

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: June 16, 2003, 11:19:02 ; Search time 6399.51 Seconds  
(without alignments)  
15794.017 Million cell updates/sec  
Title: US-09-513-888c-1\_COPY\_871\_4343  
Perfect score: 3473  
Sequence: 1 agctgcgcctggggcatct.....cgtggtgctcacgcctgca 3473

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 2054640 seqs, 14551402878 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 1000 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vl.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rtd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3473	100.0	9108	9	AF123653	Homo sapi
2	2462	70.9	173264	2	AC025853	Homo sapi
3	757	21.8	1515	9	AF123656	Homo sapi
4	757	21.8	1614	9	AF123655	Homo sapi
5	757	21.8	1692	9	AF123657	Homo sapi
6	757	21.8	1722	9	AF123658	Homo sapi
7	757	21.8	5492	9	AF123659	Homo sapi
8	214	6.2	633	9	AF123654	Homo sapi
9	39	1.1	70707	9	AC093002	Homo sapi
10	39	1.1	124882	9	AC090064	Homo sapi
11	39	1.1	185929	2	AC017085	Homo sapi
12	38	1.1	183342	9	AC087490	Homo sapi
13	38	1.1	206030	9	AC021439	Homo sapi
14	38	1.1	227884	2	AC114495	Mus muscu
15	38	1.1	263546	2	AC099416	Mus muscu
16	37	1.1	182676	2	AC104362	Homo sapi
17	35	1.0	27399	9	AL713867	Human DNA
18	35	1.0	160483	2	AC125977	Rattus no
19	35	1.0	200761	10	AC122140	Mus muscu
20	34	1.0	4005	3	G38795	C12M105 Pla
21	34	1.0	4005	3	AF030690	Plasmodiu
22	34	1.0	43593	2	AC131564	Lytechinu
23	34	1.0	66074	2	AC119882	Mus muscu
24	34	1.0	99537	2	AC111610	Rattus no
25	34	1.0	109542	2	AC131398	Rattus no
26	34	1.0	114113	2	AL160005	Homo sapi
27	34	1.0	127816	2	AC103042	Rattus no
28	34	1.0	158992	2	AC119377	Rattus no
29	34	1.0	153550	2	AL354894	Homo sapi
30	34	1.0	160483	2	AC125977	Rattus no
31	34	1.0	170799	2	AC094997	Rattus no
32	34	1.0	173523	2	AL513528	Homo sapi
33	34	1.0	178273	2	AC005308	Plasmodiu
34	34	1.0	180748	2	AC126872	Rattus no
35	34	1.0	195734	2	AC126265	Mus muscu
36	34	1.0	197171	9	CNS01DRD	Human chr
37	34	1.0	198944	8	ATCHRIV38	Arabidops
38	34	1.0	206606	8	ATFCA1	Arabidops
39	34	1.0	219726	10	AC087556	Mus muscu
40	34	1.0	222185	2	AC127697	Mus muscu
41	34	1.0	321003	2	PFMAL4P3	Plasmodiu
42	34	1.0	321003	2	PFMAL4P3	Plasmodiu
43	33	1.0	135	11	AL823652	Arabidops
44	33	1.0	11805	6	AX346651	Sequence
45	33	1.0	16596	9	AL591590	Human DNA
46	33	1.0	39969	9	HSJ645L19	Human DNA
47	33	1.0	88518	2	AL391643	Homo sapi
48	33	1.0	89944	9	AL591622	Human DNA
49	33	1.0	100785	9	AP000617	Homo sapi
50	33	1.0	101033	9	AC104090	Homo sapi
51	33	1.0	104868	8	ATF15G16	Arabidops
52	33	1.0	107135	2	AC128204	Rattus no
53	33	1.0	107328	9	AL160057	Human DNA
54	33	1.0	110000	2	PFMAL13P2_0	Plasmodiu
55	33	1.0	110000	2	PFMAL13P2_0	Plasmodiu
56	33	1.0	113333	3	AC096958	Rattus no
57	33	1.0	116696	3	PFMAL3P3	Plasmodiu
58	33	1.0	131132	9	AC103563	Homo sapi
59	33	1.0	137169	2	AC015781	Homo sapi
60	33	1.0	142001	8	ATF21F14	Arabidops
61	33	1.0	147292	2	AC023010	Homo sapi
62	33	1.0	147595	2	AC021778	Homo sapi
63	33	1.0	148689	9	AC093168	Homo sapi
64	33	1.0	149548	9	AC099066	Homo sapi
65	33	1.0	150325	2	AC018535	Homo sapi

66	33	1.0	152989	2	AC095122	AC095122 Rattus no	139	32	0.9	5908	6	AX277930	Sequence
67	33	1.0	153097	2	AC125750	AC125750 Rattus no	140	32	0.9	5908	6	AX323617	Sequence
68	33	1.0	155729	9	CNS01DWN	AL137785 Human chr	141	32	0.9	6197	6	AX344849	Sequence
69	33	1.0	157410	2	AC13816	AL137816 Homo sapi	c 142	32	0.9	6216	6	AX348318	Sequence
70	33	1.0	158041	2	AC112587	AL137816 Homo sapi	c 143	32	0.9	6216	6	AX348571	Sequence
71	33	1.0	158548	2	AC112587	AL137816 Homo sapi	c 144	32	0.9	6216	6	AX348571	Sequence
72	33	1.0	161117	2	OSJN00245	AL137816 Homo sapi	c 145	32	0.9	6769	6	AR004690	Sequence
73	33	1.0	161117	2	OSJN00245	AL137816 Homo sapi	c 146	32	0.9	6769	6	AR008176	Sequence
74	33	1.0	162884	9	AC016558	AL137816 Homo sapi	c 147	32	0.9	6769	6	AR136959	Sequence
75	33	1.0	162884	9	AC016558	AL137816 Homo sapi	c 148	32	0.9	6769	6	AR136959	Sequence
76	33	1.0	165821	2	AC020936	AC020936 Homo sapi	c 149	32	0.9	6769	6	AR136959	Sequence
77	33	1.0	167254	9	CNS05YDS	AL137816 Homo sapi	c 150	32	0.9	6769	6	AR136959	Sequence
78	33	1.0	167390	9	AC007263	AL137816 Homo sapi	c 151	32	0.9	6769	6	AR136959	Sequence
79	33	1.0	168628	2	AC119391	AL137816 Homo sapi	c 152	32	0.9	6769	6	AR136959	Sequence
80	33	1.0	169514	9	AC064869	AL137816 Homo sapi	c 153	32	0.9	6769	6	AR136959	Sequence
81	33	1.0	169794	2	AC004157	AC004157 Homo sapi	c 154	32	0.9	6769	6	AR136959	Sequence
82	33	1.0	173456	9	AL158198	AL158198 Homo sapi	c 155	32	0.9	6769	6	AR136959	Sequence
83	33	1.0	173456	9	AL158198	AL158198 Homo sapi	c 156	32	0.9	6769	6	AR136959	Sequence
84	33	1.0	173456	9	AL158198	AL158198 Homo sapi	c 157	32	0.9	6769	6	AR136959	Sequence
85	33	1.0	177250	2	AC025060	AC025060 Homo sapi	c 158	32	0.9	6769	6	AR136959	Sequence
86	33	1.0	178274	2	AC022006	AC022006 Homo sapi	c 159	32	0.9	6769	6	AR136959	Sequence
87	33	1.0	178274	2	AC022006	AC022006 Homo sapi	c 160	32	0.9	6769	6	AR136959	Sequence
88	33	1.0	180320	2	AC123135	AC123135 Rattus no	c 161	32	0.9	6769	6	AR136959	Sequence
89	33	1.0	180440	2	AC113570	AC113570 Canis fam	c 162	32	0.9	6769	6	AR136959	Sequence
90	33	1.0	181141	2	AC093621	AC093621 Homo sapi	c 163	32	0.9	6769	6	AR136959	Sequence
91	33	1.0	181503	10	AL662783	AL662783 Mouse DNA	c 164	32	0.9	6769	6	AR136959	Sequence
92	33	1.0	188717	9	CNS01DWR	AL138478 Human chr	c 165	32	0.9	6769	6	AR136959	Sequence
93	33	1.0	190830	2	AC102136	AC102136 Mus muscu	c 166	32	0.9	6769	6	AR136959	Sequence
94	33	1.0	196403	2	AL844139	AL844139 Mus muscu	c 167	32	0.9	6769	6	AR136959	Sequence
95	33	1.0	196715	2	AC094874	AC094874 Rattus no	c 168	32	0.9	6769	6	AR136959	Sequence
96	33	1.0	197171	9	CNS01DRD	AL117187 Human chr	c 169	32	0.9	6769	6	AR136959	Sequence
97	33	1.0	199551	2	AC006281	AC006281 Mus muscu	c 170	32	0.9	6769	6	AR136959	Sequence
98	33	1.0	206600	2	AC124496	AC124496 Mus muscu	c 171	32	0.9	6769	6	AR136959	Sequence
99	33	1.0	214857	10	AC122899	AC122899 Mus muscu	c 172	32	0.9	6769	6	AR136959	Sequence
100	33	1.0	224448	2	PFMAL4P4	AL035477 Plasmodiu	c 173	32	0.9	6769	6	AR136959	Sequence
101	33	1.0	232871	2	AC105826	AC105826 Rattus no	c 174	32	0.9	6769	6	AR136959	Sequence
102	33	1.0	254775	2	AC091478	AC091478 Mus muscu	c 175	32	0.9	6769	6	AR136959	Sequence
103	33	1.0	256172	2	AC005139	AC005139 Plasmodiu	c 176	32	0.9	6769	6	AR136959	Sequence
104	33	1.0	287058	2	AC095595	AC095595 Rattus no	c 177	32	0.9	6769	6	AR136959	Sequence
105	33	1.0	310779	2	AC005140	AC005140 Plasmodiu	c 178	32	0.9	6769	6	AR136959	Sequence
106	33	1.0	318221	2	PFMAL13P3	AL049184 Plasmodiu	c 179	32	0.9	6769	6	AR136959	Sequence
107	32	0.9	339247	2	AC107252	AC107252 Rattus no	c 180	32	0.9	6769	6	AR136959	Sequence
108	32	0.9	230	8	AY020871	AY020871 Rattus no	c 181	32	0.9	6769	6	AR136959	Sequence
109	32	0.9	230	8	AY020871	AY020871 Rattus no	c 182	32	0.9	6769	6	AR136959	Sequence
110	32	0.9	234	8	AY018512	AY018512 Rattus no	c 183	32	0.9	6769	6	AR136959	Sequence
111	32	0.9	236	8	AY021056	AY021056 Rattus no	c 184	32	0.9	6769	6	AR136959	Sequence
112	32	0.9	236	8	AY021062	AY021062 Rattus no	c 185	32	0.9	6769	6	AR136959	Sequence
113	32	0.9	240	8	AY021139	AY021139 Rattus no	c 186	32	0.9	6769	6	AR136959	Sequence
114	32	0.9	240	8	AY021141	AY021141 Rattus no	c 187	32	0.9	6769	6	AR136959	Sequence
115	32	0.9	242	8	AY018754	AY018754 Rattus no	c 188	32	0.9	6769	6	AR136959	Sequence
116	32	0.9	242	8	AY018755	AY018755 Rattus no	c 189	32	0.9	6769	6	AR136959	Sequence
117	32	0.9	250	8	AY021370	AY021370 Rattus no	c 190	32	0.9	6769	6	AR136959	Sequence
118	32	0.9	254	8	AY019115	AY019115 Rattus no	c 191	32	0.9	6769	6	AR136959	Sequence
119	32	0.9	254	8	AY021489	AY021489 Rattus no	c 192	32	0.9	6769	6	AR136959	Sequence
120	32	0.9	254	8	AY021506	AY021506 Rattus no	c 193	32	0.9	6769	6	AR136959	Sequence
121	32	0.9	270	8	AY019491	AY019491 Rattus no	c 194	32	0.9	6769	6	AR136959	Sequence
122	32	0.9	397	5	AF111645	AF111645 Meleagris	c 195	32	0.9	6769	6	AR136959	Sequence
123	32	0.9	838	3	LS277642	AJ277642 Litopenae	c 196	32	0.9	6769	6	AR136959	Sequence
124	32	0.9	881	6	AX477866	AX477866 Sequence	c 197	32	0.9	6769	6	AR136959	Sequence
125	32	0.9	1097	5	AF316136	AF316136 Kinostern	c 198	32	0.9	6769	6	AR136959	Sequence
126	32	0.9	1390	3	PFEXPIG	X505074 Plasmodiu	c 199	32	0.9	6769	6	AR136959	Sequence
127	32	0.9	2136	8	PVNPV30G	Z30347 P.vulgaris	c 200	32	0.9	6769	6	AR136959	Sequence
128	32	0.9	2215	3	S39048	Z30347 P.vulgaris	c 201	32	0.9	6769	6	AR136959	Sequence
129	32	0.9	3787	3	PVAL133526	AJ133526 Penaeus v	c 202	32	0.9	6769	6	AR136959	Sequence
130	32	0.9	3952	6	AX251040	AX251040 Sequence	c 203	32	0.9	6769	6	AR136959	Sequence
131	32	0.9	3952	6	AX344177	AX344177 Sequence	c 204	32	0.9	6769	6	AR136959	Sequence
132	32	0.9	3952	6	AX348944	AX348944 Sequence	c 205	32	0.9	6769	6	AR136959	Sequence
133	32	0.9	4611	3	PFA132006	AJ132006 Plasmodiu	c 206	32	0.9	6769	6	AR136959	Sequence
134	32	0.9	5218	6	AX346169	AX346169 Sequence	c 207	32	0.9	6769	6	AR136959	Sequence
135	32	0.9	5560	3	PFA132422	AJ132422 Plasmodiu	c 208	32	0.9	6769	6	AR136959	Sequence
136	32	0.9	5574	10	RNPJCF91	X57081-R.norvegicu	c 209	32	0.9	6769	6	AR136959	Sequence
137	32	0.9	5574	10	RNPJCF91	X57081-R.norvegicu	c 210	32	0.9	6769	6	AR136959	Sequence
138	32	0.9	5908	6	AX251914	AX251914 Sequence	c 211	32	0.9	6769	6	AR136959	Sequence



c 212	32	0.9 108908	3	PFMA13P8	AL034560 Plasmodium	c 285	32	0.9 154176	2	AC118829	AC118829 Rattus no
c 213	32	0.9 108979	9	AC090041	AC090041 Homo sapi	c 286	32	0.9 154364	9	AC091893	AC091893 Homo sapi
c 214	32	0.9 109200	2	AC099349	AC099349 Rattus no	c 287	32	0.9 154690	2	AC007208	AC007208 Drosophil
c 215	32	0.9 109465	9	AL158821	AL158821 Human DNA	c 288	32	0.9 155151	9	AL137143	AL137143 Human DNA
c 216	32	0.9 110000	2	AC113004_1	Continuation (2 of	c 289	32	0.9 155220	2	AC122947	AC122947 Rattus no
c 217	32	0.9 110000	2	PFMA14P1_1	Continuation (2 of	c 290	32	0.9 155560	2	AC119601	AC119601 Rattus no
c 218	32	0.9 110000	2	TBBCHRIA_06	Continuation (7 of	c 291	32	0.9 155580	9	AC024597	AC024597 Homo sapi
c 219	32	0.9 110985	8	AP004578	AP004578 Lotus jap	c 292	32	0.9 155580	9	AC024597	AC024597 Homo sapi
c 220	32	0.9 111104	9	AC117389	AC117389 Homo sapi	c 293	32	0.9 155580	9	AC024946	AC024946 Homo sapi
c 221	32	0.9 111892	2	AC128602	AC128602 Rattus no	c 294	32	0.9 155580	9	AC024946	AC024946 Homo sapi
c 222	32	0.9 113031	9	AL445672	AL445672 Human DNA	c 295	32	0.9 155592	2	AC118866	AC118866 Rattus no
c 223	32	0.9 115109	9	AC107216	AC107216 Homo sapi	c 296	32	0.9 155676	2	AC044780	AC044780 Homo sapi
c 224	32	0.9 115928	9	AC037475	AC037475 Homo sapi	c 297	32	0.9 155676	2	AC044780	AC044780 Homo sapi
c 225	32	0.9 116541	2	AC097016	AC097016 Rattus no	c 298	32	0.9 156060	2	AC004153	AC004153 Plasmodium
c 226	32	0.9 116596	3	PFMA13P3	Z98547 Plasmodium	c 299	32	0.9 156357	9	AC011456	AC011456 Homo sapi
c 227	32	0.9 117453	3	AE003670	AE003670 Drosophil	c 300	32	0.9 156874	2	AC098039	AC098039 Rattus no
c 228	32	0.9 118131	9	AC074132	AC074132 Homo sapi	c 301	32	0.9 156947	9	AL359435	AL359435 Human DNA
c 229	32	0.9 119385	5	AL645782	AL645782 Zebrafish	c 302	32	0.9 158174	8	AP003414	AP003414 Oryza sat
c 230	32	0.9 120846	9	AL365232	AL365232 Human DNA	c 303	32	0.9 158293	9	AC004746	AC004746 Homo sapi
c 231	32	0.9 121621	2	AC131559	AC131559 Rattus no	c 304	32	0.9 159176	2	AC098283	AC098283 Rattus no
c 232	32	0.9 121822	9	AC118456	AC118456 Homo sapi	c 305	32	0.9 159338	9	AC016761	AC016761 Homo sapi
c 233	32	0.9 121941	5	AL596022	AL596022 Zebrafish	c 306	32	0.9 159722	9	AC011293	AC011293 Homo sapi
c 234	32	0.9 125411	8	ATF8L15	AL392174 Arabidops	c 307	32	0.9 159761	8	AP003921	AP003921 Oryza sat
c 235	32	0.9 125497	2	AC128455	AC128455 Rattus no	c 308	32	0.9 160678	2	AC097200	AC097200 Rattus no
c 236	32	0.9 127007	10	AL627432	AL627432 Mouse DNA	c 309	32	0.9 160693	9	AC124043	AC124043 Homo sapi
c 237	32	0.9 127295	2	AL772298	AL772298 Danio rer	c 310	32	0.9 161125	2	AC128771	AC128771 Rattus no
c 238	32	0.9 127714	9	AL590677	AL590677 Human DNA	c 311	32	0.9 161896	2	AC113862	AC113862 Rattus no
c 239	32	0.9 127816	2	AC103042	AC103042 Rattus no	c 312	32	0.9 161911	2	AC021497	AC021497 Homo sapi
c 240	32	0.9 127982	2	AC104473	AC104473 Oryza sat	c 313	32	0.9 161951	2	CNS07YPU	AL713951 Oryza sat
c 241	32	0.9 128071	2	AC094497	AC094497 Rattus no	c 314	32	0.9 162025	6	AX112387	AX112387 Sequence
c 242	32	0.9 128411	5	AC07365	AC107365 Danio rer	c 315	32	0.9 162025	6	AX112388	AX112388 Sequence
c 243	32	0.9 128918	2	AL358945	AL358945 Homo sapi	c 316	32	0.9 162025	6	AX360260	AX360260 Sequence
c 244	32	0.9 131098	9	AC010607	AC010607 Homo sapi	c 317	32	0.9 162025	6	AX360261	AX360261 Sequence
c 245	32	0.9 131811	9	AC068305	AC068305 Homo sapi	c 318	32	0.9 162025	6	AX360264	AX360264 Sequence
c 246	32	0.9 132224	2	AC102898	AC102898 Mus muscu	c 319	32	0.9 162025	6	AX360265	AX360265 Sequence
c 247	32	0.9 132688	8	AC099733	AC099733 Oryza sat	c 320	32	0.9 162025	9	AC005730	AC005730 Homo sapi
c 248	32	0.9 134687	9	AL445259	AL445259 Human DNA	c 321	32	0.9 162101	8	AC027661	AC027661 Oryza sat
c 249	32	0.9 134743	9	HUAC002300	AC002300 Homo sapi	c 322	32	0.9 163115	3	AC010661	AC010661 Drosophil
c 250	32	0.9 135398	2	AC130452	AC130452 Homo sapi	c 323	32	0.9 163188	2	AC126074	AC126074 Rattus no
c 251	32	0.9 135760	2	AC118530	AC118530 Rattus no	c 324	32	0.9 163229	2	AP004651	AP004651 Oryza sat
c 252	32	0.9 136448	2	AC012231	AC012231 Homo sapi	c 325	32	0.9 163384	9	AC009180	AC009180 Homo sapi
c 253	32	0.9 136805	2	AC117958	AC117958 Rattus no	c 326	32	0.9 163387	2	AC130912	AC130912 Rattus no
c 254	32	0.9 137568	8	AC093178	AC093178 Oryza sat	c 327	32	0.9 163466	2	AC106980	AC106980 Rattus no
c 255	32	0.9 138003	2	AC018346	AC018346 Homo sapi	c 328	32	0.9 164991	9	AC092023	AC092023 Homo sapi
c 256	32	0.9 138020	9	AC108043	AC108043 Homo sapi	c 329	32	0.9 165062	2	AC098324	AC098324 Rattus no
c 257	32	0.9 138947	2	AC131011	AC131011 Homo sapi	c 330	32	0.9 165618	9	AL442636	AL442636 Human DNA
c 258	32	0.9 141430	8	AC069329	AC069329 Genomic S	c 331	32	0.9 166277	2	AC109794	AC109794 Bos tauru
c 259	32	0.9 141529	2	AC025330	AC025330 Homo sapi	c 332	32	0.9 167072	2	AC060780	AC060780 Homo sapi
c 260	32	0.9 141534	2	AP003685	AP003685 Oryza sat	c 333	32	0.9 167114	2	AP004685	AP004685 Oryza sat
c 261	32	0.9 141825	9	AL355358	AL355358 Human DNA	c 334	32	0.9 167503	2	AC129344	AC129344 Homo sapi
c 262	32	0.9 141927	2	AL645926	AL645926 Danio rer	c 335	32	0.9 167968	2	AC109799	AC109799 Bos tauru
c 263	32	0.9 141927	2	AL645926	AL645926 Danio rer	c 336	32	0.9 168080	2	AC073172	AC073172 Homo sapi
c 264	32	0.9 142429	2	AC011262	AC011262 Homo sapi	c 337	32	0.9 168310	2	AC010775	AC010775 Homo sapi
c 265	32	0.9 144249	2	AC011262	AC011262 Homo sapi	c 338	32	0.9 169845	2	AP004784	AP004784 Oryza sat
c 266	32	0.9 144713	9	AC128020	AC128020 Rattus no	c 339	32	0.9 169879	2	AC073144	AC073144 Homo sapi
c 267	32	0.9 144859	9	AC104997	AC104997 Homo sapi	c 340	32	0.9 170026	2	AC013627	AC013627 Homo sapi
c 268	32	0.9 146403	2	AC027067	AC027067 Homo sapi	c 341	32	0.9 170227	9	AC093816	AC093816 Homo sapi
c 269	32	0.9 148271	9	AL392046	AL392046 Human DNA	c 342	32	0.9 170466	2	AC129242	AC129242 Rattus no
c 270	32	0.9 149255	9	AC009262	AC009262 Homo sapi	c 343	32	0.9 171162	2	AC096402	AC096402 Rattus no
c 271	32	0.9 149291	10	AC116328	AC116328 Mus muscu	c 344	32	0.9 171426	2	AC079183	AC079183 Mus muscu
c 272	32	0.9 149548	9	AC099066	AC099066 Homo sapi	c 345	32	0.9 171462	2	AC117832	AC117832 Homo sapi
c 273	32	0.9 149704	9	AL138955	AL138955 Human DNA	c 346	32	0.9 171954	2	AC040957	AC040957 Homo sapi
c 274	32	0.9 150162	9	AC026722	AC026722 Homo sapi	c 347	32	0.9 172784	9	AC024918	AC024918 Homo sapi
c 275	32	0.9 150328	2	AP004460	AP004460 Oryza sat	c 348	32	0.9 172800	2	AL356597	AL356597 Homo sapi
c 276	32	0.9 150573	9	AC097473	AC097473 Homo sapi	c 349	32	0.9 173053	2	AC118097	AC118097 Rattus no
c 277	32	0.9 151191	2	AC117952	AC117952 Rattus no	c 350	32	0.9 173404	2	AC096147	AC096147 Rattus no
c 278	32	0.9 151367	9	AC025750	AC025750 Homo sapi	c 351	32	0.9 173434	2	AL365496	AL365496 Human DNA
c 279	32	0.9 151533	8	AC090873	AC090873 Oryza sat	c 352	32	0.9 173728	9	AL365496	AL365496 Human DNA
c 280	32	0.9 151696	9	AF240629	AF240629 Homo sapi	c 353	32	0.9 174711	2	AC104512	AC104512 Drosophil
c 281	32	0.9 152354	2	AC120598	AC120598 Homo sapi	c 354	32	0.9 174874	10	AC123054	AC123054 Mus muscu
c 282	32	0.9 152631	9	AC117432	AC117432 Homo sapi	c 355	32	0.9 175111	2	AC101999	AC101999 Mus muscu
c 283	32	0.9 152794	9	AL139376	AL139376 Human DNA	c 356	32	0.9 175179	2	AC095321	AC095321 Rattus no
c 284	32	0.9 153339	9	AC007350	AC007350 Homo sapi	c 357	32	0.9 176019	2	AC124492	AC124492 Mus muscu

358	32	0.9	176106	2	AC096415	AC096415 Rattus no	431	32	0.9	206030	9	AC021439	Homo sapi
359	32	0.9	176388	2	AC025273	AC025273 Homo sapi	432	32	0.9	206590	9	AC026951	Homo sapi
360	32	0.9	176409	2	AC097955	AC097955 Rattus no	c 433	32	0.9	206633	32	AC0109275	Mus muscu
361	32	0.9	176437	2	AC110463	AC110463 Rattus no	c 434	32	0.9	206915	10	AL663081	Mouse DNA
362	32	0.9	177034	9	AP002840	AP002840 Homo sapi	435	32	0.9	207804	2	AC011714	Homo sapi
363	32	0.9	177089	9	AC008277	AC008277 Homo sapi	436	32	0.9	208083	2	AC009649	Homo sapi
364	32	0.9	178091	2	AC126702	AC126702 Rattus no	437	32	0.9	208657	2	AC046179	Homo sapi
365	32	0.9	178273	2	AC005308	AC005308 Plasmodiu	438	32	0.9	209636	2	AL732412	Mus muscu
366	32	0.9	178384	2	AL591026	AL591026 Homo sapi	439	32	0.9	210620	2	AC094500	Rattus no
367	32	0.9	178482	2	AC119832	AC119832 Mus muscu	440	32	0.9	210636	9	AC006443	Homo sapi
368	32	0.9	178764	2	AC126507	AC126507 Rattus no	441	32	0.9	211046	2	AC115784	Mus muscu
369	32	0.9	179332	2	AC068754	AC068754 Homo sapi	442	32	0.9	211607	2	AC094844	Rattus no
370	32	0.9	179429	2	AC114933	AC114933 Homo sapi	443	32	0.9	212479	2	AC125200	Mus muscu
371	32	0.9	179685	2	AC110477	AC110477 Rattus no	444	32	0.9	212827	9	AC009412	Homo sapi
372	32	0.9	179757	9	AC006960	AC006960 Homo sapi	445	32	0.9	213743	2	AL359918	Homo sapi
373	32	0.9	179788	2	AC096900	AC096900 Rattus no	c 446	32	0.9	215516	2	AC024694	Mus muscu
374	32	0.9	179788	2	AC096900	AC096900 Rattus no	447	32	0.9	216599	2	AC087379	Homo sapi
375	32	0.9	179899	2	AL645822	AL645822 Danio rer	448	32	0.9	216800	10	AL589744	Mouse DNA
376	32	0.9	180159	2	AC110652	AC110652 Rattus no	c 449	32	0.9	216800	10	AL589744	Mouse DNA
377	32	0.9	180277	2	AC104270	AC104270 Oryza sat	450	32	0.9	217263	2	AC108831	Mus muscu
378	32	0.9	180278	9	AC092343	AC092343 Homo sapi	451	32	0.9	217454	2	AL592070	Mus muscu
379	32	0.9	180320	2	AC123135	AC123135 Rattus no	c 452	32	0.9	218900	2	AC122502	Mus muscu
380	32	0.9	180440	2	AC113570	AC113570 Canis fam	453	32	0.9	219912	2	AC020855	Mus muscu
381	32	0.9	180583	9	CNS01DW8	AL136501 Human chr	454	32	0.9	220035	2	AC122047	Mus muscu
382	32	0.9	180603	2	AC110400	AC110400 Rattus no	c 455	32	0.9	220936	2	AC113162	Rattus no
383	32	0.9	181168	2	AC103469	AC103469 Rattus no	456	32	0.9	221250	2	AC122337	Mus muscu
384	32	0.9	182223	3	AC023674	AC023674 Drosophil	457	32	0.9	222512	2	AC124497	Mus muscu
385	32	0.9	182278	30	AC067824	AC067824 Homo sapi	458	32	0.9	225481	2	AC122393	Mus muscu
386	32	0.9	183105	3	AC104606	AC104606 Drosophil	459	32	0.9	225569	2	AC097963	Rattus no
387	32	0.9	183228	2	AC097076	AC097076 Rattus no	460	32	0.9	225611	2	AC129605	Mus muscu
388	32	0.9	183273	9	AC093898	AC093898 Homo sapi	c 461	32	0.9	227184	2	AC009868	Homo sapi
389	32	0.9	183342	9	AC087490	AC087490 Homo sapi	462	32	0.9	228094	2	AC124736	Mus muscu
390	32	0.9	184178	2	AC126586	AC126586 Rattus no	463	32	0.9	228404	2	AC095672	Rattus no
391	32	0.9	184677	2	AL831760	AL831760 Mus muscu	464	32	0.9	231618	2	AC124356	Mus muscu
392	32	0.9	184894	2	AC102582	AC102582 Mus muscu	c 465	32	0.9	231618	2	AC124356	Mus muscu
393	32	0.9	184909	2	AL844863	AL844863 Mus muscu	c 466	32	0.9	231938	2	AC079025	Mus muscu
394	32	0.9	185116	9	AC005823	AC005823 Homo sapi	c 467	32	0.9	233117	2	AL844512	Danio rer
395	32	0.9	185155	2	AL807760	AL807760 Mus muscu	468	32	0.9	236121	2	AC126796	Mus muscu
396	32	0.9	185596	2	AC127921	AC127921 Rattus no	469	32	0.9	238554	2	AC020965	Mus muscu
397	32	0.9	185596	2	AC127921	AC127921 Rattus no	470	32	0.9	240438	2	AC125142	Mus muscu
398	32	0.9	185711	2	AC107087	AC107087 Rattus no	471	32	0.9	242835	2	AC079243	Mus muscu
399	32	0.9	185857	2	AC129281	AC129281 Rattus no	472	32	0.9	242913	2	AC129210	Mus muscu
400	32	0.9	186457	9	AC068359	AC068359 Homo sapi	473	32	0.9	243915	2	AC115291	Mus muscu
401	32	0.9	187088	2	AC101852	AC101852 Mus muscu	c 474	32	0.9	249088	2	AL831726	Danio rer
402	32	0.9	187142	2	AC018598	AC018598 Homo sapi	c 475	32	0.9	253576	2	AC103320	Rattus no
403	32	0.9	187473	2	AC122043	AC122043 Mus muscu	476	32	0.9	271134	2	AC124402	Mus muscu
404	32	0.9	187837	2	AC130991	AC130991 Rattus no	c 477	32	0.9	276831	2	AC126690	Mus muscu
405	32	0.9	188357	9	AL159996	AL159996 Human DNA	478	32	0.9	285272	3	AE003441	Drosophil
406	32	0.9	193281	2	AC012458	AC012458 Homo sapi	c 479	32	0.9	293431	2	PFMAL13P4	Plasmodiu
407	32	0.9	189979	2	AC118037	AC118037 Mus muscu	c 480	32	0.9	310779	2	AC005140	Plasmodiu
408	32	0.9	189994	2	AC113784	AC113784 Rattus no	481	32	0.9	318221	2	PFMAL13P3	Plasmodiu
409	32	0.9	190624	2	AC026892	AC026892 Homo sapi	482	32	0.9	333530	2	AC087242	Homo sapi
410	32	0.9	190734	2	AC120283	AC120283 Rattus no	483	32	0.9	340000	9	AP001679	Homo sapi
411	32	0.9	190937	9	AP000957	AP000957 Homo sapi	c 484	32	0.9	340000	9	HS21C002	Homo sapi
412	32	0.9	191267	2	AC129189	AC129189 Mus muscu	c 485	31	0.9	150	11	G38001	G38001 C1M39 Plasm
413	32	0.9	191420	2	AL672221	AL672221 Mus muscu	486	31	0.9	194	11	G42718	G42718 C3M86 Plasm
414	32	0.9	192518	2	HSBA539A6	AL121876 Homo sapi	c 487	31	0.9	226	8	AY018186	Oryza sat
415	32	0.9	193214	2	AC129424	AC129424 Rattus no	c 488	31	0.9	1090	5	AF316124	Kinostern
416	32	0.9	193503	2	CNS08C94	AL732381 Oryza sat	c 489	31	0.9	1094	5	AF316125	Kinostern
417	32	0.9	194076	2	AC131241	AC131241 Mus muscu	490	31	0.9	3148	3	AF323928	Plasmodiu
418	32	0.9	194612	9	AL357354	AL357354 Human DNA	491	31	0.9	4012	3	PFACAM	M59770 P.falciparu
419	32	0.9	195434	9	AC090744	AC090744 Homo sapi	492	31	0.9	4060	5	XLNRI	X34081 X.laevis mr
420	32	0.9	195434	9	AC090744	AC090744 Homo sapi	493	31	0.9	4060	5	XLNRI	X34081 X.laevis mr
421	32	0.9	196628	2	AL772388	AL772388 Danio rer	494	31	0.9	12029	3	AE001395	Plasmodiu
422	32	0.9	196877	8	AC063947	AC063947 Homo sapi	c 495	31	0.9	12029	3	AE001395	Plasmodiu
423	32	0.9	197975	8	ATCHRIV2	AL161472 Arabidops	c 496	31	0.9	15861	3	AE001413	Plasmodiu
424	32	0.9	199551	2	AC006281	AC006281 Plasmodiu	497	31	0.9	15903	2	AC115612	Dictyoste
425	32	0.9	199609	9	AC009432	AC009432 Homo sapi	c 498	31	0.9	29246	8	AP004947	Lotus jap
426	32	0.9	199639	2	AL805905	AL805905 Danio rer	499	31	0.9	41112	9	AL590323	Human DNA
427	32	0.9	200501	10	AL596086	AL596086 Mouse DNA	c 500	31	0.9	44704	9	AL672167	Human DNA
428	32	0.9	203291	2	AC117602	AC117602 Mus muscu	501	31	0.9	47519	2	AC110100	Rattus no
429	32	0.9	204185	2	AL844521	AL844521 Danio rer	502	31	0.9	61273	2	AC120141	Mus muscu
430	32	0.9	204782	2	AC011168	AC011168 Homo sapi	503	31	0.9	62263	2	AC100239	Mus muscu

504	31	0.9	63239	2	AC094243	AC094243 Rattus no	577	31	0.9	164867	9	AC103864	AC103864 Homo sapi
c 505	31	0.9	67331	2	AC067920	Homo sapi	c 578	31	0.9	166219	9	AC003084	AC003084 Human BAC
c 506	31	0.9	68105	9	HS974711	AL050339 Homo DNA	c 579	31	0.9	166796	9	AC126437	AC126437 Mus muscu
c 507	31	0.9	71990	2	AC116160	Homo sapi	c 580	31	0.9	167564	2	AP267170	Homo sapi
c 508	31	0.9	73260	5	AL606809	AL606809 Zebrafish	c 581	31	0.9	168056	2	AC099254	Rattus no
c 509	31	0.9	74562	2	HS22502	Z95124 Human DNA s	c 582	31	0.9	168223	2	AC019020	Homo sapi
c 510	31	0.9	76985	2	AC112544	AC112544 Rattus no	c 583	31	0.9	168672	2	AC027102	Homo sapi
c 511	31	0.9	77953	9	AC108031	AC108031 Homo sapi	c 584	31	0.9	169401	2	AC069056	Homo sapi
c 512	31	0.9	80578	2	PFMAL13P9	AL096783 Plasmodiu	c 585	31	0.9	169514	9	AC064869	Homo sapi
c 513	31	0.9	80518	2	PFMAL13PA	AL109815 Plasmodiu	c 586	31	0.9	169536	9	AC016496	Homo sapi
c 514	31	0.9	84730	2	AC074054	AC074054 Oryza sat	c 587	31	0.9	170588	9	CNS01RHF	Human chr
c 515	31	0.9	84838	2	AC111501	AC111501 Rattus no	c 588	31	0.9	170608	2	AC096172	Rattus no
c 516	31	0.9	86384	9	AC116172	AC116172 Homo sapi	c 589	31	0.9	170731	2	AC111988	Rattus no
c 517	31	0.9	88818	2	AC097812	AC097812 Rattus no	c 590	31	0.9	170965	9	AB017654	Homo sapi
c 518	31	0.9	92985	9	AL157378	AL157378 Human DNA	c 591	31	0.9	170996	2	AL592432	Homo sapi
c 519	31	0.9	93173	2	AC094918	AC094918 Rattus no	c 592	31	0.9	171623	2	AC107829	Homo sapi
c 520	31	0.9	94384	9	AC011718	AC011718 Homo sapi	c 593	31	0.9	171781	2	AC027510	Mus muscu
c 521	31	0.9	95727	2	AC068387	AC068387 Homo sapi	c 594	31	0.9	172402	2	AC027510	Homo sapi
c 522	31	0.9	95845	8	AF411807	AF411807 Lycopersi	c 595	31	0.9	172405	9	AC053523	Homo sapi
c 523	31	0.9	97759	2	AC097789	AC097789 Rattus no	c 596	31	0.9	173349	9	AC010600	Homo sapi
c 524	31	0.9	100132	9	AC114813	AC114813 Homo sapi	c 597	31	0.9	173450	2	AC127901	Homo sapi
c 525	31	0.9	100785	9	AP000617	AP000617 Homo sapi	c 598	31	0.9	173639	10	AL606921	Mouse DNA
c 526	31	0.9	103097	9	AL445464	AL445464 Human DNA	c 599	31	0.9	174151	2	AC011182	Homo sapi
c 527	31	0.9	103836	9	AC079791	AC079791 Homo sapi	c 600	31	0.9	174765	2	AC073103	Homo sapi
c 528	31	0.9	106642	9	AL662781	AL662781 Homo sapi	c 601	31	0.9	175645	9	AC073114	Homo sapi
c 529	31	0.9	109465	9	AL158821	AL158821 Human DNA	c 602	31	0.9	175647	2	AC110565	Mus muscu
c 530	31	0.9	110000	2	AC092450	Continuation (4 of	c 603	31	0.9	176784	2	AC099347	Rattus no
c 531	31	0.9	110000	2	PFMAL13P2_1	Continuation (2 of	c 604	31	0.9	176979	8	AP001168	Oryza sat
c 532	31	0.9	110098	9	AL358976	AL358976 Human DNA	c 605	31	0.9	177034	9	AP002840	Homo sapi
c 533	31	0.9	113596	2	AC026438	AC026438 Homo sapi	c 606	31	0.9	177670	2	AC101716	Mus muscu
c 534	31	0.9	114467	9	AP000462	AP000462 Homo sapi	c 607	31	0.9	178534	2	AC027203	Homo sapi
c 535	31	0.9	114965	9	AC108306	AC108306 Rattus no	c 608	31	0.9	178976	2	AC114702	Rattus no
c 536	31	0.9	117296	2	AC092865	AC092865 Homo sapi	c 609	31	0.9	180650	9	AC109474	Homo sapi
c 537	31	0.9	120138	2	AC024624	AC024624 Mus muscu	c 610	31	0.9	180708	9	AL590725	Human DNA
c 538	31	0.9	120450	9	AC093393	AC093393 Homo sapi	c 611	31	0.9	181265	2	AC105526	Rattus no
c 539	31	0.9	128802	2	AC123139	AC123139 Rattus no	c 612	31	0.9	181492	2	AC099587	Mus muscu
c 540	31	0.9	129422	9	AL589677	AL589677 Human DNA	c 613	31	0.9	181614	2	AC115744	Mus muscu
c 541	31	0.9	131296	9	AC105104	AC105104 Homo sapi	c 614	31	0.9	181774	2	AL844152	Danio rer
c 542	31	0.9	133651	9	AC092791	AC092791 Homo sapi	c 615	31	0.9	181829	9	AC023425	Homo sapi
c 543	31	0.9	135932	8	AC079736	AC079736 Oryza sat	c 616	31	0.9	182529	2	AC064832	Homo sapi
c 544	31	0.9	136687	9	AL662857	AL662857 Human DNA	c 617	31	0.9	183178	2	AC121981	Mus muscu
c 545	31	0.9	137463	2	AC107474	AC107474 Rattus no	c 618	31	0.9	183291	2	AC106101	Rattus no
c 546	31	0.9	140044	8	AC084406	AC084406 Oryza sat	c 619	31	0.9	184671	2	AC112648	Homo sapi
c 547	31	0.9	140363	10	AC104097	AC104097 Mus muscu	c 620	31	0.9	187045	2	AC073253	Homo sapi
c 548	31	0.9	141386	2	AC119454	AC119454 Rattus no	c 621	31	0.9	188068	2	AC109085	Rattus no
c 549	31	0.9	143614	2	AC025147	AC025147 Homo sapi	c 622	31	0.9	188212	2	AC111688	Rattus no
c 550	31	0.9	143717	2	AC083933	AC083933 Homo sapi	c 623	31	0.9	188392	2	AC095573	Rattus no
c 551	31	0.9	145220	2	AC095447	AC095447 Rattus no	c 624	31	0.9	188636	9	HUAC002287	Homo sapi
c 552	31	0.9	145510	8	AC074355	AC074355 Oryza sat	c 625	31	0.9	188807	2	AC036199	Homo sapi
c 553	31	0.9	145625	2	AC131010	AC131010 Homo sapi	c 626	31	0.9	188876	2	AC019852	Mus muscu
c 554	31	0.9	146403	2	AC027067	AC027067 Homo sapi	c 627	31	0.9	189015	2	AC090560	Homo sapi
c 555	31	0.9	150669	2	AC112836	AC112836 Rattus no	c 628	31	0.9	189486	9	AC008733	Homo sapi
c 556	31	0.9	151311	2	AP004885	AP004885 Oryza sat	c 629	31	0.9	189829	2	AC094664	Rattus no
c 557	31	0.9	151675	9	AP000470	AP000470 Homo sapi	c 630	31	0.9	190549	10	AL591512	Mouse DNA
c 558	31	0.9	151720	2	AC122663	AC122663 Rattus no	c 631	31	0.9	191136	2	AC098997	Rattus no
c 559	31	0.9	151878	9	AC093820	AC093820 Homo sapi	c 632	31	0.9	191265	2	AC130450	Homo sapi
c 560	31	0.9	152409	2	PFMAL1P1	AL031744 Plasmodiu	c 633	31	0.9	191434	9	AC087477	Homo sapi
c 561	31	0.9	153472	9	AB020868	AB020868 Homo sapi	c 634	31	0.9	191967	2	AC021962	Rattus no
c 562	31	0.9	154984	9	AC019246	AC019246 Homo sapi	c 635	31	0.9	192581	2	PFMAL13P1	Plasmodiu
c 563	31	0.9	155220	2	AC122947	AC122947 Rattus no	c 636	31	0.9	192929	2	AC005505	Plasmodiu
c 564	31	0.9	156060	2	AC004153	AC004153 Plasmodiu	c 637	31	0.9	193157	2	AC073853	Homo sapi
c 565	31	0.9	156422	2	AP016102	AP016102 Homo sapi	c 638	31	0.9	193916	2	AC123184	Rattus no
c 566	31	0.9	157756	2	AP001075	AP001075 Homo sapi	c 639	31	0.9	194076	2	AC131241	Mus muscu
c 567	31	0.9	158700	9	AC097633	AC097633 Homo sapi	c 640	31	0.9	194181	2	AC018886	Homo sapi
c 568	31	0.9	159349	2	AC027643	AC027643 Homo sapi	c 641	31	0.9	196431	2	CNS01DUS	Plasmodiu
c 569	31	0.9	160242	9	AP002778	AP002778 Homo sapi	c 642	31	0.9	198055	2	AC021333	Homo sapi
c 570	31	0.9	160253	2	AC021157	AC021157 Homo sapi	c 643	31	0.9	198130	2	AC122464	Mus muscu
c 571	31	0.9	161678	2	AC009337	AC009337 Rattus no	c 644	31	0.9	198821	2	AC123036	Homo sapi
c 572	31	0.9	162475	2	AC126737	AC126737 Rattus no	c 645	31	0.9	199434	10	AL669956	Mouse DNA
c 573	31	0.9	162743	2	CNS08CAI	AL831805 Oryza sat	c 646	31	0.9	199639	2	AL805905	Danio rer
c 574	31	0.9	163122	2	AC117930	AC117930 Papilio cyn	c 647	31	0.9	200761	10	AC122140	Mus muscu
c 575	31	0.9	163309	9	AC005434	AC005434 Homo sapi	c 648	31	0.9	200806	2	AC127265	Mus muscu
c 576	31	0.9	164216	9	AC093578	AC093578 Homo sapi	c 649	31	0.9	201106	2	AC110375	Mus muscu

C 650	31	0.9	201838	2	AC124508	AC124508 Mus muscu	C 723	30	0.9	99186	2	AL732580	Danio rer
C 651	31	0.9	203470	2	AC118155	AC118155 Rattus no	C 724	30	0.9	100000	9	AP000150	Homo sapi
C 652	31	0.9	204652	2	PFMAL13P6	AL049183 Plasmodiu	C 725	30	0.9	100871	5	AL591170	Zebrafish
C 653	31	0.9	204652	2	PFMAL13P6	AL049183 Plasmodiu	C 726	30	0.9	101965	2	AC097915	Rattus no
C 654	31	0.9	209508	2	AC111912	AL11912 Rattus no	C 727	30	0.9	102579	9	AC002375	Homo sapi
C 655	31	0.9	209507	2	AC111954	AC111954 Mus muscu	C 728	30	0.9	103566	9	AC003087	Homo sapi
C 656	31	0.9	212827	9	AC009412	AC009412 Homo sapi	C 729	30	0.9	104992	2	AC005504	Plasmodiu
C 657	31	0.9	213070	10	AL691427	AL691427 Mouse DNA	C 730	30	0.9	106360	2	CNS08C96	Continuation (4 of
C 658	31	0.9	213991	2	AC119579	AC119579 Rattus no	C 731	30	0.9	110000	2	AC125124_3	Continuation (4 of
C 659	31	0.9	217263	2	AC108831	AC108831 Mus muscu	C 732	30	0.9	110000	2	AC125124_3	Continuation (4 of
C 660	31	0.9	217374	2	AC106531	AC106531 Rattus no	C 733	30	0.9	110000	2	AL357131	Homo sapi
C 661	31	0.9	219346	10	AC098740	AC098740 Mus muscu	C 734	30	0.9	110000	2	PFMAL4P1_0	PFMAL4P1_0
C 662	31	0.9	219346	10	AC098740	AC098740 Mus muscu	C 735	30	0.9	110174	9	D83253	Homo sapien
C 663	31	0.9	219582	10	AL625764	AL625764 Mouse DNA	C 736	30	0.9	113880	3	PFMAL13P4	PFMAL13P4
C 664	31	0.9	225481	2	AC122393	AC122393 Mus muscu	C 737	30	0.9	114226	2	AC004710	Plasmodiu
C 665	31	0.9	227234	2	AC091445	AC091445 Rattus no	C 738	30	0.9	114226	2	AC004710	Plasmodiu
C 666	31	0.9	228094	2	AC124736	AC124736 Mus muscu	C 739	30	0.9	114809	2	AC083823	Homo sapi
C 667	31	0.9	229420	2	AL772373	AL772373 Danio rer	C 740	30	0.9	115565	2	OSIG000046	OSIG000046
C 668	31	0.9	231772	2	AC125217	AC125217 Mus muscu	C 741	30	0.9	116147	2	AC097254	Rattus no
C 669	31	0.9	234112	2	PFMAL4P2	AL035475 Plasmodiu	C 742	30	0.9	116788	9	AC007247	Homo sapi
C 670	31	0.9	239890	2	AL591542	AL591542 Mus muscu	C 743	30	0.9	116969	9	AL450423	Human DNA
C 671	31	0.9	253305	3	PFMAL13P7	AL034559 Plasmodiu	C 744	30	0.9	120450	9	AC093393	Homo sapi
C 672	31	0.9	293431	3	PFMAL13P4	AL049181 Plasmodiu	C 745	30	0.9	122032	9	AL513187	Human DNA
C 673	31	0.9	340000	9	AP001689	AP001689 Homo sapi	C 746	30	0.9	122969	2	AC098862	Homo sapi
C 674	31	0.9	347342	2	AL831721	AL831721 Danio rer	C 747	30	0.9	123204	10	AL672005	AL672005
C 675	30	0.9	226	8	AY020725	AY020725 Oryza sat	C 748	30	0.9	123233	2	AC084100	Homo sapi
C 676	30	0.9	400	11	GI6297	GI6297 human SFS S	C 749	30	0.9	124010	9	HS340G1	HS340G1
C 677	30	0.9	694	4	BTMSAT16	X71509 B.taurus mi	C 750	30	0.9	126736	2	AC044788	AC044788
C 678	30	0.9	2085	3	PFTHIORED	X87095 P.falciparu	C 751	30	0.9	128500	9	AC069426	Homo sapi
C 679	30	0.9	6012	6	AX344487	AX344487 Sequence	C 752	30	0.9	129517	2	AC016400	Homo sapi
C 680	30	0.9	6012	6	AX348896	AX348896 Sequence	C 753	30	0.9	131004	2	AC084184	Homo sapi
C 681	30	0.9	6552	6	AX251432	AX251432 Sequence	C 754	30	0.9	134856	2	AC098220	Rattus no
C 682	30	0.9	8451	6	AX339147	AX339147 Sequence	C 755	30	0.9	135378	9	AL390060	Human DNA
C 683	30	0.9	8451	6	AX345561	AX345561 Sequence	C 756	30	0.9	135736	9	AL391645	Human DNA
C 684	30	0.9	8451	6	AX348369	AX348369 Sequence	C 757	30	0.9	138176	2	AC117887	Rattus no
C 685	30	0.9	8561	6	AX281215	AX281215 Sequence	C 758	30	0.9	142318	2	AC121392	Rattus no
C 686	30	0.9	8961	6	AX323814	AX323814 Sequence	C 759	30	0.9	142994	2	CNS08C7P	CNS08C7P
C 687	30	0.9	12029	3	AE001381	AE001381 Plasmodiu	C 760	30	0.9	143534	9	AC113380	Homo sapi
C 688	30	0.9	12029	3	AE001427	AE001427 Plasmodiu	C 761	30	0.9	143701	2	AC022853	Homo sapi
C 689	30	0.9	12404	3	AE001424	AE001424 Plasmodiu	C 762	30	0.9	144138	9	AC011196	Homo sapi
C 690	30	0.9	13951	3	AE001406	AE001406 Plasmodiu	C 763	30	0.9	144162	2	AC008434	Homo sapi
C 691	30	0.9	14005	3	AE001409	AE001409 Plasmodiu	C 764	30	0.9	144406	2	AC008396	Homo sapi
C 692	30	0.9	16422	3	AE001421	AE001421 Plasmodiu	C 765	30	0.9	147009	2	AC084179	Homo sapi
C 693	30	0.9	17470	3	AE001402	AE001402 Plasmodiu	C 766	30	0.9	148295	9	AC090510	Homo sapi
C 694	30	0.9	28670	9	AC104621	AC104621 Homo sapi	C 767	30	0.9	148757	2	AC130885	Homo sapi
C 695	30	0.9	40100	2	AC130558	AC130558 Rattus no	C 768	30	0.9	148807	9	AC007028	Homo sapi
C 696	30	0.9	40668	9	AC003112	AC003112 Human DNA	C 769	30	0.9	148872	2	AC073168	Homo sapi
C 697	30	0.9	47844	9	AC008998	AC008998 Homo sapi	C 770	30	0.9	148876	9	AC011455	Homo sapi
C 698	30	0.9	54940	9	AL596211	AL596211 Human DNA	C 771	30	0.9	149218	2	AC023997	Homo sapi
C 699	30	0.9	58346	2	AC100546	AC100546 Mus muscu	C 772	30	0.9	149366	9	AC127223	Mus muscu
C 700	30	0.9	62043	9	AL161893	AL161893 Human DNA	C 773	30	0.9	149869	9	AC006026	Homo sapi
C 701	30	0.9	64386	2	AC104222	AC104222 Mus muscu	C 774	30	0.9	150573	9	AC097473	Homo sapi
C 702	30	0.9	66448	9	AC091286	AC091286 Homo sapi	C 775	30	0.9	151324	9	AC098936	Homo sapi
C 703	30	0.9	66448	9	AC091286	AC091286 Homo sapi	C 776	30	0.9	151745	2	AC102069	Mus muscu
C 704	30	0.9	69324	2	AL117589	AL117589 Mus muscu	C 777	30	0.9	152039	9	AC097489	Homo sapi
C 705	30	0.9	70788	2	AL353144	AL353144 Homo sapi	C 778	30	0.9	152345	9	AP000009	Homo sapi
C 706	30	0.9	74126	9	AC055825	AC055825 Homo sapi	C 779	30	0.9	152409	2	PFMAL1P1	PFMAL1P1
C 707	30	0.9	78866	9	AL358452	AL358452 Human DNA	C 780	30	0.9	154386	2	AC016314	Homo sapi
C 708	30	0.9	80518	2	PFMAL13P3A	AL109815 Plasmodiu	C 781	30	0.9	154530	9	AL160151	Human DNA
C 709	30	0.9	81851	9	HSJ719K3	AL109931 Human DNA	C 782	30	0.9	155421	2	AC109554	Rattus no
C 710	30	0.9	83110	2	PFMAL13P8	AL109814 Plasmodiu	C 783	30	0.9	155523	2	AC025367	Homo sapi
C 711	30	0.9	83351	8	AC010657	AC010657 Genomic s	C 784	30	0.9	156585	9	AC128023	Rattus no
C 712	30	0.9	85691	9	AP001429	AP001429 Homo sapi	C 785	30	0.9	156947	9	AL359435	Human DNA
C 713	30	0.9	87974	2	AC021283	AC021283 Homo sapi	C 786	30	0.9	157665	10	AC069018	Mus muscu
C 714	30	0.9	88037	2	PFMAL13P8	AL096782 Plasmodiu	C 787	30	0.9	158835	2	AC130857	Rattus no
C 715	30	0.9	90050	9	HSJ136A11	AL121962 Human DNA	C 788	30	0.9	159288	2	AP005533	Oryza sat
C 716	30	0.9	92501	2	AC107549	AC107549 Rattus no	C 789	30	0.9	160135	9	AL590427	Human DNA
C 717	30	0.9	95560	2	AC103136	AC103136 Rattus no	C 790	30	0.9	160324	9	AC079117	Homo sapi
C 718	30	0.9	97083	9	AF130249	AF130249 Homo sapi	C 791	30	0.9	160519	2	AC128328	Rattus no
C 719	30	0.9	97898	9	AL353613	AL353613 Human DNA	C 792	30	0.9	160519	2	AC128328	Rattus no
C 720	30	0.9	98341	9	AC074024	AC074024 Homo sapi	C 793	30	0.9	160562	2	AC098172	Rattus no
C 721	30	0.9	98734	2	PFMAL1P2	AL031745 Plasmodiu	C 794	30	0.9	160707	2	AC044899	Homo sapi
C 722	30	0.9	99145	2	AC112379	AC112379 Rattus no	C 795	30	0.9	161067	2	AL607133	Homo sapi

C 796	30	0.9	161083	2	AC129224	AC129224	Oryza sat
C 797	30	0.9	161876	2	AC073634	AC073634	Homo sapi
C 798	30	0.9	162549	9	AC090802	AC090802	Homo sapi
799	30	0.9	162803	2	AC032000	AC032000	Homo sapi
C 800	30	0.9	163361	2	AC128954	AC128954	Rattus no
C 801	30	0.9	163521	10	AC121966	AC121966	Mus muscu
C 802	30	0.9	164118	2	AL732629	AL732629	Danio rer
C 803	30	0.9	164217	9	AC093264	AC093264	Homo sapi
C 804	30	0.9	164217	9	AC093264	AC093264	Homo sapi
C 805	30	0.9	164399	3	PFMAL3P6	PFMAL3P6	
C 806	30	0.9	164399	3	PFMAL3P6	PFMAL3P6	
C 807	30	0.9	165010	9	HSDJ339B4	HSDJ339B4	
C 808	30	0.9	165425	2	AC120888	AC120888	Oryza sat
C 809	30	0.9	166395	5	AL627383	AL627383	Zebratfish
C 810	30	0.9	166459	2	AC016092	AC016092	Homo sapi
C 811	30	0.9	166572	2	AC097102	AC097102	Homo sapi
C 812	30	0.9	166796	2	AC126437	AC126437	Mus muscu
C 813	30	0.9	167087	2	AF004001	AF004001	Oryza sat
C 814	30	0.9	167346	9	AC096640	AC096640	Homo sapi
C 815	30	0.9	167409	2	AC073374	AC073374	Homo sapi
816	30	0.9	168008	2	AC027488	AC027488	Homo sapi
C 817	30	0.9	168008	2	AC027488	AC027488	Homo sapi
C 818	30	0.9	168062	30	AC022292	AC022292	Homo sapi
C 819	30	0.9	168506	9	AC007404	AC007404	Homo sapi
C 820	30	0.9	168662	2	AC022241	AC022241	Homo sapi
C 821	30	0.9	169546	2	AC004157	AC004157	Plasmodi
C 822	30	0.9	169869	2	AC005867	AC005867	Homo sapi
C 823	30	0.9	170512	2	AC021806	AC021806	Homo sapi
C 824	30	0.9	170789	2	AC106198	AC106198	Rattus no
C 825	30	0.9	171026	9	AL590416	AL590416	Human DNA
C 826	30	0.9	171152	2	AC110183	AC110183	Mus muscu
C 827	30	0.9	171578	2	AC011791	AC011791	Homo sapi
C 828	30	0.9	172180	9	AC109494	AC109494	Homo sapi
C 829	30	0.9	172248	2	AC124336	AC124336	Mus muscu
C 830	30	0.9	172433	2	AC118973	AC118973	Rattus no
C 831	30	0.9	172747	9	AL358835	AL358835	Human DNA
C 832	30	0.9	172758	2	AC117918	AC117918	Rattus no
C 833	30	0.9	173415	9	AL591890	AL591890	Human DNA
C 834	30	0.9	173532	2	AC040890	AC040890	Homo sapi
C 835	30	0.9	173696	2	AC111981	AC111981	Rattus no
C 836	30	0.9	174402	9	AC016991	AC016991	Homo sapi
C 837	30	0.9	176634	2	AC118163	AC118163	Homo sapi
C 838	30	0.9	177076	2	AC092949	AC092949	Homo sapi
C 839	30	0.9	177127	2	AC026287	AC026287	Homo sapi
C 840	30	0.9	177519	9	AC068702	AC068702	Homo sapi
C 841	30	0.9	178116	2	AC073491	AC073491	Homo sapi
C 842	30	0.9	178328	9	AC092547	AC092547	Homo sapi
C 843	30	0.9	178480	2	AC125834	AC125834	Rattus no
C 844	30	0.9	178524	9	AC006427	AC006427	Homo sapi
C 845	30	0.9	179410	9	AC091174	AC091174	Homo sapi
C 846	30	0.9	179410	9	AC090968	AC090968	Homo sapi
C 847	30	0.9	180120	9	AC090857	AC090857	Homo sapi
C 848	30	0.9	180430	9	AC096768	AC096768	Homo sapi
C 849	30	0.9	180559	2	AL671919	AL671919	Mus muscu
C 850	30	0.9	180602	9	AC010873	AC010873	Homo sapi
C 851	30	0.9	180789	2	AC024633	AC024633	Homo sapi
C 852	30	0.9	181588	2	AC126574	AC126574	Rattus no
C 853	30	0.9	182852	2	AC118821	AC118821	Rattus no
C 854	30	0.9	183357	9	AC068759	AC068759	Homo sapi
C 855	30	0.9	184050	2	AC025748	AC025748	Homo sapi
C 856	30	0.9	184346	2	AC069138	AC069138	Homo sapi
C 857	30	0.9	185457	2	AC118123	AC118123	Rattus no
C 858	30	0.9	185593	9	AC068970	AC068970	Homo sapi
C 859	30	0.9	186224	9	AC105901	AC105901	Homo sapi
C 860	30	0.9	186682	2	AC123097	AC123097	Papio cyn
C 861	30	0.9	187008	2	AC125219	AC125219	Mus muscu
C 862	30	0.9	187266	2	AC073984	AC073984	Homo sapi
C 863	30	0.9	187835	2	AC119382	AC119382	Rattus no
C 864	30	0.9	187835	2	AC119382	AC119382	Rattus no
C 865	30	0.9	188148	2	AC036220	AC036220	Homo sapi
C 866	30	0.9	188151	2	AC095270	AC095270	Rattus no
C 867	30	0.9	188840	9	AC046144	AC046144	Homo sapi
C 868	30	0.9	189574	2	AL8088113	AL8088113	Mus muscu
C 869	30	0.9	190624	2	AC026892	AC026892	Homo sapi
C 870	30	0.9	190848	9	AC113416	AC113416	Homo sapi
C 871	30	0.9	191027	2	AC022271	AC022271	Homo sapi
C 872	30	0.9	191136	2	AC098997	AC098997	Rattus no
C 873	30	0.9	191161	2	AC107539	AC107539	Rattus no
C 874	30	0.9	191241	2	AC116461	AC116461	Mus muscu
C 875	30	0.9	195634	2	AC013464	AC013464	Homo sapi
C 876	30	0.9	196490	2	AC005507	AC005507	Plasmodi
C 877	30	0.9	196490	2	AC005507	AC005507	Plasmodi
C 878	30	0.9	196946	2	AC067934	AC067934	Homo sapi
C 879	30	0.9	196966	2	AC031975	AC031975	Homo sapi
C 880	30	0.9	196999	2	AF172173	AF172173	Mus muscu
C 881	30	0.9	197778	9	AF130358	AF130358	Homo sapi
C 882	30	0.9	197915	9	AC005725	AC005725	Homo sapi
C 883	30	0.9	198480	2	AC025077	AC025077	Homo sapi
C 884	30	0.9	198952	10	AL773600	AL773600	Mouse DNA
C 885	30	0.9	199610	2	AC109243	AC109243	Mus muscu
C 886	30	0.9	199610	2	AC109243	AC109243	Mus muscu
C 887	30	0.9	200966	10	AL596108	AL596108	Mouse DNA
C 888	30	0.9	202563	9	AC021192	AC021192	Homo sapi
C 889	30	0.9	204254	2	AC087783	AC087783	Homo sapi
C 890	30	0.9	204358	2	AC111121	AC111121	Mus muscu
C 891	30	0.9	204480	2	AC019083	AC019083	Homo sapi
C 892	30	0.9	205429	2	AC005506	AC005506	Plasmodi
C 893	30	0.9	206214	2	AC095934	AC095934	Rattus no
C 894	30	0.9	210233	2	AC104431	AC104431	Homo sapi
C 895	30	0.9	210282	9	AP001274	AP001274	Homo sapi
C 896	30	0.9	211325	2	AP002757	AP002757	Homo sapi
C 897	30	0.9	215891	2	AL732451	AL732451	Mus muscu
C 898	30	0.9	220633	9	HU091321	HU091321	Human Chrom
C 899	30	0.9	222572	10	AL691519	AL691519	Mouse DNA
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\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* 39462 39561: gap of 100 bp  
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\* Location/Qualifiers  
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DEFINITION Homo sapiens clone T8D145M4 FEZ1 (FEZ1) mRNA, alternatively  
spliced, complete cds.  
ACCESSION AF123655

AF123655.1 GI:4572467  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1614)  
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,  
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.  
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
and its expression is altered in multiple human tumors  
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
99199287  
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2 (bases 1 to 1614)  
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,  
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.  
Direct Submission  
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
Institute, 2338 10th street, Philadelphia, PA 19107, USA  
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Best Local Similarity 99.9%; Pred. No. 0;  
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## RESULT 5

AF123657  
LOCUS Homo sapiens clone G3611 FEZ1 (FEZ1) mRNA, alternatively spliced, complete cds.  
DEFINITION

ACCESSION AF123657

VERSION AF123657.1

KEYWORDS GI:4572471

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1692)

AUTHORS Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H., Mori.M., Fidanza.V., Alder.H. and Croce.C.M.

TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)

MEDLINE 99199297

PUBMED 10097140

REFERENCE 2 (bases 1 to 1692)

AUTHORS Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H., Mori.M., Fidanza.V., Alder.H. and Croce.C.M.

TITLE Direct Submission

JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer Institute, 233S 10th street, Philadelphia, PA 19107, USA

FEATURES Location/Qualifiers

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Db 345 GGGTCCGAGAAGGTCAGTGAAGGCCACAGCCTTCAAGCCTGTGTGCCACCGTCAGG 404

Qy 836 AGGCATCTGCATCTCTCCCGGAGAGTGCAGCACCAGCTGCACCCGCGCCCTCCAGA 895

Db 405 AGGCATCTGCATCTCTCCCGGAGAGTGCAGCACCAGCTGCACCCGCGCCCTCCAGA 464

Qy 896 CAAGCCCAAGGAGCAGAGCTGAAGCTGGCCTGTGCTTGGGGCGCTGCAGACTCCGG 955

Db 465 CAAGCCCAAGGAGCAGAGCTGAAGCTGGCCTGTGCTTGGGGCGCTGCAGACTCCGG 524

Qy 956 CCGGAATCTCATGTCCAGCCTGCCACACAGCAGCAGCAGCAGCTACAGCTGGACCC 1015

Db 525 CCGGAATCTCATGTCCAGCCTGCCACACAGCAGCAGCAGCAGCTACAGCTGGACCC 584

Qy 1016 GTGGTCCACACCGTGGGACCCACAGCCGTTTTTGGGGGCTCCGCCACAAATCAGCCA 1075

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Db 705 AGGTAGCAAGCTGGGCGCACTCGAACAAGGCGAGACAAGGCGCCCTCGTGTGTCCTCC 764

Qy 1196 CATCTCCAGCAGAGTGCAGATCCAGGAGCTGGAACAGAGCTGTGGAGAGGAGGG 1255

Db 765 CATCTCCAGCAGAGTGCAGATCCAGGAGCTGGAACAGAGCTGTGGAGAGGAGGG 824

Qy 1256 CGCCCTCCAGAGCTGCAGCGCAGCTTTGAGGAGAGGAGCTTCCTCCAGCTGGGCTA 1315

Db 825 CGCCCTCCAGAGCTGCAGCGCAGCTTTGAGGAGAGGAGCTTCCTCCAGCTGGGCTA 884

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Qy 1436 ACTCAGCTTCAGCAGGAGAGCGCAGCTCCGCGAGGAGCTTCGAGAGCTTCATGAAGGA 1495

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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1722)		
JOURNAL	Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.		
MEDLINE	The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors		
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)		
AUTHORS	99199287		
TITLE	2 (bases 1 to 1722)		
JOURNAL	Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.		
MEDLINE	Direct Submission		
PUBMED	Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer Institute, 233S 10th street, Philadelphia, PA 19107, USA		
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REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 5492)		
JOURNAL	Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.		
MEDLINE	The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors		
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)		
AUTHORS	99199287		
TITLE	2 (bases 1 to 5492)		
JOURNAL	Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.		

TITLE Direct Submission  
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
Institute, 2338 10th street, Philadelphia, PA 19107, USA  
FEATURES Location/Qualifiers  
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Best Local Similarity 99.9%; Pred. No. 0;  
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DB 876 CATCTCCAGGACGAGTGCAGATCCAGAGCTGGAAACAGAGCTGTTGGAGAGGAGGG 935  
QY 1256 CCCCTCCAGAGCTGCAGCGAGCTTTCAGGAGAGGAGCTTGCTCCAGCTCGCCTA 1315  
DB 936 CCCCTCCAGAGCTGCAGCGAGCTTTCAGGAGAGGAGCTTGCTCCAGCTCGCCTA 995  
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DB 996 CGAGGAGCGGCGCGCTGCAGGAGCGAGCTGGAGGCGCGGAGCCCAAGGCGGCAA 1055  
QY 1376 CRAAGCTCAACGAGCGCTCGCAGAGAGCAGCCGCGCAGCAGCTCTCGACCTGCAGGT 1435  
DB 1056 CRAAGCTCAACGAGCGCTCGCAGAGAGCAGCCGCGCAGCAGCTCTCGACCTGCAGGT 1115  
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DB 1116 ACTGCACTTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTTCATGAAGGA 1175  
QY 1496 GCAGGACCTCTCGAGACCAAGCTCAGGTCTTACGAGAGGAGAGCAGCTTCGCGCC 1555  
DB 1176 GCAGGACCTCTCGAGACCAAGCTCAGGTCTTACGAGAGGAGAGCAGCTTCGCGCC 1235  
QY 1556 CGCGCTGGAGAGACCCAGTGGGAGGTG 1583  
DB 1236 CGCGCTGGAGAGACCCAGTGGGAGGTG 1263  
RESULT 8  
AF123654 Homo sapiens clone E264162 FEZ1 (FEZ1) mRNA linear PRI 07-APR-1999  
LOCUS complete cds.  
DEFINITION AF123654  
ACCESSION AF123654.1 GI:4572465  
VERSION  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 633)  
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,  
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.  
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
and its expression is altered in multiple human tumors  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
MEDLINE 99199287  
PUBMED 10097140  
REFERENCE 2 (bases 1 to 633)  
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,  
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.  
TITLE Direct Submission  
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
Institute, 2338 10th street, Philadelphia, PA 19107, USA  
FEATURES Location/Qualifiers  
source 1. 633  
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Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGTCTGCCACCGTCCAGG 835



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Qy 896 CAAGCCCAAGAGAGAGAGTGAAGCTGGCTGTGCTCTGGGCGCTGTGCAGACTCCGG 955
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Db 525 CCGGAATCCATGTCAGCTGCCACACACAGC 558

RESULT 9
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LOCUS AC093002 70707 bp DNA linear PRI 07-MAR-2002
DEFINITION Homo sapiens 3q BAC RP11-490H13 (Roswell Park Cancer Institute
AC093002 Human BAC Library) complete sequence.
ACCESSION AC093002
VERSION AC093002.4 GI:18873802
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70707)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.B., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davis,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Gabis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homai,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulsegh,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
Nickerson,E., Nwokenwo,S., Ogih,M., Okuwonu,G., Oragunye,N.,
Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,
Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,E.,
Sonaikhe,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
Vera,V., Villalon,D., Vinson,N., Wang,Q., Wang,S., Ward-Moore,S.,
Warren,R., Washington,C., Watlington,S., Williams,G.,
Williamson,A., Wlezyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 70707)

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# AUTHORS TITLE JOURNAL

## REFERENCE AUTHORS TITLE JOURNAL

## REFERENCE AUTHORS TITLE JOURNAL

## REFERENCE AUTHORS TITLE JOURNAL

## COMMENT

Worley, K.C.  
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 70707)  
Worley, K.C.  
Direct Submission  
Submitted (23-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
4 (bases 1 to 70707)  
Worley, K.C.  
Direct Submission  
Submitted (26-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
5 (bases 1 to 70707)  
Worley, K.C.  
Direct Submission  
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Feb 23, 2002 this sequence version replaced gi:17646866.  
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
[gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the  
entire insert of this clone. Overlapping regions of clones are only  
sequenced and submitted once, so the sequence for the remainder of  
the insert may be found in the record for the adjacent clones.  
Overlapping clones are noted at the beginning and end of the  
Features listing.

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches  
of a local database that includes entries from dbSTS, GDB, and  
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,  
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST  
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the  
EST and cDNA sequences. Genes demonstrate at least two exons  
flanked by consensus splice sites that maintained sequence  
continuity across the splice junctions. Sequences that are not  
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
standard of double strand coverage with a minimum of 2 clones and 2  
reads with no ambiguities or 2 chemistries with a minimum of 2  
clones and 3 reads with no ambiguities. If the sequence quality for  
a region does not meet this standard, it will be indicated in the  
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
standards - estimated error rate less than 1 per 10,000 bases.  
Reports of lowest quality individual bases and measures of base  
quality are listed below. Description of the metrics can be found  
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

## QUALSTAT-REPORT.

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repeat_region	1649..1918

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repeat_region complement(2160..2302)
repeat_region /rpt_family="AluJo"
repeat_region 2303..2332 /rpt_family="(TTA)n"
repeat_region complement(2333..2448)
repeat_region /rpt_family="AluJo"
repeat_region 2607..2669 /rpt_family="AT-rich"
repeat_region 2716..2900 /rpt_family="THE1B"
repeat_region 2901..3184 /rpt_family="THE1B"
repeat_region 3185..3351 /rpt_family="AluSg"
repeat_region /rpt_family="THE1B"
repeat_region 3358..3490 /rpt_family="AluY"
repeat_region 3495..3802 /rpt_family="AluY"
repeat_region 4345..4813 /rpt_family="L1PAL3"
repeat_region 4860..5153 /standard_name="178146"
STS 5312..6561 /rpt_family="L1M1"
repeat_region complement(6582..7596)
repeat_region /rpt_family="L1PAG"
repeat_region 7607..9349 /rpt_family="L1M1"
repeat_region 9350..9564 /rpt_family="MER30"
repeat_region 9565..9726 /rpt_family="L1M1"
repeat_region 9727..9995 /rpt_family="AluSg1"
repeat_region 9996..10167 /rpt_family="L1M1"
repeat_region 10164..10294 /rpt_family="L1"
repeat_region 13559..13921 /rpt_family="THE1B"
repeat_region complement(14072..14400)
repeat_region /rpt_family="L2"
repeat_region complement(14388..14468)
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repeat_region complement(15317..15413)
repeat_region /rpt_family="MLT2E"
repeat_region 15884..15915 /rpt_family="AT-rich"
repeat_region 16775..16812 /rpt_family="(TTTC)n"
repeat_region complement(16813..17110)
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repeat_region complement(17223..17378)
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repeat_region 17970..18012 /rpt_family="LTR33A"
repeat_region 18900..19020 /rpt_family="CT-rich"
repeat_region 19511..19673 /rpt_family="MIR"
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repeat_region complement(20162..20288)
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Db 1196 TATATTTTATATATATATATATATATATATATATATAT 1234

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LOCUS Homo sapiens chromosome 5 clone CTB-43C3, complete sequence.
DEFINITION AC090064
ACCESSION AC090064.3 GI:20340448
VERSION HTG.
KEYWORDS SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 124882)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE 2 (bases 1 to 124882)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE 3 (bases 1 to 124882)
TITLE Submitted (14-FEB-2001) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 124882)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE 5 (bases 1 to 124882)
TITLE Submitted (30-APR-2002) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 30, 2002 this sequence version replaced gi:15290406.
Draft Sequence Produced by DOE Joint Genome Institute
www.igi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 143kb). It is clipped at the overlap with AC011407. The
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Best Local Similarity 100.0%; Pred. No. 1.1e-09; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0;

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LOCUS Homo sapiens chromosome 3 clone RP11-490H13, WORKING DRAFT
DEFINITION AC017085
ACCESSION AC017085
VERSION AC017085.5 GI:10198573
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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## RESULT 13

AC021439/C

LOCUS

DEFINITION

AC021439

AC021439.9

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AC021439 206030 bp DNA linear PRI 25-MAY-2002  
Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

AC021439 206030 bp DNA linear PRI 25-MAY-2002  
Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

AC021439 206030 bp DNA linear PRI 25-MAY-2002  
Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

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Homo sapiens chromosome 15, clone RP11-484P15, complete sequence.

## ----- Project Information

Center project name: L5100

Center clone name: 484\_P15

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complement(2925. 4060)

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6624. 6795

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6801. 6855

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9607. 9910

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9926. 10062

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10101. 10134

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10165. 10262

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10269. 10646

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12318. 12613

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JOURNAL

REFERENCE

AUTHORS

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Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WDR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WDR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)



```

Center project name: L23473
Center clone name: 171_P_5
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 225162 bases at least Q40
Consensus quality: 226535 bases at least Q30
Consensus quality: 227117 bases at least Q20
Insert size: 225000; agarose-fp
Insert size: 227484; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; agarose-fp
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 301: contig of 301 bp in length
* 302 401: gap of 100 bp
* 402 5831: contig of 5430 bp in length
* 5832 5931: gap of 100 bp
* 5932 173029: contig of 167098 bp in length
* 173030 173129: gap of 100 bp
* 173130 210061: contig of 36932 bp in length
* 210062 210161: gap of 100 bp
* 210162 227884: contig of 17723 bp in length.
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        /db_xref="taxon:10090"
        /clone="RP23-171P5"
        /clone_lib="RPCI-23 Female Mouse BAC"
        1. .301
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        clone end:SP6
        vector_side:left"
        402. .5831
        /note="assembly_fragment"
        5932. .173029
        /note="assembly_fragment"
        173130. .210061
        /note="assembly_fragment"
        210162. .227884
        /note="assembly_fragment
        clone end:T7
        vector_side:right"
BASE COUNT 65784 a 48825 c 49902 g 62967 t 402 others
ORIGIN
Query Match 1.1%; Score 38; DB 2; Length 227884;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 807 GCCTTCAGCCTGTGCTGCCAGGTCCAGGACCAATCCT 844
      |||||||
Db 84402 GCCTTCAGCCTGTGCTGCCAGGTCCAGGACCAATCCT 84439
      |||||||
RESULT 15
AC099416/c AC099416 263546 bp DNA linear HTG 23-MAY-2002
LOCUS Mus musculus chromosome UNK clone RP23-122M11, WORKING DRAFT
DEFINITION SEQUENCE, 8 unordered pieces.
AC099416 AC099416
AC099416.2 GI:21105058
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Mus musculus.

```

```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Unpublished
The sequence of Mus musculus clone
REFERENCE
2 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (14-NOV-2001) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 23, 2002 this sequence version replaced gi:16924178.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M BAO122M11
----- Summary Statistics -----
Sequencing vector: M13; 32%
Sequencing vector: plasmid; 68%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 278310 bases at least Q40
Consensus quality: 282938 bases at least Q30
Consensus quality: 286149 bases at least Q20
Insert size: 250000; agarose-fp
Insert size: 387570; sum-of-contigs
Quality coverage: 25.74 in Q20 bases; agarose-fp
Quality coverage: 16.86 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1204: contig of 1204 bp in length
* 1205 1304: gap of unknown length
* 1305 2524: contig of 1220 bp in length
* 2525 2624: gap of unknown length
* 2626 4136: contig of 1512 bp in length
* 4137 4236: gap of unknown length
* 4237 16434: contig of 12198 bp in length
* 16435 16534: gap of unknown length
* 16535 32106: contig of 15572 bp in length
* 32107 32206: gap of unknown length
* 32207 140224: contig of 108018 bp in length
* 140225 140324: gap of unknown length
* 140325 262693: contig of 122369 bp in length
* 262694 262793: gap of unknown length
* 262794 263546: contig of 753 bp in length.
FEATURES
    Location/Qualifiers
        1. .263546
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /chromosome="UNK"
        /clone="RP23-122M11"
        1. .1204
        /note="assembly_name:Contig127"
        1305. .2524
        misc_feature
        misc_feature

```

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misc_feature /note="assembly_name:Contig157"
2625..4136
misc_feature /note="assembly_name:Contig360"
4237..16434
misc_feature /note="assembly_name:Contig396"
16535..32106
misc_feature /note="assembly_name:Contig397"
32207..140224
misc_feature /note="assembly_name:Contig398"
140325..262693
misc_feature /note="assembly_name:Contig399"
262794..263546
misc_feature /note="assembly_name:Contig154"
BASE COUNT 76628 a 56149 c 55623 g 74436 t 710 others
ORIGIN
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Query Match 1.1%; Score 38; DB 2; Length 263546;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 807 GCCTCAAGCCTGTGCTGCCACGGTCAGGAGCCATCCT 844
Db 250484 GCCTCAAGCCTGTGCTGCCACGGTCAGGAGCCATCCT 250447
```

Search completed: June 17, 2003, 03:55:22  
Job time : 6462.51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 613.119 Seconds  
(without alignments)  
12756.396 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_871\_4343

Perfect score: 3473

Sequence: 1 agctgcgcctgggggcatct.....cgtggtggtcagcctgca 3473

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq.101002.\*

- 1: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*
- 4: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*
- 5: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*
- 6: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*
- 7: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*
- 8: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*
- 9: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*
- 10: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*
- 11: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*
- 12: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*
- 13: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*
- 14: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*
- 15: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*
- 16: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*
- 17: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*
- 18: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*
- 19: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*
- 20: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SID22/gcgcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	3473	100.0	9048	21 AAA64507 Nucleotide sequenc
2	1677	48.3	2411	22 AAS30637 DNA encoding novel
3	1677	48.3	2411	22 AAS28699 Genomic sequence #
4	757	21.8	1512	21 AAA64513 Nucleotide sequenc
5	757	21.8	1614	21 AAA64512 Nucleotide sequenc
6	757	21.8	1692	21 AAA64514 Nucleotide sequenc
7	757	21.8	1722	21 AAA64515 Nucleotide sequenc
8	757	21.8	1791	21 AAA64509 cDNA sequence enco
9	757	21.8	5492	21 AAA64508 cDNA sequence of t

10	475	13.7	560	22	AAS30595	DNA encoding novel
11	475	13.7	560	22	AAS28127	Novel cDNA encodin
12	214	6.2	633	21	AAA64511	Nucleotide sequenc
c 13	33	1.0	11805	24	ABL33749	Human immune svste
c 14	32	0.9	388	22	AAH93292	Plasmodium falci
c 15	32	0.9	881	24	ABN9110	Human prostate spe
c 16	32	0.9	3952	22	AAS46286	Tumour suppressor
c 17	32	0.9	3952	24	ABL70512	Chemically treated
c 18	32	0.9	3952	24	ABK31181	Signal transductio
c 19	32	0.9	4468	21	AAC62126	DNA encoding a cal
c 20	32	0.9	4611	21	AAC62127	DNA encoding a cal
c 21	32	0.9	5218	24	ABL33267	Human immune svste
c 22	32	0.9	5908	22	AAS45386	Chemically pretrea
c 23	32	0.9	5908	24	AAS61216	Human gene regulat
c 24	32	0.9	5908	24	ABK28231	DNA transcrip
c 25	32	0.9	6197	24	ABN80257	Human chemically m
c 26	32	0.9	6216	24	ABL70139	Human chemically t
c 27	32	0.9	6216	24	ABK39932	Human chemically p
c 28	32	0.9	7238	24	ABL33618	Human immune svste
c 29	32	0.9	10553	22	ABAI6395	Human nervous syst
c 30	32	0.9	10553	22	AAK69113	Human immune/haema
c 31	32	0.9	24025	17	AAT17455	Mutated BRCA1 geno
c 32	32	0.9	24025	17	AAT17515	Mutated BRCA1 geno
c 33	32	0.9	24026	17	AAT32612	BRCA1, human breas
c 34	32	0.9	24026	17	AAT17512	Mutated BRCA1 geno
c 35	32	0.9	24026	17	AAT17513	Mutated BRCA1 geno
c 36	32	0.9	24026	17	AAT17514	Mutated BRCA1 geno
c 37	32	0.9	24026	17	AAT17516	Mutated BRCA1 geno
c 38	32	0.9	24026	17	AAT17517	Mutated BRCA1 geno
c 39	32	0.9	24026	17	AAT17518	Mutated BRCA1 geno
c 40	32	0.9	24026	17	AAT17519	Mutated BRCA1 geno
c 41	32	0.9	24026	17	AAT17521	Mutated BRCA1 geno
c 42	32	0.9	24026	17	AAT17522	Mutated BRCA1 geno
c 43	32	0.9	24026	17	AAT17523	Mutated BRCA1 geno
c 44	32	0.9	24026	17	AAT17524	Mutated BRCA1 geno
c 45	32	0.9	24026	17	AAT17526	Mutated BRCA1 geno
c 46	32	0.9	24026	17	AAT17527	Mutated BRCA1 geno
c 47	32	0.9	24026	17	AAT17528	Mutated BRCA1 geno
c 48	32	0.9	24026	17	AAT17529	Mutated BRCA1 geno
c 49	32	0.9	24026	17	AAT17530	BRCA1 genomic requ
c 50	32	0.9	24026	17	AAT18325	BRCA1, human breas
c 51	32	0.9	24029	17	AAT17520	Mutated BRCA1 geno
c 52	32	0.9	24031	17	AAT17525	Mutated BRCA1 geno
c 53	32	0.9	32203	22	AAS36349	Human cardiovascular
c 54	32	0.9	47513	22	AAK74979	Human immune/haema
c 55	32	0.9	154465	24	AAD28763	Human AKAP allelic
c 56	32	0.9	158245	24	AAD28762	Human AKAP allelic
c 57	32	0.9	161425	22	AAH02340	Human AKAP10 gene
c 58	32	0.9	162025	22	AAH02339	Human AKAP10 gene
c 59	32	0.9	162025	24	AAD28758	Human AKAP allelic
c 60	32	0.9	162025	24	AAD28759	Human AKAP allelic
c 61	31	0.9	3147	21	AAK82996	P. falciparum gcpe
c 62	30	0.9	1941	21	AAK70122	Plasmodium falci
c 63	30	0.9	6012	24	ABL70484	Chemically treated
c 64	30	0.9	6012	24	ABL70484	Signal transductio
c 65	30	0.9	6552	22	AAS46678	Tumour suppressor
c 66	30	0.9	8451	24	ABK39982	Human chemically p
c 67	30	0.9	8451	24	ABL32659	Human immune svste
c 68	30	0.9	8451	24	AAS63319	Chemically pretrea
c 69	30	0.9	8961	24	ABL49380	Human polynucleoti
c 70	30	0.9	8961	24	ABL28428	DNA transcrip
c 71	29	0.8	40668	24	ABQ88150	Human osteoblast d
c 72	29	0.8	158	22	AAI61616	Soybean 318013 reg
c 73	29	0.8	549	21	AAC95291	Cat flea head and
c 74	29	0.8	4601	23	ABL18948	Drosophila melanog
c 75	29	0.8	5586	22	AAS46798	Tumour suppressor
c 76	29	0.8	5586	24	ABL34183	Human immune svste
c 77	29	0.8	5760	6	AAH50530	Sequence encoding
c 78	29	0.8	8676	24	ABL70452	Chemically treated
c 79	29	0.8	8676	24	AAS61415	Human gene regulat
c 80	29	0.8	9770	24	ABL32032	Human immune svste
c 81	29	0.8	9770	24	ABL32033	Human immune svste
c 82	29	0.8	11745	24	ABK28332	DNA transcrip

83	29	0.8	17213	24	ABL33482	Human immune syste	156	26	0.7	12477	22	AA531480	Human DNA for a no
84	29	0.8	37322	24	ABL61996	Colon adenocarcino	157	26	0.7	12477	22	AA535051	DNA #1 encoding hu
85	29	0.8	119950	20	AA390201	Human yes1 gene.	158	26	0.7	12477	24	ABQ66804	Human polynucleoti
86	29	0.8	513445	22	AAI61373	Soybean 318013 reg	c 159	26	0.7	13165	22	ABA07140	Human pancreatic c
87	28	0.8	154	22	AAH93350	Human polynucleoti	c 160	26	0.7	13165	22	AAK89348	Human digestive sy
88	28	0.8	344	22	AAH93307	Plasmodium falcipa	c 161	26	0.7	16271	22	ABA19209	Human nervous syst
89	28	0.8	745	15	AAQ71372	DNA probe (Y1) use	c 162	26	0.7	16271	22	ABA19210	Human nervous syst
90	28	0.8	881	24	ABN89110	Human prostate spe	c 163	26	0.7	16602	24	ABN80069	Human chemically m
91	28	0.8	4320	23	ABL04688	Drosophila melanog	c 164	26	0.7	16602	24	ABL32727	Human immune syste
92	28	0.8	17280	22	AA546771	Tumour suppressor	c 165	26	0.7	17183	24	ABL32486	Human immune syste
93	28	0.8	19124	18	AA72882	Plasmodium var-7 g	166	26	0.7	17280	22	AA546772	Tumour suppressor
94	28	0.8	19124	21	AAZ98287	Plasmodium var-7 p	c 167	26	0.7	17379	22	AA328427	Genomic sequence #
95	28	0.8	154902	24	ABQ88198	Human osteoblast d	c 168	26	0.7	17379	22	AAK71667	Human immune/haema
96	28	0.8	1082138	21	AA222305	Arabidopsis thalia	c 169	26	0.7	17569	24	ABK39756	cDNA encoding clon
97	27	0.8	554	22	AAH10798	Human cDNA clone (	c 170	26	0.7	17594	24	ABL34026	Human immune syste
98	27	0.8	926	21	ABN81102	Shrimp polynucleot	c 171	26	0.7	18357	24	ABQ67084	Human angiogenesis
99	27	0.8	1449	24	ABQ13550	Oligonucleotide fo	172	26	0.7	20579	24	ABQ67074	Human angiogenesis
100	27	0.8	1449	24	ABQ13551	Oligonucleotide fo	173	26	0.7	25131	22	AAK84544	Human immune/haema
101	27	0.8	1837	19	AAV21647	P. falciparum chor	c 174	26	0.7	34769	22	AA546775	Tumour suppressor
102	27	0.8	1837	21	AA588980	Plasmodium falcipa	175	26	0.7	48436	24	ABN89533	Human corneal N-ac
103	27	0.8	2051	22	AAH15970	Human cDNA sequenc	176	26	0.7	160552	22	AAQ02697	Human glycosyl sul
104	27	0.8	3205	23	ABL15080	Drosophila melanog	177	25	0.7	105	22	AAH93322	Plasmodium falcipa
105	27	0.8	3935	23	ABL05834	Drosophila melanog	178	25	0.7	402	21	AAH70130	Plasmodium falcipa
106	27	0.8	5759	24	ABL33704	Human immune syste	c 179	25	0.7	488	22	AAI90613	Human polynucleoti
107	27	0.8	5878	24	ABL33541	Human immune syste	c 180	25	0.7	588	23	ABV54666	Human prostate exp
108	27	0.8	6431	24	ABQ67119	Human angiogenesis	181	25	0.7	1920	24	ABA01809	P. falciparum isopr
109	27	0.8	6431	24	ABQ67120	Human angiogenesis	c 182	25	0.7	3783	22	AAK71130	Human immune/haema
110	27	0.8	6432	22	AA546557	Tumour suppressor	c 183	25	0.7	3925	22	AAI61171	Human polynucleoti
111	27	0.8	6432	22	AA546558	Tumour suppressor	c 184	25	0.7	4282	21	AAK77113	Human ORFX ORF2668
112	27	0.8	6965	21	AA588985	Toxoplasma gondii	c 185	25	0.7	5276	22	AAI59690	Human polynucleoti
113	27	0.8	7047	24	ABK28386	DNA transcription	186	25	0.7	5316	22	AAI57904	Human polynucleoti
114	27	0.8	10132	24	ABL54371	Chemically treated	187	25	0.7	5666	24	ABL33772	Human immune syste
115	27	0.8	10132	24	ABL54372	Chemically treated	188	25	0.7	5860	24	ABL70524	Chemically treated
116	27	0.8	10132	24	ABL34080	Human immune syste	189	25	0.7	5860	24	AA561373	Human gene regulat
117	27	0.8	10132	24	ABL34081	Human immune syste	190	25	0.7	5860	24	ABK31457	Signal transductio
118	27	0.8	10471	22	ABAI6396	Human nervous syst	c 191	25	0.7	6107	24	ABL70354	Chemically treated
119	27	0.8	14353	24	ABL34434	Human immune syste	c 192	25	0.7	6107	24	AA561315	Human gene regulat
120	27	0.8	16258	24	ABL70376	Chemically treated	c 193	25	0.7	6151	24	ABL33610	Human immune syste
121	27	0.8	16258	24	ABK40038	Human chemically p	c 194	25	0.7	6151	24	ABK28275	DNA transcription
122	27	0.8	47108	24	ABK31510	Signal transductio	c 195	25	0.7	6173	21	AA513380	Chromosome 16q tum
123	26	0.7	53	22	AAH93331	Plasmodium falcipa	196	25	0.7	6834	22	AA205314	Human reproductive
124	26	0.7	209	22	AAH93332	Plasmodium falcipa	c 197	25	0.7	6834	22	AA205314	Human immunoglobul
125	26	0.7	396	22	AAH93303	Plasmodium falcipa	c 198	25	0.7	7592	23	ABL19452	Drosophila melanog
126	26	0.7	1195	11	AAQ04474	Human vascular per	c 199	25	0.7	7592	23	ABL19452	Drosophila melanog
127	26	0.7	1195	20	AA504098	Human vascular end	200	25	0.7	7864	24	ABL33608	Human immune syste
128	26	0.7	1618	16	AAQ75423	Human 4-1BB-L poly	201	25	0.7	7864	24	ABL33608	DNA transcription
129	26	0.7	1618	18	AAI91025	Human 4-1BB ligand	c 202	25	0.7	8305	24	ABL33569	Human immune syste
130	26	0.7	1618	24	ABL54046	Human cytokine 4-1	203	25	0.7	8404	22	AA546500	Tumour suppressor
131	26	0.7	1619	19	AAV39013	Nucleotide sequenc	204	25	0.7	8404	24	ABL33595	Human immune syste
132	26	0.7	1619	24	ABK94188	Human cDNA differe	205	25	0.7	8588	22	AA545470	Chemically pretrea
133	26	0.7	1619	24	ABN96784	Gene #3282 used to	206	25	0.7	8588	24	ABK28326	DNA transcription
134	26	0.7	1873	19	AAV15103	Human vascular end	c 207	25	0.7	9217	23	ABL29242	Drosophila melanog
135	26	0.7	1873	20	AA321568	Vascular endotheli	208	25	0.7	10024	24	ABN95933	Gene #2431 used to
136	26	0.7	2361	21	AAC98144	Human colon cancer	209	25	0.7	10092	23	ABL17246	Drosophila melanog
137	26	0.7	2552	23	ABL03744	Drosophila melanog	c 210	25	0.7	10553	22	ABA16395	Human nervous syst
138	26	0.7	2914	22	AAK70730	Human immune/haema	c 211	25	0.7	10553	22	ABA16395	Human immune/haema
139	26	0.7	2914	22	AAK70730	Human immune/haema	c 212	25	0.7	10842	21	AA513381	Chromosome 16q tum
140	26	0.7	3001	21	AAH51782	Chromosome 13q31-q	c 213	25	0.7	12069	24	ABK39930	Human chemically p
141	26	0.7	3001	21	AAH51787	Chromosome 13q31-q	214	25	0.7	14551	24	ABK34584	Human metastasis a
142	26	0.7	3166	24	ABL59546	Human vascular end	215	25	0.7	14809	22	AA534708	Human DNA for a no
143	26	0.7	4601	23	ABL18948	Drosophila melanog	c 216	25	0.7	16107	22	AAK78528	Human immune/haema
144	26	0.7	5776	24	ABL92225	Chemically treated	c 217	25	0.7	16107	22	AAK78528	Human secreted pro
145	26	0.7	5776	24	ABL92225	Chemically treated	c 218	25	0.7	16914	24	ABL70315	Chemically treated
146	26	0.7	6621	24	ABL70156	Human immune syste	c 219	25	0.7	16914	24	AA561253	Human gene regulat
147	26	0.7	6621	24	ABK33933	Human DNA for stag	c 220	25	0.7	17280	22	AA546771	Tumour suppressor
148	26	0.7	6621	24	AA561098	Human gene regulat	c 221	25	0.7	18535	22	AA330121	Human lung antigen
149	26	0.7	6831	24	ABL33486	Human immune syste	222	25	0.7	21477	22	AAK66626	Human immune/haema
150	26	0.7	7167	24	ABL32401	Human immune syste	223	25	0.7	21480	22	AAK66626	Human immune/haema
151	26	0.7	8129	22	AA546763	Tumour suppressor	c 224	25	0.7	113515	24	ABL34174	Human immune syste
152	26	0.7	9810	24	ABL32427	Human immune syste	c 225	25	0.7	122186	22	AAK89560	Human histone deac
153	26	0.7	12477	22	ABA06765	Human genomic DNA	226	25	0.7	130263	24	ABK83573	Human cDNA differe
154	26	0.7	12477	22	AAK85389	Human immune/haema	227	25	0.7	178896	24	ABQ88146	Human osteoblast d
155	26	0.7	12477	22	AAI63967	Human polynucleoti	228	25	0.7	1503900	22	AAK95240	Human neuregulin-1



229	25	0.7	1503900	22	AAK96733	Human neuregulin-1
c 230	24	0.7	125	21	AAC25418	Human secreted pro
c 231	24	0.7	426	21	AAC36828	Human cardiovascular
c 232	24	0.7	487	21	AAC68735	Human TSC39 cDNA f
c 233	24	0.7	504	24	ABO17474	Oligonucleotide fo
c 234	24	0.7	504	24	ABO17475	Oligonucleotide fo
c 235	24	0.7	505	23	ABV58881	Human prostate exp
c 236	24	0.7	633	13	AAQ20241	Pfsl6 gene. Plasm
c 237	24	0.7	789	12	AAQ10792	Bovine vascular en
c 238	24	0.7	789	14	AAQ44255	Partial bovine VEG
c 239	24	0.7	829	12	AAQ10796	Bovine vascular en
c 240	24	0.7	961	12	AAQ10791	Bovine vascular en
c 241	24	0.7	961	14	AAQ44259	Bovine VEGF-164 co
c 242	24	0.7	1543	11	AAQ06600	Clone lambda.vegf.
c 243	24	0.7	1547	21	AAC68736	Human TSC39 cDNA.
c 244	24	0.7	1560	24	ABK48976	Physics-based gene
c 245	24	0.7	1698	21	AAA81571	N meningitidis pa
c 246	24	0.7	2141	21	AAZ50203	Petunia hybrida ne
c 247	24	0.7	2141	21	AAZ35496	Petunia nectary-sp
c 248	24	0.7	2459	23	ABL26096	Drosophila melanog
c 249	24	0.7	2461	23	ABL13728	Drosophila melanog
c 250	24	0.7	2500	23	ABL28394	Drosophila melanog
c 251	24	0.7	2780	23	ABL27136	Drosophila melanog
c 252	24	0.7	2948	24	ABL19697	Mouse ischaemic co
c 253	24	0.7	3054	24	ABK36165	cdna sequence #556
c 254	24	0.7	3175	23	ABL02810	Drosophila melanog
c 255	24	0.7	4578	22	AAS27741	DNA encoding novel
c 256	24	0.7	4578	22	AAS27742	DNA encoding novel
c 257	24	0.7	4684	23	ABL18548	Drosophila melanog
c 258	24	0.7	5005	23	ABL28704	Drosophila melanog
c 259	24	0.7	5204	24	ABL32900	Human immune syste
c 260	24	0.7	5457	24	ABL33130	Human immune syste
c 261	24	0.7	5457	24	ABL33131	Human immune syste
c 262	24	0.7	5497	23	ABL04596	Drosophila melanog
c 263	24	0.7	5557	24	ABL33546	Human immune syste
c 264	24	0.7	5814	24	ABL33560	Human immune syste
c 265	24	0.7	5956	24	ABL70325	Chemically treated
c 266	24	0.7	5956	24	AAS61272	Human gene regulat
c 267	24	0.7	5956	24	ABK31368	Signal transductio
c 268	24	0.7	5989	22	AAS46515	Tumour suppressor
c 269	24	0.7	5995	22	AAS46720	Tumour suppressor
c 270	24	0.7	6103	24	ABL34171	Human immune syste
c 271	24	0.7	6103	24	ABL34171	Signal transductio
c 272	24	0.7	6454	23	ABK31513	Drosophila melanog
c 273	24	0.7	6853	22	AAK87155	Human immune/haema
c 274	24	0.7	7862	24	ABL34054	Human immune syste
c 275	24	0.7	7913	22	AAS46311	Tumour suppressor
c 276	24	0.7	7913	24	ABL70531	Chemically treated
c 277	24	0.7	7913	24	AAS61128	Human gene regulat
c 278	24	0.7	7913	24	ABL31216	Signal transductio
c 279	24	0.7	7928	24	ABL70123	Chemically treated
c 280	24	0.7	7928	24	ABL32094	Human immune syste
c 281	24	0.7	7928	24	AAS61055	Human gene regulat
c 282	24	0.7	7928	24	ABK31168	Signal transductio
c 283	24	0.7	8237	22	AAS46801	Tumour suppressor
c 284	24	0.7	8447	24	ABN80093	Human chemically m
c 285	24	0.7	10483	22	AAK90686	Human immune/haema
c 286	24	0.7	10619	22	AAS45296	Chemically pretrea
c 287	24	0.7	10619	24	ABL92192	Chemically treated
c 288	24	0.7	10619	24	ABL49303	Human polynucleoti
c 289	24	0.7	10619	24	ABL32070	Human immune syste
c 290	24	0.7	10619	24	ABK28127	DNA transcription
c 291	24	0.7	12202	23	ABL02770	Drosophila melanog
c 292	24	0.7	12202	23	ABL21186	Drosophila melanog
c 293	24	0.7	15037	22	AAI99283	Human excretory re
c 294	24	0.7	15037	22	AAI63633	Human kidney relat
c 295	24	0.7	15548	24	ABL34155	Human immune syste
c 296	24	0.7	16258	24	ABL70376	Chemically treated
c 297	24	0.7	16258	24	ABK40038	Human chemically p
c 298	24	0.7	16602	24	ABN80068	Human immune syste
c 299	24	0.7	16602	24	ABL32726	Human immune syste
c 300	24	0.7	17239	22	AAS36826	Human cardiovascular
c 301	24	0.7	17792	22	AAS32727	Human genomic DNA
229	302	0.7	17792	22	AAS36099	Human cardiovascular
230	303	0.7	17809	23	ABK42246	Genomic sequence #
231	304	0.7	18357	24	ABO67083	Human angiogenesis
232	305	0.7	32221	22	AAS39766	Genomic sequence #
233	306	0.7	32221	22	AAK90119	Human digestive sy
234	307	0.7	34769	22	AAS46774	Tumour suppressor
235	308	0.7	40324	24	ABO67149	Human angiogenesis
236	309	0.7	42573	23	ABU28622	Drosophila melanog
237	310	0.7	49999	24	AAZ23902	Human LOBO homolog
238	311	0.7	50000	24	ABL56201	AnEPV genome fragm
239	312	0.7	58708	22	AAK64739	Human immune/haema
240	313	0.7	103929	21	AAF22287	BAC containing rep
241	314	0.7	113515	24	ABU34175	Human immune syste
242	315	0.7	237326	19	AAV57903	Hereditary haemoch
243	316	0.7	23	21	AAA64525	PCR primer G20 use
244	317	0.7	23	21	AAA64527	PCR primer G32 use
245	318	0.7	23	21	AAA64541	Nucleotide sequenc
246	319	0.7	151	22	AAI61595	Soybean 318013 reg
247	320	0.7	236	22	AAH93306	Plasmodium falcipa
248	321	0.7	238	22	AAI61524	Soybean 240017 reg
249	322	0.7	269	22	AAI61702	Soybean 318013 reg
250	323	0.7	286	24	ABN96424	Gene #2922 used to
251	324	0.7	300	20	AAZ13456	Human gene express
252	325	0.7	377	22	AAI81403	Human polynucleoti
253	326	0.7	453	22	AAI93193	Human polynucleoti
254	327	0.7	470	22	AAH93301	Plasmodium falcipa
255	328	0.7	472	21	AAZ28226	Human secreted pro
256	329	0.7	480	24	ABK62665	Rat sequence diffe
257	330	0.7	509	22	ABK61512	Human foetal liver
258	331	0.7	509	22	ABA29232	Probe #7698 for ge
259	332	0.7	509	22	AAK09812	Human brain expres
260	333	0.7	509	22	AAK35706	Human bone marrow
261	334	0.7	509	22	AAI41421	Probe #10107 used
262	335	0.7	509	24	ABSO9980	Human genome-deriv
263	336	0.7	543	22	ABA21513	Human nervous syst
264	337	0.7	543	22	ABA21514	Human nervous syst
265	338	0.7	543	22	ABA21515	Human nervous syst
266	339	0.7	582	22	AAH93310	Plasmodium falcipa
267	340	0.7	582	22	AAH93310	Plasmodium falcipa
268	341	0.7	703	22	AAH87363	Human developmenta
269	342	0.7	742	22	AAH07077	Human cDNA clone (
270	343	0.7	809	22	AAH29793	S cerevisiae apopt
271	344	0.7	821	20	AAZ16428	Human gene express
272	345	0.7	824	24	ABN89109	Human prostate spe
273	346	0.7	844	22	AAH03515	Human cDNA clone (
274	347	0.7	944	22	AAH33445	Human colon cancer
275	348	0.7	1501	22	AAH13748	Human cDNA sequenc
276	349	0.7	1514	24	ABK34631	Human cDNA for nov
277	350	0.7	1560	24	ABK48976	Physics-based gene
278	351	0.7	1636	22	ABA19549	Human nervous syst
279	352	0.7	1636	22	AAI99154	Human excretory re
280	353	0.7	1636	22	AAH32848	Human genomic DNA
281	354	0.7	1636	22	AAH63504	Human kidney relat
282	355	0.7	1731	24	ABU64393	Stomach cancer rel
283	356	0.7	1764	24	ABK48066	cDNA encoding conl
284	357	0.7	1829	7	AAH60863	Sequence encoding
285	358	0.7	1843	22	AAH74307	Human H11 coding s
286	359	0.7	1843	22	AAH74328	Human H11 coding s
287	360	0.7	1966	21	AAH77664	Human cancer assoc
288	361	0.7	2093	22	AAH15345	Human cDNA sequenc
289	362	0.7	2273	20	AAZ77465	Human ovarian tumo
290	363	0.7	2562	23	ABL13566	Drosophila melanog
291	364	0.7	2707	23	ABK43641	DNA encoding novel
292	365	0.7	2780	23	ABL271136	Drosophila melanog
293	366	0.7	2780	23	ABL271136	Drosophila melanog
294	367	0.7	2780	23	ABL271136	Drosophila melanog
295	368	0.7	3350	13	AAQ29361	Ocean pout DNA seq
296	369	0.7	3391	22	ABLO1932	Drosophila melanog
297	370	0.7	3730	22	ABLO19745	Human nervous syst
298	371	0.7	3975	13	AAH81157	Malaria-specific g
299	372	0.7	3975	13	AAQ22959	SERP gene. Plasm
300	373	0.7	3997	24	ABL99812	Human secretory po
301	374	0.7	4400	22	ABL29072	Drosophila melanog
	374	0.7	4515	22	AAK85745	Human immune/haema

375	23	0.7	4762	23	ABL24574	Drosophila melanog	c 448	23	0.7	31718	22	AAL06415	Human reproductive
c 376	23	0.7	4858	24	ABK33961	Human DNA for stag	c 449	23	0.7	31718	22	AAL06416	Human reproductive
c 377	23	0.7	5037	24	ABN59798	Novel human coding	450	23	0.7	31718	22	AAK73104	Human immune/haema
c 378	23	0.7	5218	24	ABL33266	Human immune syste	451	23	0.7	31718	22	AAK73120	Human immune/haema
c 379	23	0.7	5586	24	AAS63356	Chemically pretrea	c 452	23	0.7	31718	22	AAK87442	Human immune/haema
c 380	23	0.7	5591	23	ABL05500	Drosophila melanog	c 453	23	0.7	31718	22	AAK87443	Human immune/haema
c 381	23	0.7	5795	24	ABN80232	Human chemically m	454	23	0.7	31718	22	AAK87573	Human immune/haema
c 382	23	0.7	5795	24	ABL33768	Human immune syste	455	23	0.7	31718	22	AAK87592	Human immune/haema
c 383	23	0.7	5818	22	AAS46635	Tumour suppressor	c 456	23	0.7	31718	22	AAK90359	Human digestive sy
c 384	23	0.7	5908	22	AAS45386	Chemically pretrea	c 457	23	0.7	31718	22	AAK90360	Human digestive sy
c 385	23	0.7	5908	24	AAS61216	Human gene regulat	c 458	23	0.7	32192	22	ABA17963	Human nervous syst
c 386	23	0.7	5908	24	ABK28231	DNA transcription	c 459	23	0.7	42573	23	ABL28622	Drosophila melanog
c 387	23	0.7	5930	24	ABL32517	Human immune syste	c 460	23	0.7	44211	22	AAK85974	Human immune/haema
c 388	23	0.7	5995	22	AAS46720	Tumour suppressor	461	23	0.7	56153	22	AAS46794	Tumour suppressor
c 389	23	0.7	6025	22	AAS45338	Chemically pretrea	462	23	0.7	149671	24	ABK84797	Human cdna differe
c 390	23	0.7	6048	24	ABQ67001	Human angiogenesis	463	23	0.7	335913	22	AAI61371	Soybean 240017 reg
c 391	23	0.7	6065	24	ABL32505	Human immune syste	464	23	0.7	335913	22	AAI61372	Soybean 240017 reg
c 392	23	0.7	6124	11	AAQ03568	Sequence encoding	465	23	0.7	513445	22	AAI61373	Soybean 318013 reg
c 393	23	0.7	6124	24	ABK15042	Plasmodium gene fo	c 466	22	0.6	22	21	AAA64524	PCR primer G17 use
c 394	23	0.7	6145	24	ABL32973	Human immune syste	c 467	22	0.6	22	21	AAA64528	PCR primer IntBCR
c 395	23	0.7	6155	24	ABK28361	DNA transcription	c 468	22	0.6	22	21	AAU32385	Human SNP oligonuc
c 396	23	0.7	6168	22	AAK85162	Human immune/haema	c 469	22	0.6	100	21	AAI19497	Human secreted pro
c 397	23	0.7	6170	22	AAK85163	Human immune/haema	c 470	22	0.6	177	22	AAH93314	Plasmodium falci
c 398	23	0.7	6216	24	ABL70139	Chemically treated	471	22	0.6	200	24	ABL86078	Human ovarian canc
c 399	23	0.7	6216	24	ABK39932	Human chemically p	472	22	0.6	209	22	AAH93323	Plasmodium falci
c 400	23	0.7	6306	22	AAK85746	Human immune/haema	c 473	22	0.6	218	22	AAH93315	Plasmodium falci
c 401	23	0.7	6430	24	ABN80122	Human chemically m	474	22	0.6	250	21	AAF21208	Human low adenosin
c 402	23	0.7	7109	22	ABAI19555	Human nervous syst	475	22	0.6	250	21	AAA35086	Human adenosine re
c 403	23	0.7	7109	22	AAI99157	Human excretory re	476	22	0.6	256	21	AAA32079	Plant microsatelli
c 404	23	0.7	7109	22	AAS32850	Human genomic DNA	477	22	0.6	300	20	AAI213456	Human gene express
c 405	23	0.7	7109	22	AAI63507	Human kidney relat	478	22	0.6	300	21	AAA32050	Plant microsatelli
c 406	23	0.7	7134	24	ABL32482	Human immune syste	c 479	22	0.6	333	21	AAI07773	Human secreted pro
c 407	23	0.7	7498	24	ABL32257	Human immune syste	c 480	22	0.6	333	22	ABA14783	Human nervous syst
c 408	23	0.7	7570	23	ABL06842	Drosophila melanog	c 481	22	0.6	348	23	ABV34186	Human prostate exp
c 409	23	0.7	8085	22	AAS46479	Tumour suppressor	c 482	22	0.6	366	23	ABV43047	Human prostate exp
c 410	23	0.7	8085	24	ABK33986	Human DNA for stag	c 483	22	0.6	375	23	ABV13065	Human prostate exp
c 411	23	0.7	8210	24	ABK32506	Human prostate spe	c 484	22	0.6	386	22	AAI89642	Human polynucleoti
c 412	23	0.7	8310	20	AAZ29911	CDNA encoding a SC	c 485	22	0.6	402	21	AAI70130	Plasmodium falci
c 413	23	0.7	8588	22	AAS45469	Chemically pretrea	c 486	22	0.6	409	22	AAI87008	Human polynucleoti
c 414	23	0.7	8588	24	ABK28325	DNA transcription	c 487	22	0.6	410	24	ABI79733	Human ovarian canc
c 415	23	0.7	8693	24	ABL32808	Human immune syste	c 488	22	0.6	412	22	AAH93300	Plasmodium falci
c 416	23	0.7	8693	24	ABL32809	Human immune syste	c 489	22	0.6	419	24	ABL87259	Human ovarian canc
c 417	23	0.7	8842	24	ABL33448	Human immune syste	c 490	22	0.6	426	21	AAA32069	Plant microsatelli
c 418	23	0.7	8842	24	ABK33334	Human immune syste	c 491	22	0.6	437	22	AAK62516	Human immune/haema
c 419	23	0.7	8896	24	AAS83337	Chemically pretrea	c 492	22	0.6	437	22	AAK62516	Plant microsatelli
c 420	23	0.7	8920	15	AAQ62924	Carbamoyl-phosphat	c 493	22	0.6	437	21	AAA32052	Plant microsatelli
c 421	23	0.7	9402	22	AAS46672	Tumour suppressor	c 494	22	0.6	479	21	AAH933295	Arabidopsis thalia
c 422	23	0.7	9566	22	ABA20411	Human nervous syst	c 495	22	0.6	479	24	AAH933295	Plasmodium falci
c 423	23	0.7	9566	22	AAI37121	Human musculocele	c 496	22	0.6	495	24	ABN64967	Human cancer relat
c 424	23	0.7	9566	22	AAS26794	Human genomic DNA	c 497	22	0.6	496	24	ABL86815	Human ovarian canc
c 425	23	0.7	9840	22	AAK67429	Human immune/haema	c 498	22	0.6	502	22	AAH11854	Human cdna clone (
c 426	23	0.7	10329	24	ABL34123	Human immune syste	c 499	22	0.6	516	22	AAH11579	Human cdna clone (
c 427	23	0.7	10425	22	ABAI7962	Human nervous syst	c 500	22	0.6	521	24	ABQ29480	Oligonucleotide fo
c 428	23	0.7	10697	24	ABN80330	Human chemically m	c 501	22	0.6	549	21	AAQ95216	Oligonucleotide fo
c 429	23	0.7	11394	24	ABK28221	DNA transcription	c 502	22	0.6	549	21	AAQ95306	Cat flea head and
c 430	23	0.7	11662	24	ABL33901	Human immune syste	c 503	22	0.6	553	21	AAQ79990	Cat flea head and
c 431	23	0.7	12069	24	ABK39931	Human chemically p	c 504	22	0.6	553	21	AAQ79990	Human secreted pro
c 432	23	0.7	13774	22	AAK83209	Human immune/haema	c 505	22	0.6	585	22	AAK82704	Human immune/haema
c 433	23	0.7	15548	24	ABL34154	Human immune syste	c 506	22	0.6	585	22	AAK82705	Human immune/haema
c 434	23	0.7	16299	22	AAK71100	Human immune/haema	c 507	22	0.6	566	22	AAK83940	Human polynucleoti
c 435	23	0.7	17949	22	AAH92228	Human signal trans	c 508	22	0.6	637	22	AAQ07877	Human secreted pro
c 436	23	0.7	18647	21	AAF21059	Human low adenosin	c 509	22	0.6	637	24	ABQ24140	Oligonucleotide fo
c 437	23	0.7	18648	21	AAK34937	Human adenosine re	c 510	22	0.6	642	21	ABQ24141	Oligonucleotide fo
c 438	23	0.7	18648	24	ABL65840	Lung cancer relate	c 511	22	0.6	649	24	ABQ52678	Oligonucleotide fo
c 439	23	0.7	18648	24	ABL69114	Kidney cancer rela	c 512	22	0.6	649	24	ABQ52679	Oligonucleotide fo
c 440	23	0.7	21537	24	ABL33998	Human immune syste	c 513	22	0.6	670	21	AAQ36232	Arabidopsis thalia
c 441	23	0.7	21748	23	ABL02520	Drosophila melanog	c 514	22	0.6	710	24	ABQ20510	Oligonucleotide fo
c 442	23	0.7	24012	22	AAK74877	Human immune/haema	c 515	22	0.6	710	24	ABQ20511	Oligonucleotide fo
c 443	23	0.7	25012	22	ABAI5431	Human nervous syst	c 516	22	0.6	750	14	AAQ35214	Rat synaptophysin
c 444	23	0.7	25955	22	ABAI9852	Human nervous syst	c 517	22	0.6	819	24	ABK35901	cdna sequence #292
c 445	23	0.7	28149	22	ABAI7961	Human nervous syst	c 518	22	0.6	936	24	ABQ48606	Oligonucleotide fo
c 446	23	0.7	31718	22	AAS39915	Genomic sequence #	c 519	22	0.6	936	24	ABQ48607	Oligonucleotide fo
c 447	23	0.7	31718	22	AAS39916	Genomic sequence #	c 520	22	0.6	937	19	AAV52661	Human native hepat

c 521	22	0.6	954	14	AAQ46148	NKG2. Tropaeolum	c 594	22	0.6	6129	24	ABK31237	Signal transductio
c 522	22	0.6	1006	24	ABN74683	Bovine embryonic g	595	22	0.6	6149	24	AAS63306	Chemically pretrea
c 523	22	0.6	1167	24	ADN17481	Rat glucose-depend	596	22	0.6	6239	24	ABL333776	Human immune syste
c 524	22	0.6	1297	20	AAS56827	X. laevis pRNDkk-1	597	22	0.6	6239	24	ABK28297	DNA transcription
c 525	22	0.6	1361	24	AAJ38827	Human PSNA cDNA #7	c 598	22	0.6	6253	24	ABK83716	Human cDNA differe
c 526	22	0.6	1409	21	AAZ97090	Human secreted pro	c 599	22	0.6	6254	24	ABL33620	Human immune syste
c 527	22	0.6	1545	24	ABQ67136	Human angiogenesis	c 600	22	0.6	6261	22	AAS46644	Tumour suppressor
c 528	22	0.6	1614	23	ABL25018	Drosophila melanog	c 601	22	0.6	6261	22	AAS46644	Tumour suppressor
c 529	22	0.6	1620	24	ABK48975	Physics-based gene	c 602	22	0.6	6261	22	AAS46644	Tumour suppressor
c 530	22	0.6	1894	22	ADN17491	Rat glucose-depend	c 603	22	0.6	6261	22	AAS61046	Human gene regulat
c 531	22	0.6	2192	23	ABV24684	Human prostate exp	c 604	22	0.6	6261	24	ABK31160	Signal transductio
c 532	22	0.6	2192	23	ABV25567	Human prostate exp	c 605	22	0.6	6261	24	ABK31161	Signal transductio
c 533	22	0.6	2192	23	ABV25890	Human prostate exp	c 606	22	0.6	6261	24	ABK31161	Signal transductio
c 534	22	0.6	2226	24	ABL24114	Drosophila melanog	c 607	22	0.6	6298	24	ABL32434	Human immune syste
c 535	22	0.6	2334	22	AAI58874	Human polynucleoti	c 608	22	0.6	6298	24	ABL32435	Human immune syste
c 536	22	0.6	2349	22	AAH41951	Putative human CLA	c 609	22	0.6	6436	24	ABL33693	Human immune syste
c 537	22	0.6	2441	23	ABL10994	Drosophila melanog	c 610	22	0.6	6436	24	ABL33693	Human immune syste
c 538	22	0.6	2451	20	AAV82439	Vascular endotheli	c 611	22	0.6	6475	24	ABL334249	Human immune syste
c 539	22	0.6	2567	20	AAZ52889	Human prostate tum	c 612	22	0.6	6588	23	ABU24492	Human immune syste
c 540	22	0.6	2582	22	AAH16248	Human cDNA sequenc	c 613	22	0.6	6615	24	ABQ67035	Human angiogenesis
c 541	22	0.6	2634	16	AAQ87841	Human neuronal cal	c 614	22	0.6	6615	24	ABQ67035	Human immune syste
c 542	22	0.6	2634	21	AAV1722	Human calcium chan	c 615	22	0.6	6775	24	ABQ67159	Human angiogenesis
c 543	22	0.6	2642	22	AAH14538	Human cDNA sequenc	c 616	22	0.6	6831	24	ABL33486	Human immune syste
c 544	22	0.6	2704	24	ABK88007	CDNA encoding huma	c 617	22	0.6	6852	24	ABL70311	Chemically treated
c 545	22	0.6	2712	16	AAQ87836	Human neuronal cal	c 618	22	0.6	6852	24	ABL70311	Chemically treated
c 546	22	0.6	2712	21	AAV17133	Human calcium chan	c 619	22	0.6	6852	24	AAS61249	Human gene regulat
c 547	22	0.6	2760	22	AAI26764	Human breast cance	c 620	22	0.6	6852	24	AAS61250	Human gene regulat
c 548	22	0.6	2772	22	AAS26279	Human cDNA encodin	c 621	22	0.6	6988	24	ABL34440	Human immune syste
c 549	22	0.6	2970	16	AAQ87835	Human neuronal cal	c 622	22	0.6	7070	24	ABN80054	Human chemically m
c 550	22	0.6	2970	21	AAV17132	Human calcium chan	c 623	22	0.6	7109	22	ABAI19555	Human nervous syst
c 551	22	0.6	2975	19	AAV15529	Human lymphoid-spe	c 624	22	0.6	7109	22	AAI199157	Human excretory re
c 552	22	0.6	2993	24	ABK84329	Human cDNA differe	c 625	22	0.6	7109	22	AAS32850	Human genomic DNA
c 553	22	0.6	2999	23	ABL17028	Drosophila melanog	c 626	22	0.6	7109	22	AAI63507	Human kidney relat
c 554	22	0.6	3001	21	AAH51775	Chromosome 13q31-q	c 627	22	0.6	7238	24	ABL33618	Human immune syste
c 555	22	0.6	3022	24	ABQ54722	Human ovarian anti	c 628	22	0.6	7346	22	AAI05261	Human reproductive
c 556	22	0.6	3129	22	ABAI16690	Human nervous syst	c 629	22	0.6	7346	23	ABU98145	Human testicular a
c 557	22	0.6	3230	23	ABL24328	Drosophila melanog	c 630	22	0.6	7471	22	AAS32548	Human genomic DNA
c 558	22	0.6	3240	19	AAV15530	Human lymphoid-spe	c 631	22	0.6	7593	23	ABL07930	Drosophila melanog
c 559	22	0.6	3471	14	AAQ46673	P mySB cDNA clone.	c 632	22	0.6	7635	23	ABL11336	Drosophila melanog
c 560	22	0.6	3720	24	ABK17123	Eucalyptus grandis	c 633	22	0.6	7669	24	ABL32629	Human immune syste
c 561	22	0.6	3741	22	AAQ91367	Peroxidase Swpa2 c	c 634	22	0.6	7903	22	AAS45403	Chemically pretrea
c 562	22	0.6	3742	22	AAQ91365	Peroxidase Swpa2 c	c 635	22	0.6	7903	24	ABL33363	Human immune syste
c 563	22	0.6	3957	22	ABA06411	Human cDNA SEQ ID	c 636	22	0.6	7903	24	ABL33363	DNA transcription
c 564	22	0.6	4282	23	AAI41898	Human GA733-2 gene	c 637	22	0.6	8087	24	ABL32742	Human immune syste
c 565	22	0.6	4809	23	ABL07632	Drosophila melanog	c 638	22	0.6	8087	24	ABL32743	Human immune syste
c 566	22	0.6	4936	23	ABL30286	Drosophila melanog	c 639	22	0.6	8319	22	AAS32546	Human immune syste
c 567	22	0.6	5040	24	ABL34405	Human immune syste	c 640	22	0.6	8413	24	ABL70519	Chemically treated
c 568	22	0.6	5152	22	AAK70178	Human immune/haema	c 641	22	0.6	8413	24	ABL34496	Human metastasis a
c 569	22	0.6	5170	22	AAI06377	Human reproductive	c 642	22	0.6	8577	24	ABL333787	Human immune syste
c 570	22	0.6	5179	24	ABL33397	Human immune syste	c 643	22	0.6	8753	24	ABL92271	Chemically treated
c 571	22	0.6	5179	24	ABK28404	DNA transcription	c 644	22	0.6	8998	24	ABL333707	Human immune syste
c 572	22	0.6	5413	22	AAS46694	Tumour suppressor	c 645	22	0.6	9021	22	AAS46326	Tumour suppressor
c 573	22	0.6	5413	23	ABL11337	Drosophila melanog	c 646	22	0.6	9789	17	AAI41852	CDNA encoding Plas
c 574	22	0.6	5426	22	ABAI16522	Human nervous syst	c 647	22	0.6	9899	24	ABL34443	Human immune syste
c 575	22	0.6	5525	24	ABK33929	Human DNA for stag	c 648	22	0.6	9965	24	ABL33527	Human immune syste
c 576	22	0.6	5525	24	ABL34462	Human metastasis a	c 649	22	0.6	10023	19	AAV52731	Human hepatocyte n
c 577	22	0.6	5546	24	ABK34004	Human DNA for stag	c 650	22	0.6	10132	24	ABL54372	Chemically treated
c 578	22	0.6	5546	24	ABL32390	Human immune syste	c 651	22	0.6	10132	24	ABL34081	Human immune syste
c 579	22	0.6	5632	24	ABL32436	Human immune syste	c 652	22	0.6	10140	22	AAH49201	Human CHO promote
c 580	22	0.6	5814	22	ABL70586	Chemically treated	c 653	22	0.6	10329	24	ABL34122	Human immune syste
c 581	22	0.6	5834	22	AAS45429	Chemically pretrea	c 654	22	0.6	10425	22	ABAI17962	Human nervous syst
c 582	22	0.6	5923	22	AAI90320	Pea auxin-induced	c 655	22	0.6	10736	22	ABK80161	Human immune/haema
c 583	22	0.6	5951	24	ABL33005	Human immune syste	c 656	22	0.6	10736	22	AAK89460	Human digestive sy
c 584	22	0.6	6031	22	AAS46622	Tumour suppressor	c 657	22	0.6	10762	24	ABL92322	Chemically treated
c 585	22	0.6	6059	22	ABL33480	Human immune syste	c 658	22	0.6	11046	24	ABK31537	Signal transductio
c 586	22	0.6	6063	24	ABL32748	Human immune syste	c 659	22	0.6	11735	22	AAS45329	Chemically pretrea
c 587	22	0.6	6120	24	ABN80277	Human chemically m	c 660	22	0.6	11735	24	AAS61142	Human gene regulat
c 588	22	0.6	6120	24	ABL70462	Chemically treated	c 661	22	0.6	11735	24	ABK28168	DNA transcription
c 589	22	0.6	6120	24	AAS61429	Human gene regulat	c 662	22	0.6	11836	22	AAS45394	Chemically pretrea
c 590	22	0.6	6120	24	ABK31489	Signal transductio	c 663	22	0.6	11836	22	AAS45395	Chemically pretrea
c 591	22	0.6	6128	24	ABQ67040	Human angiogenesis	c 664	22	0.6	11836	24	ABK28239	DNA transcription
c 592	22	0.6	6129	24	ABL70538	Chemically treated	c 665	22	0.6	11836	24	ABK28240	DNA transcription
c 593	22	0.6	6129	24	AAS61150	Human gene regulat	c 666	22	0.6	11934	22	AAK82197	Human immune/haema

c 667	22	0.6	12010	23	ABL06138	Drosophila melanog	c 740	22	0.6	66804	24	ABK87050	Human transporter
c 668	22	0.6	12620	22	ABA16691	Human nervous syst	c 741	22	0.6	68356	22	AAK67283	Human immune/haema
c 669	22	0.6	13158	22	AAK68742	Human immune/haema	c 742	22	0.6	68356	22	AAK83212	Human immune/haema
c 670	22	0.6	13573	24	ABL33869	Human immune syste	c 743	22	0.6	68940	20	AAK57351	Human chromosome 6
c 671	22	0.6	13830	22	AAO02659	Tomato chromosome	c 744	22	0.6	73334	24	ABL92319	Chemically treated
c 672	22	0.6	14253	24	ABL33495	Human immune syste	c 745	22	0.6	73334	24	ABL34125	Human immune syste
c 673	22	0.6	14426	22	AAK71817	Human immune/haema	c 746	22	0.6	81369	21	AAA97997	Human T gene DNA
c 674	22	0.6	14426	22	AAK73115	Human immune/haema	c 747	22	0.6	84539	24	ABL64158	Stomach cancer rel
c 675	22	0.6	14426	22	AAK87586	Human immune/haema	c 748	22	0.6	107820	22	AAI16230	Human ATP-binding
c 676	22	0.6	14426	22	AAI162924	Human genomic DNA	c 749	22	0.6	109906	24	ABK94411	DNA encoding endot
c 677	22	0.6	14448	22	AAK71815	Human immune/haema	c 750	22	0.6	112460	24	ABK83567	Human cDNA differe
c 678	22	0.6	14448	22	AAK73111	Human immune/haema	c 751	22	0.6	126512	24	ABN83429	Human transporter
c 679	22	0.6	14448	22	AAK87580	Human immune/haema	c 752	22	0.6	127197	24	AAI161370	Soybean 515002 reg
c 680	22	0.6	14448	22	AAI62922	Human genomic DNA	c 753	22	0.6	154465	24	AAD28763	Human AKAP allelic
c 681	22	0.6	14451	22	AAK71818	Human immune/haema	c 754	22	0.6	158245	24	AAD28762	Human AKAP allelic
c 682	22	0.6	14451	22	AAK87587	Human immune/haema	c 755	22	0.6	161425	22	AAH02340	Human AKAP10 gene
c 683	22	0.6	14451	22	AAI62925	Human genomic DNA	c 756	22	0.6	162025	24	AAH02339	Human AKAP10 gene
c 684	22	0.6	14451	22	AAI62925	Human genomic DNA	c 757	22	0.6	162025	24	AAH02339	Human AKAP allelic
c 685	22	0.6	14537	22	AAK46355	Tumour suppressor	c 758	22	0.6	162025	24	AAH02339	Human AKAP allelic
c 686	22	0.6	15201	22	AAK83176	Human immune/haema	c 759	22	0.6	183999	22	AAH02339	Human AKAP allelic
c 687	22	0.6	15364	22	AAK83152	Human immune/haema	c 760	22	0.6	222930	24	ABK84349	Human cDNA differe
c 688	22	0.6	15743	24	ABK28396	DNA transcription	c 761	22	0.6	319608	21	AAH51601	Human chromosome 1
c 689	22	0.6	15772	22	AAK83220	Human immune/haema	c 762	22	0.6	319608	22	AAH51601	Human chromosome 1
c 690	22	0.6	15811	23	ABL12090	Drosophila melanog	c 763	22	0.6	319608	22	AAH51601	Human chromosome 1
c 691	22	0.6	16037	22	AAK78529	Human immune/haema	c 764	22	0.6	1503900	22	AAK95240	Human neuroregulin-1
c 692	22	0.6	16037	24	ABK59947	Human secreted pro	c 765	21	0.6	1503900	22	AAK95240	Human neuroregulin-1
c 693	22	0.6	16107	22	AAK78528	Human immune/haema	c 766	21	0.6	21	21	AAK64523	PCR primer Int. ABF
c 694	22	0.6	16107	22	AAK65948	Human secreted pro	c 767	21	0.6	21	21	AAK64523	PCR primer G21. use
c 695	22	0.6	16235	22	AAK86192	Human immune/haema	c 768	21	0.6	32	22	AAK64523	Primer 603 to ampl
c 696	22	0.6	16235	22	AAK86192	Human immune/haema	c 769	21	0.6	41	22	AAK64523	hFIX gene AE3, age
c 697	22	0.6	18110	24	ABK15357	Human interleukin	c 770	21	0.6	50	22	AAK64523	hFIX gene AE3, age
c 698	22	0.6	18281	24	ABK132963	Human immune syste	c 771	21	0.6	51	22	AAK64523	Human SNP oligonuc
c 699	22	0.6	18340	22	AAI19368	Mammalian interleu	c 772	21	0.6	51	22	AAK64523	Human SNP oligonuc
c 700	22	0.6	18488	22	AAK83173	Human immune/haema	c 773	21	0.6	51	22	AAK64523	Human silent SNP c
c 701	22	0.6	18663	22	AAK67485	Human immune/haema	c 774	21	0.6	79	22	AAK64523	Human secreted pro
c 702	22	0.6	20300	24	ABK47337	Genomic nucleotide	c 775	21	0.6	101	22	AAK64523	hFIX gene AE3, age
c 703	22	0.6	20829	23	ABL14502	Drosophila melanog	c 776	21	0.6	102	24	ABL81741	hFIX gene AE3, el
c 704	22	0.6	21621	22	AAK74867	Human immune/haema	c 777	21	0.6	123	22	AAK64523	Human ovarian canc
c 705	22	0.6	23457	22	AAK74866	Human immune/haema	c 778	21	0.6	124	22	AAK64523	hFIX gene AE3, ag
c 706	22	0.6	23544	22	AAO05829	Human reproductive	c 779	21	0.6	125	22	AAK64523	hFIX gene AE3, ag
c 707	22	0.6	23544	23	ABL98393	Human testicular a	c 780	21	0.6	126	22	AAK64523	hFIX gene AE3, ag
c 708	22	0.6	23670	24	ABA97077	Tomato Hero gene c	c 781	21	0.6	127	22	AAK64523	hFIX gene AE3, ag
c 709	22	0.6	23683	24	ABL70482	Chemically treated	c 782	21	0.6	128	22	AAK64523	hFIX gene AE3, ag
c 710	22	0.6	23683	24	ABL34623	Human metastasis a	c 783	21	0.6	129	22	AAK64523	hFIX gene AE3, ag
c 711	22	0.6	24161	22	AAK80711	Human immune/haema	c 784	21	0.6	130	22	AAK64523	hFIX gene AE3, ag
c 712	22	0.6	25378	22	AAK80709	Human immune/haema	c 785	21	0.6	131	22	AAK64523	hFIX gene AE3, ag
c 713	22	0.6	26997	22	AAK46748	Tumour suppressor	c 786	21	0.6	132	22	AAK64523	hFIX gene AE3, ag
c 714	22	0.6	27689	24	AAK19494	Arabidopsis RPW8 c	c 787	21	0.6	133	22	AAK64523	hFIX gene AE3, ag
c 715	22	0.6	28136	22	AAK69755	Human immune/haema	c 788	21	0.6	134	22	AAK64523	hFIX gene AE3, ag
c 716	22	0.6	28149	22	ABA17961	Human nervous syst	c 789	21	0.6	134	22	AAK64523	hFIX gene AE3, ag
c 717	22	0.6	31405	22	AAK67293	Human immune/haema	c 790	21	0.6	135	22	AAK64523	hFIX gene AE3, ag
c 718	22	0.6	31405	22	AAK74865	Human immune/haema	c 791	21	0.6	135	22	AAK64523	hFIX gene AE3, ag
c 719	22	0.6	31405	22	AAK83153	Human immune/haema	c 792	21	0.6	136	22	AAK64523	hFIX gene AE3, ag
c 720	22	0.6	32192	22	ABA17963	Human nervous syst	c 793	21	0.6	136	22	AAK64523	hFIX gene AE3, ag
c 721	22	0.6	32193	22	AAK27848	DNA encoding novel	c 794	21	0.6	137	22	AAK64523	hFIX gene AE3, ag
c 722	22	0.6	32248	22	ABA20412	Human nervous syst	c 795	21	0.6	137	22	AAK64523	Human immune/haema
c 723	22	0.6	32248	22	AAK37122	Human musculoskele	c 796	21	0.6	137	22	AAK64523	Human immune/haema
c 724	22	0.6	32248	22	AAK26795	Human genomic DNA	c 797	21	0.6	137	22	AAK64523	hFIX gene AE3, ag
c 725	22	0.6	33942	22	AAK80281	Human immune/haema	c 798	21	0.6	137	22	AAK64523	hFIX gene AE3, ag
c 726	22	0.6	33942	22	AAK862174	Human immune/haema	c 799	21	0.6	138	22	AAK64523	hFIX gene AE3, ag
c 727	22	0.6	34769	22	AAK46778	Tumour suppressor	c 800	21	0.6	138	22	AAK64523	hFIX gene AE3, ag
c 728	22	0.6	38186	20	AAK32028	Human METHI relate	c 801	21	0.6	139	22	AAK64523	hFIX gene AE3, ag
c 729	22	0.6	38186	22	AAK90085	AC004449 cDNA clon	c 802	21	0.6	139	22	AAK64523	hFIX gene AE3, ag
c 730	22	0.6	41783	21	AAK21221	Human low adenosin	c 803	21	0.6	140	22	AAK64523	hFIX gene AE3, ag
c 731	22	0.6	41783	21	AAA35099	Human adenosine re	c 804	21	0.6	140	22	AAK64523	hFIX gene AE3, ag
c 732	22	0.6	41477	24	ABK84481	Human cDNA differe	c 805	21	0.6	141	22	AAK64523	hFIX gene AE3, ag
c 733	22	0.6	47108	24	ABK31511	Signal transductio	c 806	21	0.6	141	22	AAK64523	hFIX gene AE3, ag
c 734	22	0.6	49634	24	ABL68647	Kidney cancer rela	c 807	21	0.6	142	22	AAK64523	hFIX gene AE3, ag
c 735	22	0.6	53522	24	AAK30228	Human PKD1 gene.	c 808	21	0.6	142	22	AAK64523	hFIX gene AE3, ag
c 736	22	0.6	53526	17	AAK94101	Human PKD1 gene.	c 809	21	0.6	143	22	AAK64523	hFIX gene AE3, ag
c 737	22	0.6	53577	19	AAK18551	Human polycystic k	c 810	21	0.6	143	22	AAK64523	hFIX gene AE3, ag
c 738	22	0.6	53577	19	AAK94108	Human PKD1 locus b	c 811	21	0.6	144	22	AAK64523	hFIX gene AE3, ag
c 739	22	0.6	65057	23	ABL03490	Drosophila melanog	c 812	21	0.6	144	22	AAK64523	hFIX gene AE3, ag

813	21	0.6	145	22	AAF54096	hFIX gene AE3'' ag	C 886	21	0.6	404	23	ABV18543	Human prostate exp
814	21	0.6	145	22	AAF54127	hFIX gene AE3'' ag	C 887	21	0.6	408	23	ABV04866	Human prostate exp
815	21	0.6	146	22	AAF54095	hFIX gene AE3'' ag	C 888	21	0.6	409	23	AAI89061	Human polynucleoti
816	21	0.6	146	22	AAF54126	hFIX gene AE3'' ag	C 889	21	0.6	409	23	ABV10144	Human prostate exp
817	21	0.6	147	22	AAF54094	hFIX gene AE3'' ag	C 890	21	0.6	410	24	ABL79733	Human ovarian can
818	21	0.6	147	22	AAF54125	hFIX gene AE3'' ag	C 891	21	0.6	410	24	ABV32285	Human prostate exp
819	21	0.6	148	22	AAF54093	hFIX gene AE3'' ag	C 892	21	0.6	412	23	AAK58934	Human immune/haem
820	21	0.6	148	22	AAF54124	hFIX gene AE3'' ag	C 893	21	0.6	413	22	ABV31230	Human prostate exp
821	21	0.6	149	22	AAF54092	hFIX gene AE3'' ag	C 894	21	0.6	416	22	AAK96685	Human immune/haem
822	21	0.6	149	22	AAF54123	hFIX gene AE3'' ag	C 895	21	0.6	416	22	AAK98178	Human neuregulin g
823	21	0.6	150	22	AAF54091	hFIX gene AE3'' ag	C 896	21	0.6	416	22	AAK98178	Human polynucleoti
824	21	0.6	150	22	AAF54122	hFIX gene AE3'' ag	C 897	21	0.6	416	22	AAI91938	Human prostate exp
825	21	0.6	151	22	AAF54090	hFIX gene AE3'' ag	C 898	21	0.6	416	23	ABV35141	Human prostate exp
826	21	0.6	151	22	AAF54121	hFIX gene AE3'' ag	C 899	21	0.6	416	23	ABV35141	Human prostate exp
827	21	0.6	152	22	AAF54089	hFIX gene AE3'' ag	C 900	21	0.6	420	22	AAI87096	Human polynucleoti
828	21	0.6	152	22	AAF54120	hFIX gene AE3'' ag	C 901	21	0.6	422	23	ABV51084	Human prostate exp
829	21	0.6	153	22	AAF54088	hFIX gene AE3'' ag	C 902	21	0.6	422	23	AAI89138	Human polynucleoti
830	21	0.6	153	22	AAF54119	hFIX gene AE3'' ag	C 903	21	0.6	424	22	AAI84041	Human polynucleoti
831	21	0.6	154	22	AAF54087	hFIX gene AE3'' ag	C 904	21	0.6	426	23	ABV10058	Human prostate exp
832	21	0.6	160	22	AAI61473	Soybean 240017 reg	C 905	21	0.6	427	21	AAA28561	Human PC-1 gene in
833	21	0.6	170	21	AAI61548	Human secreted pro	C 906	21	0.6	428	22	AAK66386	Human immune/haem
834	21	0.6	188	22	AAI61667	Soybean 318013 reg	C 907	21	0.6	430	22	AAI17775	Human breast cance
835	21	0.6	193	22	AAK67054	Human immune/haem	C 908	21	0.6	436	22	AAI10700	Human breast cance
836	21	0.6	193	22	AAK67055	Human immune/haem	C 909	21	0.6	441	21	AAI1834	Human secreted pro
837	21	0.6	213	19	AAV16134	Microsatellite mar	C 910	21	0.6	443	22	AAI83572	Human polynucleoti
838	21	0.6	227	22	AAI61521	Soybean 240017 reg	C 911	21	0.6	448	23	ABV31316	Human prostate exp
839	21	0.6	239	22	AAI614403	Human reproductive	C 912	21	0.6	448	23	ABV40285	Human prostate exp
840	21	0.6	239	22	AAI614403	Human reproductive	C 913	21	0.6	449	22	AAK32417	Human bone marrow
841	21	0.6	240	22	AAI91712	Human genomic DNA	C 914	21	0.6	449	23	AAK32417	Human prostate exp
842	21	0.6	244	22	AAI61525	Soybean 240017 reg	C 915	21	0.6	449	24	ABV05849	Human prostate exp
843	21	0.6	247	21	AAI61532	Human secreted pro	C 916	21	0.6	460	23	ABV07201	Human genome-deriv
844	21	0.6	252	24	ABL68431	Kidney cancer rela	C 917	21	0.6	462	23	ABV43326	Human prostate exp
845	21	0.6	268	21	AAI61532	Human secreted pro	C 918	21	0.6	462	23	ABV43326	Human prostate exp
846	21	0.6	269	22	AAI61532	Human secreted pro	C 919	21	0.6	463	23	ABV40335	Human prostate exp
847	21	0.6	275	21	AAI61532	Human secreted pro	C 920	21	0.6	469	23	ABV59953	Human prostate exp
848	21	0.6	277	21	AAI61532	Human secreted pro	C 921	21	0.6	480	16	AAQ81474	HMG2 promoter II.
849	21	0.6	296	23	ABV59802	Human prostate exp	C 922	21	0.6	480	16	AAQ81474	HMG2 promoter II.
850	21	0.6	299	22	ABV59784	Human nervous syst	C 923	21	0.6	484	23	ABV15018	Human prostate exp
851	21	0.6	299	22	AAK64933	Human immune/haem	C 924	21	0.6	485	22	AAI16193	Human breast cance
852	21	0.6	299	22	AAK70243	Human immune/haem	C 925	21	0.6	487	23	AAI16193	DNA encoding novel
853	21	0.6	299	22	AAK70244	Human immune/haem	C 926	21	0.6	488	23	AAI16178	Human breast cance
854	21	0.6	304	23	AAI61532	Human immune/haem	C 927	21	0.6	492	23	ABV22727	Human prostate exp
855	21	0.6	305	22	AAK68337	cDNA #11 encoding	C 928	21	0.6	492	23	ABV22727	Human prostate exp
856	21	0.6	308	23	ABV59784	Human immune/haem	C 929	21	0.6	496	24	ABL86815	Human ovarian can
857	21	0.6	312	21	AAI61532	Human prostate exp	C 930	21	0.6	500	23	ABV39099	Human prostate exp
858	21	0.6	313	22	AAK70243	Human secreted pro	C 931	21	0.6	502	22	AAI11854	Human prostate exp
859	21	0.6	315	21	AAK70243	Human immune/haem	C 932	21	0.6	505	22	AAI12818	Human cDNA clone (
860	21	0.6	315	21	AAK70243	Human breast cance	C 933	21	0.6	515	22	AAH09732	Human cDNA clone (
861	21	0.6	317	23	ABV60229	Human immune/haem	C 934	21	0.6	517	24	ABN62972	Human cancer relat
862	21	0.6	326	21	AAI61532	Human prostate exp	C 935	21	0.6	526	23	ABV32217	Human prostate exp
863	21	0.6	334	22	AAI61532	Human secreted pro	C 936	21	0.6	526	23	ABV41148	Human prostate exp
864	21	0.6	339	22	AAK62643	Human polynucleoti	C 937	21	0.6	530	24	ABV01902	Human prostate exp
865	21	0.6	343	23	ABV61438	Human immune/haem	C 938	21	0.6	530	24	ABN64214	Human cancer relat
866	21	0.6	344	22	AAH93307	Human prostate exp	C 939	21	0.6	532	22	AAK65304	Human immune/haem
867	21	0.6	346	21	AAI61532	Plasmodium falci	C 940	21	0.6	547	24	ABQ14986	Oligonucleotide fo
868	21	0.6	356	22	AAI61532	Human secreted pro	C 941	21	0.6	547	24	ABQ14987	Oligonucleotide fo
869	21	0.6	360	21	AAI61532	Novel human diag	C 942	21	0.6	550	21	AAK94842	Cat flea hindgut a
870	21	0.6	373	24	ABL64614	Human secreted pro	C 943	21	0.6	552	22	AAK88826	Human digestive sy
871	21	0.6	375	22	AAK78393	Stomach cancer rel	C 944	21	0.6	553	21	AAK79900	Human secreted pro
872	21	0.6	375	22	AAK78393	Human immune/haem	C 945	21	0.6	561	21	AAK69740	Human ovarian can
873	21	0.6	375	22	AAK78393	Human immune/haem	C 946	21	0.6	561	24	ABN72634	Ovarian carcinoma
874	21	0.6	380	22	AAI61532	Novel human polynu	C 947	21	0.6	562	24	ABN60958	Human cancer relat
875	21	0.6	383	22	AAI61532	Human polynucleoti	C 948	21	0.6	563	22	AAH10207	Human cDNA clone (
876	21	0.6	388	24	ABL81123	Human breast cance	C 949	21	0.6	570	22	AAH13416	Human cDNA clone (
877	21	0.6	389	22	AAI99402	Human ovarian can	C 950	21	0.6	572	20	AAV88520	EST clone GM153
878	21	0.6	389	22	AAI99402	Human excretory re	C 951	21	0.6	572	22	AAH09154	Human cDNA clone (
879	21	0.6	389	22	AAI99402	Human polynucleoti	C 952	21	0.6	575	22	AAK80944	Human immune/haem
880	21	0.6	393	22	AAI61532	Human kidney relat	C 953	21	0.6	575	23	ABK42954	Genomic sequence #
881	21	0.6	393	22	AAI61532	Human breast cance	C 954	21	0.6	579	24	ABN63192	Human cancer relat
882	21	0.6	394	22	AAI91857	Human polynucleoti	C 955	21	0.6	580	22	AAK64801	Human immune/haem
883	21	0.6	395	22	AAI93016	Novel human diag	C 956	21	0.6	582	24	ABQ36542	Oligonucleotide fo
884	21	0.6	400	22	AAI61532	Human polynucleoti	C 957	21	0.6	582	24	ABQ36543	Oligonucleotide fo
885	21	0.6	401	22	AAI80907	Human polynucleoti	C 958	21	0.6	589	23	ABV58556	Human cDNA clone (

959 21 0.6 592 22 ABA62687 Human foetal liver  
960 21 0.6 592 22 ABA29991 Probe #8457 for ge  
961 21 0.6 592 22 AAK11065 Human brain expres  
962 21 0.6 592 22 AAK36891 Human bone marrow  
963 21 0.6 592 22 AAI17741 Probe #7674 for ge  
964 21 0.6 592 22 AAI42689 Probe #11375 used  
965 21 0.6 601 23 ABV52214 Human prostate exp  
966 21 0.6 608 23 ABV1216 Human prostate exp  
967 21 0.6 610 23 ABV30324 Human prostate exp  
968 21 0.6 610 23 ABV50324 Human prostate exp  
969 21 0.6 612 22 AAL25036 Human breast cance  
970 21 0.6 615 23 ABV14940 Human prostate exp  
971 21 0.6 615 23 ABK25236 Genomic sequence #  
972 21 0.6 616 22 AAH87648 Peppermint plant o  
973 21 0.6 624 22 AAK74618 Human immune/haema  
974 21 0.6 624 22 AAK74619 Human immune/haema  
975 21 0.6 624 22 AAK74620 Human immune/haema  
976 21 0.6 624 23 ABV39025 Human prostate exp  
977 21 0.6 624 23 ABV44812 Human prostate exp  
978 21 0.6 624 23 ABV44885 Human prostate exp  
979 21 0.6 625 21 AAZ80509 Human colon cancer  
980 21 0.6 626 23 AAV48170 Human prostate exp  
981 21 0.6 627 22 AAL12591 Human breast cance  
982 21 0.6 627 22 AAK59153 Human immune/haema  
983 21 0.6 637 22 AAD07877 Human secreted pro  
984 21 0.6 654 22 AAL37107 Human musculoskele  
985 21 0.6 662 24 ABQ14046 Oligonucleotide fo  
986 21 0.6 662 24 ABQ14047 Oligonucleotide fo  
987 21 0.6 672 22 AAL36427 Human musculoskele  
988 21 0.6 699 22 ABA21522 Human nervous syst  
989 21 0.6 700 22 AAH92455 Human inflammatory  
990 21 0.6 700 22 AAH92911 Human inflammatory  
991 21 0.6 709 24 ABQ31714 Oligonucleotide fo  
992 21 0.6 709 24 ABQ31715 Oligonucleotide fo  
993 21 0.6 715 23 ABV11139 Human prostate exp  
994 21 0.6 735 22 AAL21464 Human breast cance  
995 21 0.6 739 22 AAS28421 Genomic sequence #  
996 21 0.6 739 22 AAS28422 Genomic sequence #  
997 21 0.6 739 23 ABV18384 Human prostate exp  
998 21 0.6 749 21 AAC46565 Zea mays DNA fragm  
999 21 0.6 749 21 AAC46565 Zea mays DNA fragm  
c1000 21 0.6 757 22 AAI96793 Human neuroblastom

ALIGNMENTS

RESULT 1  
ID AAA64507 standard; DNA; 9048 BP.  
XX  
AC AAA64507;  
XX  
DT  
XX  
XX  
02-JAN-2001 (first entry)  
DE Nucleotide sequence comprising the human FEZ1 gene.  
XX  
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200050565-A2.  
XX  
PD 31-AUG-2000.  
XX  
PF 25-FEB-2000; 2000WO-US04950.  
XX  
PR 25-FEB-1999; 99US-0121537.  
XX

PA (UVJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Croce CM, Ishii H;  
XX WPI; 2000-558396/51.  
XX  
XX  
PT New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -  
XX  
XX Claim 2; Fig 5A; 255pp; English.  
XX  
XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour  
XX suppressor gene, located at chromosome location 8p22. Decreased or no  
XX expression of FEZ1 is detected in a variety of cancer cells. Expression  
XX of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts  
XX with tubulin, with microtubules, and with protein Efi-gamma.  
XX Post-translational phosphorylation and dephosphorylation modulates the  
XX effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are  
XX useful for inducing cells to proliferate. Compounds which modulate FEZ1  
XX association with tubulin are useful for alleviating tubulin hyper- or  
XX hypo- polymerisation disorders, such as those associated with aberrant  
XX initiation of mitosis, modulation of the initiation and rate of cell  
XX proliferation and cell growth, modulation of cell shape, cell rigidity,  
XX cell motility, rate and stage of cellular DNA replication, intracellular  
XX distribution of organelles, metastatic potential of cell and cellular  
XX transformation from a non-cancerous to cancerous phenotype. Compounds  
XX which modulate FEZ1 binding and phosphorylation are also useful for  
XX alleviating a disorder, such as tumorigenesis, tumour survival, growth  
XX and metastasis.  
SQ Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;  
Query Match 100.0%; Score 3473; DB 21; Length 9048;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGCTGCCCTGGGGGCATCTTGAATACAGCTGGAGCTTTGTGCATCATTTACACAGA 60  
Db 871 AGCTGCCCTGGGGGCATCTTGAATACAGCTGGAGCTTTGTGCATCATTTACACAGA 930  
Qy 61 CTAGGGCAAAAGGAGGCCAGGCTGAGAAATCAGCCCTCACACAGCTCAAGCCCTCG 120  
Db 931 CTAGGGCAAAAGGAGGCCAGGCTGAGAAATCAGCCCTCACACAGCTCAAGCCCTCG 990  
Qy 121 TCGTCCACAGTGGGACACTGAAATCAATTTCTTATTCAGTCTCTGCCCCCTTGCCT 180  
Db 991 TCGTCCACAGTGGGACACTGAAATCAATTTCTTATTCAGTCTCTGCCCCCTTGCCT 1050  
Qy 181 GGGGAATGAATCCCGGCTTTGATTTACTAGGAAGAGCCCTCTATGTTTGCATAGAGC 240  
Db 1051 GGGGAATGAATCCCGGCTTTGATTTACTAGGAAGAGCCCTCTATGTTTGCATAGAGC 1110  
Qy 241 ATTACAGCTTTCAAATTAAGGGCTTGTAACTCTGAAGCACTCTACAGGAAATTTAC 300  
Db 1111 ATTACAGCTTTCAAATTAAGGGCTTGTAACTCTGAAGCACTCTACAGGAAATTTAC 1170  
Qy 301 AGTTTTAAAAGAGTCTGATTTGGAGTGAGCCCTCCCAACCCCTGTAAAGGAGCCAGTC 360  
Db 1171 AGTTTTAAAAGAGTCTGATTTGGAGTGAGCCCTCCCAACCCCTGTAAAGGAGCCAGTC 1230  
Qy 361 CGTCTCTTGTCTCAGGCTTAAATGGAAGAGGCACTGAACAGGAAGAGGGATGACCTTAA 420  
Db 1231 CGTCTCTTGTCTCAGGCTTAAATGGAAGAGGCACTGAACAGGAAGAGGGATGACCTTAA 1290  
Qy 421 AGAGGGAAGCAAGCTCGGCCAGCTGATGCCCTTAATTTGCCCCCACACAGAGACTAGAG 480  
Db 1291 AGAGGGAAGCAAGCTCGGCCAGCTGATGCCCTTAATTTGCCCCCACACAGAGACTAGAG 1350  
Qy 481 CAGGAGCTCAAGATGGTATTATACCTCGGGAGGCTGGGCAAGCTGGTGGCAGTT 540  
Db 1351 CAGGAGCTCAAGATGGTATTATACCTCGGGAGGCTGGGCAAGCTGGTGGCAGTT 1410





Db 3571 TCCTTTCTCTATTTCCACCCCTATCCCCCATCAAAATTTGGCCAGAGCATGATGA 3630  
Qy 2761 AAACCGAAGCCACAGGTTAGACCCATGTCCTCTGGATCTTGGCCATCTGGGGTCATGGG 2820  
Db 3631 AAACCGAAGCCACAGGTTAGACCCATGTCCTCTGGATCTTGGCCATCTGGGGTCATGGG 3690  
Qy 2821 AGACCAAGGCCAGTCTGGCTGAATCTTAAGAGTGAATGAAGTCCAGAGCATGTGGCTCTA 2880  
Db 3691 AGACCAAGGCCAGTCTGGCTGAATCTTAAGAGTGAATGAAGTCCAGAGCATGTGGCTCTA 3750  
Qy 2881 CAGAAATGATCTTTGGAACTAGCCCTGGAAAGCCACCTTTCACATTTCTTTACAGTAGAAA 2940  
Db 3751 CAGAAATGATCTTTGGAACTAGCCCTGGAAAGCCACCTTTCACATTTCTTTACAGTAGAAA 3810  
Qy 2941 TTTCCCTTGGCCCTCAGTGAACACTGACAGTCTCTGGAGAAATCCGACCTACCCAGG 3000  
Db 3811 TTTCCCTTGGCCCTCAGTGAACACTGACAGTCTCTGGAGAAATCCGACCTACCCAGG 3870  
Qy 3001 ATGGTGCTTGGGACCAAGAAATTTTCATTCGAAGGCCAACCTGTATTTCATGCCACGAAGG 3060  
Db 3871 ATGGTGCTTGGGACCAAGAAATTTTCATTCGAAGGCCAACCTGTATTTCATGCCACGAAGG 3930  
Qy 3061 CAGTGACACAGTCTAGTGGCTGAGGATGGCCCTGGCTTTGAACCTCAGCTTGACCACTTAT 3120  
Db 3931 CAGTGACACAGTCTAGTGGCTGAGGATGGCCCTGGCTTTGAACCTCAGCTTGACCACTTAT 3990  
Qy 3121 GATCAGGTGATTTGAATACATTAAGCATGGTGGCAATGGGGTATAGTAACTGT 3180  
Db 3991 GATCAGGTGATTTGAATACATTAAGCATGGTGGCAATGGGGTATAGTAACTGT 4050  
Qy 3181 TGGGATCAAACTCTACCTTATATTTATATATATATATATATATATATATATATATATAT 3240  
Db 4051 TGGGATCAAACTCTACCTTATATTTATATATATATATATATATATATATATATATATAT 4110  
Qy 3241 ATATATTAGCCCTCAGGCTGGTCTCACTTCCAGAGCTTTTGTATCATAACTCTCTGTGC 3300  
Db 4111 ATATATTAGCCCTCAGGCTGGTCTCACTTCCAGAGCTTTTGTATCATAACTCTCTGTGC 4170  
Qy 3301 CTCAGTTTCATGATTAATAGGACTACTATAGTACCTTCTATCCTGCTGCTGCTGCTGCTG 3360  
Db 4171 CTCAGTTTCATGATTAATAGGACTACTATAGTACCTTCTATCCTGCTGCTGCTGCTGCTG 4230  
Qy 3361 GAATAGATGAGCAATGATGGCTTGGCACTTATATAACACTACAAATATTATAGTGAAGT 3420  
Db 4231 GAATAGATGAGCAATGATGGCTTGGCACTTATATAACACTACAAATATTATAGTGAAGT 4290  
Qy 3421 ATGTTTATAATAATATCTTCTGTGGCTAGGCGTGGTGGCTCAGCCTGCA 3473  
Db 4291 ATGTTTATAATAATATCTTCTGTGGCTAGGCGTGGTGGCTCAGCCTGCA 4343

RESULT 2  
ID AAS30637  
XX AAS30637 standard; DNA; 2411 BP.  
AC AAS30637;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE DNA encoding novel lung cancer antigen, Seq ID No 89.  
XX  
KW Human; lung cancer; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW neotropic; neuroprotective; antibacterial; virucide; fungicide;  
KW ophthalmological; autoimmune disease; rheumatoid arthritis; neoplasm;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; skin aging;  
KW ocular disorder; wound healing; organ transplantation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155300-A2.  
XX

PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01238.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI; 2001-465565/50.  
XX  
PT Isolated nucleic acid molecule encoding a lung cancer antigen is used  
in preventing, treating or ameliorating a medical condition  
XX  
PS Disclosure; SEQ ID No 89; 475pp; English.  
XX  
CC The invention relates to novel isolated lung cancer antigen  
polynucleotides (I) and polypeptides (II). (I) and (II) are used to  
prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are  
also used in diagnosing a pathological condition or susceptibility to a  
pathological condition, in particular, lung cancer. The antibodies to  
(II) can also be used in alleviating symptoms associated with the  
disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
treated include autoimmune diseases e.g. rheumatoid arthritis,  
hyperproliferative disorders e.g. neoplasms of the breast or liver,  
cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
ocular disorders e.g. corneal infection. The polypeptides can also be  
used to aid wound healing and epithelial cell proliferation, to prevent  
skin aging due to sunburn, to maintain organs before transplantation, for  
supporting cell culture of primary tissues, to regenerate tissues and in  
chemotaxis. AAS30580-AAS30685 represent novel human lung cancer antigen  
coding sequences, PCR primers and related sequences of the invention.  
CC Note: The sequence data for this patent did not form part of the  
printed specification, but was obtained in electronic format directly  
from WIPO at: ffp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2411 BP; 558 A; 681 C; 733 G; 439 T; 0 other;  
Query Match 48.3%; Score 1677; DB 22; Length 2411;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 AGCTGCGCCTGGGGGCATCTTTGAATACAGGCTGGAGTTTGTGCATCATTACCAGAGA 60  
Db 531 AGCTGCGCCTGGGGGCATCTTTGAATACAGGCTGGAGTTTGTGCATCATTACCAGAGA 590  
Qy 61 CTAGGGCAAGAGGAGGCCAGGCACTGAGAAATCCAGCCCTCACACAGCTCAAGCCCTCG 120  
Db 591 TTAGGGCAAGAGGAGGCCAGGCACTGAGAAATCCAGCCCTCACACAGCTCAAGCCCTCG 650  
Qy 121 TGCCTCCACAGTGGACACTGAAATCAATTTTCTTATTCAGTCTCTGCCCCCTGGCCT 180  
Db 651 TGCCTCCACAGTGGACACTGAAATCAATTTTCTTATTCAGTCTCTGCCCCCTGGCCT 710  
Qy 181 GGGGAAATGAATCCCGGCTTTTGAATTTACTAGGAAGAGCCCTTTATGTTTGCATAGAGC 240  
Db 711 GGGGAAATGAATCCCGGCTTTTGAATTTACTAGGAAGAGCCCTTTATGTTTGCATAGAGC 770  
Qy 241 ATTACAGCTTTTCAAAATTAAGGGCTTGTAACTGTGAAGCACTCTACAGGGAATTTAC 300  
Db 771 ATTACAGCTTTTCAAAATTAAGGGCTTGTAACTGTGAAGCACTCTACAGGGAATTTAC 830  
Qy 301 AGTTTAAAAAGGATCGTGAATTTGGAGTGGAGCTCCCAACCCCTGTAGGAGGCCAGTGC 360  
Db 831 AGTTTAAAAAGGATCGTGAATTTGGAGTGGAGCTCCCAACCCCTGTAGGAGGCCAGTGC 890  
Qy 361 CGTGTCTCTGCTCCAGGCTTAATGAAGAGGCACTGAACAGGAAGAGGATGGAACCTTAA 420



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Db 891 CGTGTCTTGTCTCAGGCTTAATGGAAGAGGAGTGAACAGAGAGGAGTGAACCTAA 950
Qy 421 AGAGGACAGCAAGCTCGGCCAGGCTGATGCCCTAACTTGGCCCAACAGAGAGCTAGAG 480
Db 951 AGAGGACAGCAAGCTCGGCCAGGCTGATGCCCTAACTTGGCCCAACAGAGAGCTAGAG 1010
Qy 481 CAGAGAGCTCAGATGGTATTATACCTCGGAGGCTGGGCAAGCTGGTGGCAGGTT 540
Db 1011 CAGAGAGCTCAGATGGTATTATACCTCGGAGGCTGGGCAAGCTGGTGGCAGGTT 1070
Qy 541 GCTATTTTCATAGAAACAAAGTCCCAAGTCGCATTTAGGGTTTTTCCCTTCCTAAAGAGAT 600
Db 1071 GCTATTTTCATAGAAACAAAGTCCCAAGTCGCATTTAGGGTTTTTCCCTTCCTAAAGAGAT 1130
Qy 601 GACATTCAGCTGCTTCAAAGCAACAGGCAAGGTCTGTGAGCAATGACCAAGAGGGGT 660
Db 1131 GACATTCAGCTGCTTCAAAGCAACAGGCAAGGTCTGTGAGCAATGACCAAGAGGGGT 1190
Qy 661 GCTGGTGGCTCAGAGAGCCAGACTGGCTCAAGTCCGACCGGTGCTGGGAGGGA 720
Db 1191 GCTGGTGGCTCAGAGAGCCAGACTGGCTCAAGTCCGACCGGTGCTGGGAGGGA 1250
Qy 721 GGGTGCAATGCGCGCAGGAGGAGCATGAGTCAACCGGCTCTTTCTCTACAGGCT 780
Db 1251 GGGTGCAATGCGCGCAGGAGGAGCATGAGTCAACCGGCTCTTTCTCTACAGGCT 1310
Qy 781 CCGAAGAGGTGCAAGTGAAGCCCAACAGCCTTTCAAGCCTGTGTGCTGCCAGGTCAGAGCCA 840
Db 1311 CCGAAGAGGTGCAAGTGAAGCCCAACAGCCTTTCAAGCCTGTGTGCTGCCAGGTCAGAGCCA 1370
Qy 841 TCCTGCACTCTCCCGGAGAGTCCAGCCACAGCTGCAACCCGCCCTCCAGACAGC 900
Db 1371 TCCTGCACTCTCCCGGAGAGTCCAGCCACAGCTGCAACCCGCCCTCCAGACAGC 1430
Qy 901 CCAAGGAGCAGGAGCTGAAGCCTGCGCTGTGCTCTGGGGCGCTGTCAAGCTCCCGCGGA 960
Db 1431 CCAAGGAGCAGGAGCTGAAGCCTGCGCTGTGCTCTGGGGCGCTGTCAAGCTCCCGCGGA 1490
Qy 961 ACTCATGTTCAGGCTGCCCCACACACAGCACAGCAGCAGCAGTACAGCTGGACCCGCTGG 1020
Db 1491 ACTCATGTTCAGGCTGCCCCACACACAGCACAGCAGCAGTACAGCTGGACCCGCTGG 1550
Qy 1021 TCACACCGTGGGACCCACAGCCGTTTTGGGGGCTCGGCCCAACATACCCAGGGCA 1080
Db 1551 TCACACCGTGGGACCCACAGCCGTTTTGGGGGCTCGGCCCAACATACCCAGGGCA 1610
Qy 1081 TCCTCTCCAGGACAGCAACATGATGAGCTGGAAGGCTCTGTCTCTTCGACCGAGGTA 1140
Db 1611 TCCTCTCCAGGACAGCAACATGATGAGCTGGAAGGCTCTGTCTCTTCGACCGAGGTA 1670
Qy 1141 GCAAGCTGGGCCACTCGAAACAGGCAGACAAGGGCCCTCGTGTGTCCGCTTCCGCCATCT 1200
Db 1671 GCAAGCTGGGCCACTCGAAACAGGCAGACAAGGGCCCTCGTGTGTCCGCTTCCGCCATCT 1730
Qy 1201 CCAGGAGAGTGCAGCATCCAGAGCTGGAACAGAGCTGTTGGAGGAGGAGGGCGCC 1260
Db 1731 CCAGGAGAGTGCAGCATCCAGAGCTGGAACAGAGCTGTTGGAGGAGGAGGGCGCC 1790
Qy 1261 TCAGAGAGCTCAGCGAGCTTTCAGGAGAGGAGCTTGCCTCCAGCTGSCCTACGAGG 1320
Db 1791 TCAGAGAGCTCAGCGAGCTTTCAGGAGAGGAGCTTGCCTCCAGCTGSCCTACGAGG 1850
Qy 1321 AGCGCCCGCGCTGTCAGGAGCAGCTGAGGGCCCGGAGCCCAAGAGCGGCAACAGC 1380
Db 1851 AGCGCCCGCGCTGTCAGGAGCAGCTGAGGGCCCGGAGCCCAAGAGCGGCAACAGC 1910
Qy 1381 TCAGAGAGCTTCCAGAGAGCCAGCGCGGAGAGCTTCTGCACTGTCAGGTACTGC 1440
Db 1911 TCAGAGAGCTTCCAGAGAGCCAGCGCGGAGAGCTTCTGCACTGTCAGGTACTGC 1970
Qy 1441 AGCTTCAGAGGAGAGCGGAGCTCCGCGAGGAGCTTCGAGAGCTCATGAGGAGCAGG 1500
Db 1971 AGCTTCAGAGGAGAGCGGAGCTTCGCGAGGAGCTTCGAGAGCTCATGAGGAGCAGG 2030
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Qy 1501 ACCTGCTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAACACAGCTTCGGCCCCCGGC 1560
Db 2031 ACCTGCTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAACACAGCTTCGGCCCCCGGC 2090
Qy 1561 TGGAGGAGACCCAGTGGAGGTGAGGCCACACAGGGCTCATGGTTTGGGTGGTTCAGCGG 1620
Db 2091 TGGAGGAGACCCAGTGGAGGTGAGGCCACACAGGGCTCATGGTTTGGGTGGTTCAGCGG 2150
Qy 1621 TTTGGCCCAAGTACCCCTCTCTCTTCTGGTGTGGCCAAATAGCGTGCAAAACACAGACCG 1680
Db 2151 TTTGGCCCAAGTACCCCTCTCTCTTCTGGTGTGGCCAAATAGCGTGCAAAACACAGACCG 2210
Qy 1681 CGCAGGCAAGCGGGCTTAATGTGTGCTTTATCACCACAAAGAGGGGCTCCCTGCAAAAC 1740
Db 2211 CGCAGGCAAGCGGGCTTAATGTGTGCTTTATCACCACAAAGAGGGGCTCCCTGCAAAAC 2270
Qy 1741 CATGTTGGGGATCGACTTACATCTGAGCTTCTCTGTCCCAACCATCACCCTCATGGC 1800
Db 2271 CATGTTGGGGATCGACTTACATCTGAGCTTCTCTGTCCCAACCATCACCCTCATGGC 2330
Qy 1801 TCCTAGATTTTCAGTTTCCCAAGTGAAGCTTAAATCATGAAGCCGGAAGCCAGATGACCA 1860
Db 2331 TCCTAGATTTTCAGTTTCCCAAGTGAAGCTTAAATCATGAAGCCGGAAGCCAGATGACCA 2390
Qy 1861 AGCCCCAGCCAGGCTGTGGGC 1881
Db 2391 AGCCCCAGCCAGGCTGTGGGC 2411

RESULT 3
AAS28699
ID AAS28699 standard; DNA; 2411 BP.
XX
AC AAS28699;
XX
XX
DT 07-NOV-2001 (first entry)
XX
DE Genomic sequence #539 encoding for novel human respiratory antigen.
XX
KW Human; respiratory antigen; respiratory disorder; throat disorder;
KW lung disorder; nose disorder; lung cancer; gene therapy; cycostatic;
KW anti allergic; anti asthmatic; anti inflammatory; olfactory;
KW respiratory active; ds.
XX
OS Homo sapiens.
XX
XX
PN WO200155448-A1.
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US01333.
XX
XX
PR 31-JAN-2000; 2000US-0179055.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
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Query Match		48.3%;	Score 1677;	DB 22;	Length 2411;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1877;		Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	AGCTGCGCTCGGGGCATCTTTGTAATACAGCTGGAGTTTGTCTATCATTTACCAGAGA	60		
Db	531	AGCTGCGCTCGGGGCATCTTTGTAATACAGCTGGAGTTTGTCTATCATTTACCAGAGA	590		
Qy	61	CTAGGGCAAGAGAGGCCCGCCAGCAGCTGAGAAATTCAGAGCCCTCACACCACTCAAGCCCTCG	120		
Db	591	TTAGGGCAAGAGAGGCCCGCCAGCAGCTGAGAAATTCAGAGCCCTCACACCACTCAAGCCCTCG	650		
Qy	121	TGCGTCCACAGTGGACACCTGAAATCAATTTTCTATTCAGTCTCTGCCCCCTTGCCCT	180		
Db	651	TGCGTCCACAGTGGACACCTGAAATCAATTTTCTATTCAGTCTCTGCCCCCTTGCCCT	710		
Qy	181	GGGGAATGATCCCGGCTTTGATTTACTAGGAAGAGCTCTTATGTTTGCATAGAGC	240		
Db	711	GGGGAATGATCCCGGCTTTGATTTACTAGGAAGAGCTCTTATGTTTGCATAGAGC	770		
Qy	241	ATTCAGCTTTTCAAAATTAAGGGCTTGTAAACTGTGAAGCACTCTACCAAGGAAATTAAC	300		
Db	771	ATTCAGCTTTTCAAAATTAAGGGCTTGTAAACTGTGAAGCACTCTACCAAGGAAATTAAC	830		
Qy	301	AGTTTAAAAAGGATCGTGATTTTGGAGTGAGCCCTCCCAACCCCTGTAAAGGAGGCCAGGTC	360		
Db	831	AGTTTAAAAAGGATCGTGATTTTGGAGTGAGCCCTCCCAACCCCTGTAAAGGAGGCCAGGTC	890		
Qy	361	CGTGCTCTTGCTCCAGGCTTAATGGAAGAGGAGTGAACAGGAAGAGGATGACACTTAA	420		
Db	891	CGTGCTCTTGCTCCAGGCTTAATGGAAGAGGAGTGAACAGGAAGAGGATGGAACCTTAA	950		
Qy	421	AGAGGGACAGCAAGCTCGGCCAGCTGATGCCCTAACTTGGCCACACAGAGAGCTAGAG	480		
Db	951	AGAGGGACAGCAAGCTCGGCCAGCTGATGCCCTAACTTGGCCACACAGAGAGCTAGAG	1010		
Qy	481	CAGGAGCCTCAAGATGTTATTTATCACCTCGGGAGGCTGGGGCAAGCTGGTGCGAGGTT	540		
Db	1011	CAGGAGCCTCAAGATGTTATTTATCACCTCGGGAGGCTGGGGCAAGCTGGTGCGAGTT	1070		
Qy	541	GCTATTTATAGAACAAAGTCCCAAGTCCGCAATAGGGTTTTCCTCTCAAGAGAGAT	600		
Db	1071	GCTATTTATAGAACAAAGTCCCAAGTCCGCAATAGGGTTTTCCTCTCAAGAGAGAT	1130		
Qy	601	GACATTGAGCTGCTTCAAGCAACAGGCAAGTCTGCTGAGACAAATTCACCAAGAGGGGT	660		
Db	1131	GACATTGAGCTGCTTCAAGCAACAGGCAAGTCTGCTGAGACAAATTCACCAAGAGGGGT	1190		
Qy	661	GCTGCTGCTCTCAGAGAGCCAGACTGGCTCAAGGTCGGCACGCGTGCCTGGGGAGGGA	720		
Db	1191	GCTGCTGCTCTCAGAGAGCCAGACTGGCTCAAGGTCGGCACGCGTGCCTGGGGAGGGA	1250		
Qy	721	GGGTGCAATGCGCGCAGAGGAGGAGCATGAGTCAACCGGCTCTTTTCTCTACAGGGCT	780		
Db	1251	GGGTGCAATGCGCGCAGAGGAGGAGCATGAGTCAACCGGCTCTTTTCTCTACAGGGCT	1310		
Qy	781	CCGAGAGGGTGCAAGTGGAGGCCACAGCTTCAAGCCTGTCTGCCAGGTCAGGAGCCA	840		
Db	1311	CCGAGAGGGTGCAAGTGGAGGCCACAGCTTCAAGCCTGTCTGCCAGGTCAGGAGCCA	1370		
Qy	841	TCCTGCACTCTCTCCCGGAGAGTCCAGCCACCACTGACCTGACCCCGCCCTCCAGACAAGC	900		
Db	1371	TCCTGCACTCTCTCCCGGAGAGTCCAGCCACCACTGACCTGACCCCGCCCTCCAGACAAGC	1430		
Qy	901	CCAGGAGCAGAGCTGAAGCTTGCCCTGTGCTCTGGGGCGCTGTACAGCTCCCGCCGGA	960		
Db	1431	CCAGGAGCAGAGCTGAAGCTTGCCCTGTGCTCTGGGGCGCTGTACAGCTCCCGCCGGA	1490		
Qy	961	ACTCCATGCTCAGCTGCCACACACAGCAGCAGCAGTACAGCTGACCGCTGG	1020		
Db	1491	ACTCCATGCTCAGCTGCCACACACAGCAGCAGCAGTACAGCTGACCGCTGG	1550		

Qy	1021	TCACACCCGTGGGACCCCAAGCCGTTTTTGGGGCTCCGCCCAACAACATCACCCAGGGCA	1080
Db	1551	TCACACCCGTGGGACCCCAAGCCGTTTTTGGGGCTCCGCCCAACAACATCACCCAGGGCA	1610
Qy	1081	TCGTCTCTCCAGGACAGCAACATGATGAGCTCTGAAGGCTCTGTCTCTTCTCCACGGAGTA	1140
Db	1611	TCGTCTCTCCAGGACAGCAACATGATGAGCTCTGAAGGCTCTGTCTCTTCTCCACGGAGTA	1670
Qy	1141	GCAAGCTGGGCACTCTCGAAACAAGGCAGACAAGGSCCTCTCGTGTCTCGCTCCCCCATCT	1200
Db	1671	GCAAGCTGGGCACTCTCGAAACAAGGCAGACAAGGSCCTCTCGTGTCTCGCTCCCCCATCT	1730
Qy	1201	CCACGGACGAGTGCAGCATCCAGAGCTGGAACAAGAGCTCTTGGAGAGGAGGCGGCC	1260
Db	1731	CCACGGACGAGTGCAGCATCCAGAGCTGGAACAAGAGCTCTTGGAGAGGAGGCGGCC	1790
Qy	1261	TCCAGAGCTGCAGCGCAGCTTTTTCAGGAGAGGAGCTTGCCCTCCAGCTGCGCTACGAGG	1320
Db	1791	TCCAGAGCTGCAGCGCAGCTTTTTCAGGAGAGGAGCTTGCCCTCCAGCTGCGCTACGAGG	1850
Qy	1321	AGCGCGCGCGCGCTGCAGGAGCGAGCTGGAGGSCCGGAGCCCAAAAGGCGGCAACAAGC	1380
Db	1851	AGCGCGCGCGCGCTGCAGGAGCGAGCTGGAGGSCCGGAGCCCAAAAGGCGGCAACAAGC	1910
Qy	1381	TCAAGCAGGCTCTCGACAAGAGCCAGCGCGCAGCAGGCTCCTGCACCTGCAGGTACTGC	1440
Db	1911	TCAAGCAGGCTCTCGACAAGAGCCAGCGCGCAGCAGGCTCCTGCACCTGCAGGTACTGC	1970
Qy	1441	AGCTTCAGCAGGAGAAAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTCTATGAAGAGCAGG	1500
Db	1971	AGCTTCAGCAGGAGAAAGCGGCGAGCTCCGCGCAGGAGCTCGAGAGCTCTATGAAGAGCAGG	2030
Qy	1501	ACCTGCTGGAGACCAAGCTCAGGCTCTACGAGAGGAGAGACCAAGCTTCGGGCCCGCGC	1560
Db	2031	ACCTGCTGGAGACCAAGCTCAGGCTCTACGAGAGGAGAGACCAAGCTTCGGGCCCGCGC	2090
Qy	1561	TGGAGGAGACCCAGTGGAGGTGAGGCCACACAGGCTCATGGGTTTGGGTGGTCAAGCG	1620
Db	2091	TGGAGGAGACCCAGTGGAGGTGAGGCCACACAGGCTCATGGGTTTGGGTGGTCAAGCG	2150
Qy	1621	TTTGGGCCAGTACCCCTCTCTCTGCTGCTGGCCCAATAGCGTGCMAACACAGACCG	1680
Db	2151	TTTGGGCCAGTACCCCTCTCTCTGCTGCTGGCCCAATAGCGTGCMAACACAGACCG	2210
Qy	1681	CGCAGCAAGCGGGCTTAATGCTGCTTATCACCCAAAGAGGGGCTCCCTGCAAAAC	1740
Db	2211	CGCAGCAAGCGGGCTTAATGCTGCTTATCACCCAAAGAGGGGCTCCCTGCAAAAC	2270
Qy	1741	CATGTTGGGGATCGACTTACATCTGAGCTTCTCTCTGCTCCCAACCATCACCTCATGGC	1800
Db	2271	CATGTTGGGGATCGACTTACATCTGAGCTTCTCTCTGCTCCCAACCATCACCTCATGGC	2330
Qy	1801	TCCTAGATTTTCAAGTTCGCAAGTGCATTTAAATCATGAAGCGGAGAGCCAGATGACCA	1860
Db	2331	TCCTAGATTTTCAAGTTCGCAAGTGCATTTAAATCATGAAGCGGAGAGCCAGATGACCA	2390
Qy	1861	AGSCCCACGACGAGCTGTGGC	1881
Db	2391	AGSCCCACGACGAGCTGTGGC	2411

RESULT 4

AAA64513  
ID AAA64513 standard; cDNA; 1512 BP.

XX AAA64513;

XX AC

DT 02-JAN-2001 (first entry)

XX Nucleotide sequence of truncated FEZ1 transcript D14.

DE Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;

XX tumour proliferation; tubulin; microtubule; protein EF1-gamma;

KW

KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
 XX tumorigenesis; tumour survival; metastasis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 1..1512  
 FT /\*tag= a  
 FT /product= "truncated FEZ1"

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX P-PSDB; AAB08720.

XX New polynucleotide homologous with a portion of one strand of the human  
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
 PT cancer -

XX Disclosure; Fig 5F; 255pp; English.

XX The present sequence encodes a truncated human FEZ1 polypeptide. The  
 CC encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour  
 CC suppressor gene, located at chromosome location 8p22. Decreased  
 CC or no expression of FEZ1 is detected in a variety of cancer cells.  
 CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
 CC also interacts with tubulin, with microtubules, and with protein  
 CC EPI-gamma. Post-translational phosphorylation and dephosphorylation  
 CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
 CC expression are useful for inducing cells to proliferate. Compounds  
 CC which modulate FEZ1 association with tubulin are useful for alleviating  
 CC tubulin hyper- or hypo- polymerisation disorders, such as those  
 CC associated with aberrant initiation of mitosis, modulation of the  
 CC initiation and rate of cell proliferation and cell growth, modulation of  
 CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
 CC DNA replication, intracellular distribution of organelles, metastatic  
 CC potential of cell and cellular transformation from a non-cancerous to  
 CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
 CC phosphorylation are also useful for alleviating a disorder, such as  
 CC tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 1512 BP; 335 A; 483 C; 481 G; 213 T; 0 other;

Query Match 21.8%; Score 757; DB 21; Length 1512;  
 Best Local Similarity 99.9%; Pred No. 0;  
 Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 GGGCTCCGAGAGGGTGCAGTGCAGGCCACACAGCCTTCAAGCCTGTGTCGCCACGGTCAAG 835  
 Db 345 GGGCTCCGAGAGGGTGCAGTGCAGGCCACACAGCCTTCAAGCCTGTGTCGCCACGGTCAAG 404  
 QY 836 AGCCATCTGCATCTCTCCCGGAGAGTGCAGGCCACACAGCCTGCACCCGGCCCTCCAGA 895  
 Db 405 AGCCATCTGCATCTCTCCCGGAGAGTGCAGGCCACACAGCCTGCACCCGGCCCTCCAGA 464  
 QY 896 CAAGCCCAAGGAGGAGTGAAGCCTGGCTGTGCTCTGGGGCGCTGTGAGACTCCGG 955  
 Db 465 CAAGCCCAAGGAGGAGTGAAGCCTGGCTGTGCTCTGGGGCGCTGTGAGACTCCGG 524  
 QY 956 CGGGAATCCATGTCCAGCCTGCCACACACAGCAGCAGCAGCAGTACCAAGCTGGACCC 1015  
 PR 525 CGGGAATCCATGTCCAGCCTGCCACACACAGCAGCAGCAGCAGTACCAAGCTGGACCC 584

QY 1016 GCTGGTCAACCCGTGGAGCCACACAGCCGTTTTGGGGGCTCCGCCACACATCACCCA 1075  
 Db 585 GCTGGTCAACCCGTGGAGCCACACAGCCGTTTTGGGGGCTCCGCCACACATCACCCA 644  
 QY 1076 GGGCATCGTCTCCAGGACAGCAACATGATGAGCCTGAAGGCTCTGTCTTCTCCGACGG 1135  
 Db 645 GGGCATCGTCTCCAGGACAGCAACATGATGAGCCTGAAGGCTCTGTCTTCTCCGACGG 704  
 QY 1136 AGGTAGCAAGCTGGGCCACTTCGAAACAAGGACAGCAAGGGCCCTCTGTGTCTCCCTCCC 1195  
 Db 705 AGGTAGCAAGCTGGGCCACTTCGAAACAAGGACAGCAAGGGCCCTCTGTGTCTCCCTCCC 764  
 QY 1196 CATCTCCACGGAGTGCAGCATCCAGAGCTGGACAGACAGCTGTGGAGGGGAGGG 1255  
 Db 765 CATCTCCACGGAGTGCAGCATCCAGAGCTGGACAGACAGCTGTGGAGGGGAGGG 824  
 QY 1256 CGCCCTCCAGAACTGCAGCGCAGCTTTGAGGAGAAAGAGCTTGCCTCCAGCCTGGCCTA 1315  
 Db 825 CGCCCTCCAGAACTGCAGCGCAGCTTTGAGGAGAAAGAGCTTGCCTCCAGCCTGGCCTA 884  
 QY 1316 CGAGGAGCGCGCGCGCTGCAGGGACAGAGCTGGAGGGCCCGAGGCCCAAGCGCGCAA 1375  
 Db 885 CGAGGAGCGCGCGCGCTGCAGGGACAGAGCTGGAGGGCCCGAGGCCCAAGCGCGCAA 944  
 QY 1376 CAAGCTCAAGCAGCGCTCGCAGAGAGCCAGCGCGCGCAGCAGCTCTGCACCTGCAGGT 1435  
 Db 945 CAAGCTCAAGCAGCGCTCGCAGAGAGCCAGCGCGCGCAGCAGCTCTGCACCTGCAGGT 1004  
 QY 1436 ACTGCAGCTTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTTCGAGAGCCTCATGAAGGA 1495  
 Db 1005 ACTGCAGCTTTCAGCAGGAGAGCGGCGAGCTCCGCGCAGGAGCTTCGAGAGCCTCATGAAGGA 1064  
 QY 1496 GCAGGACCTCTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACCAAGCTTCGGGCC 1555  
 Db 1065 GCAGGACCTCTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACCAAGCTTCGGGCC 1124  
 QY 1556 CGCGCTGGAGGAGACCCAGTGGGAGGTG 1583  
 Db 1125 CGCGCTGGAGGAGACCCAGTGGGAGGTG 1152

# RESULT 5

AAA64512 ID AAA64512 standard; cDNA; 1614 BP.

XX AAA64512;

XX AC

DT 02-JAN-2001 (first entry)

XX Nucleotide sequence of truncated FEZ1 transcript T8D145M4.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
 KW tumour proliferation; tubulin; microtubule; protein EPI-gamma;  
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
 KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..633

FT /\*tag= a

FT /product= "truncated FEZ1"

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.



EPI-gamma. Post-translational phosphorylation and dephosphorylation modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are useful for inducing cells to proliferate. Compounds which modulate FEZ1 association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility, rate and stage of cellular DNA replication, intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate FEZ1 binding and dephosphorylation are also useful for alleviating a disorder, such as tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 1692 BP; 380 A; 523 C; 553 G; 236 T; 0 other;  
Query Match 21.8%; Score 757; DB 21; Length 1692;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 GGGCTCCGAGAGGGTGCAGTGCAGCCACAGCCTTCAAGCTGTGCTGCACCGTCAGG 835  
Db 345 GGGCTCCGAGAGGGTGCAGTGCAGCCACAGCCTTCAAGCTGTGCTGCACCGTCAGG 404  
QY 836 AGCCATCTGCACCTCTCCCGGAGAGTCCAGCCACAGCTGCACCGCCCTCCAGA 895  
Db 405 AGCCATCTGCACCTCTCCCGGAGAGTCCAGCCACAGCTGCACCGCCCTCCAGA 464  
QY 896 CAAGCCCAAGGAGGAGAGCTGAAGCCTGGCTGTGCTCTGGGGCGCTGTGAGACTCCGG 955  
Db 465 CAAGCCCAAGGAGGAGAGCTGAAGCCTGGCTGTGCTCTGGGGCGCTGTGAGACTCCGG 524  
QY 956 CGGNACTCATGTTCAGCTGCCACACAGACACAGCAGCAGCAGCTACAGCTGGAGCC 1015  
Db 525 CGGNACTCATGTTCAGCTGCCACACAGACACAGCAGCAGCAGCTACAGCTGGAGCC 584  
QY 1016 GCTGTGTACACCGTGGGACCCACAGCCGTTTTGGGGGCTCCGCCACACATCACCCA 1075  
Db 585 GCTGTGTACACCGTGGGACCCACAGCCGTTTTGGGGGCTCCGCCACACATCACCCA 644  
QY 1076 GGGCATCTCTCTCCAGGACAGCAACATGATGAGCTGAAGCTCTGTCTTCTCCGACGG 1135  
Db 645 GGGCATCTCTCTCCAGGACAGCAACATGATGAGCTGAAGCTCTGTCTTCTCCGACGG 704  
QY 1136 AGGTAGCAAGCTGGCCACTGCACAGGAGAGAGAGGCGCCCTCGTGTGCTCCCTCCC 1195  
Db 705 AGGTAGCAAGCTGGCCACTGCACAGGAGAGAGAGGCGCCCTCGTGTGCTCCCTCCC 764  
QY 1196 CATCTCCACGAGGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAGGGAGGG 1255  
Db 765 CATCTCCACGAGGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAGGGAGGG 824  
QY 1256 CGCCCTCCAGAGCTGCAGCGCAGCTTTGAGGAGAGGAGCTTGCTCCAGCCTGGCCTA 1315  
Db 825 CGCCCTCCAGAGCTGCAGCGCAGCTTTGAGGAGAGGAGCTTGCTCCAGCCTGGCCTA 884  
QY 1316 CGAGAGCGGCGCGCGCTGCAGGAGCAGCTGCAGGCGCCGAGCCCAAGAGGGGCAA 1375  
Db 885 CGAGAGCGGCGCGCGCTGCAGGAGCAGCTGCAGGCGCCGAGCCCAAGAGGGGCAA 944  
QY 1376 CAAGCTCAAGCAGGCTCGCAGAGAGCAGCGCGCAGAGGCTTCGCACTTCAGGT 1435  
Db 945 CAAGCTCAAGCAGGCTCGCAGAGAGCAGCGCGCAGAGGCTTCGCACTTCAGGT 1004  
QY 1436 ACTGAGCTTCAGCAGGAGAGCGCAGCTCCGCGAGAGCTTCGAGAGCCTCATGAAGA 1495  
Db 1005 ACTGAGCTTCAGCAGGAGAGCGCAGCTCCGCGAGAGCTTCGAGAGCCTCATGAAGA 1064  
QY 1496 CGAGACCTGTGGAGACCAAGCTCAGCTCAGTGTACAGAGGAGAGAGCAGCTTCGGCCC 1555  
Db 1065 CGAGACCTGTGGAGACCAAGCTCAGTGTTCAGAGAGGAGAGAGCAGCTTCGGCCC 1124  
QY 1556 CGCGTGGAGGAGAGCCAGTGGAGGTG 1583

Db 1125 CGCGCTGGAGGAGACCCAGTGGGAGGTG 1152  
RESULT 7  
AAA64515  
ID AAA64515 standard; cDNA; 1722 BP.  
XX AAA64515;  
AC AAA64515;  
XX 02-JAN-2001 (first entry)  
DT  
XX Nucleotide sequence of truncated FEZ1 transcript G3612.  
DE  
XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein EPI-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 1..1722  
CDS /\*tag= a  
FT /product= "truncated FEZ1"  
FT  
XX WO200050565-A2.  
PN  
XX 31-AUG-2000.  
PD  
XX 25-FEB-2000; 2000WO-US04950.  
PF  
XX 25-FEB-1999; 99US-0121537.  
PR  
XX (UJJE-) UNIV JEFFERSON THOMAS.  
PA  
XX Croce CM, Ishii H;  
PI  
XX WPI; 2000-558396/51.  
DR P-PSDB; AAB08722.  
XX  
XX New polynucleotide homologous with a portion of one strand of the human  
FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
cancer -  
XX  
XX Disclosure; Fig 5H; 255pp; English.  
XX  
XX The present sequence encodes a truncated human FEZ1 polypeptide. The  
encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour  
suppressor gene, located at chromosome location 8p22. Decreased  
or no expression of FEZ1 is detected in a variety of cancer cells.  
Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
also interacts with tubulin, with microtubules, and with protein  
EPI-gamma. Post-translational phosphorylation and dephosphorylation  
modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
expression are useful for inducing cells to proliferate. Compounds  
which modulate FEZ1 association with tubulin are useful for alleviating  
tubulin hyper- or hypo- polymerisation disorders, such as those  
associated with aberrant initiation of mitosis, modulation of the  
initiation and rate of cell proliferation and cell growth, modulation of  
cell shape, cell rigidity, cell motility, rate and stage of cellular  
DNA replication, intracellular distribution of organelles, metastatic  
potential of cell and cellular transformation from a non-cancerous to  
cancerous phenotype. Compounds which modulate FEZ1 binding and  
dephosphorylation are also useful for alleviating a disorder, such as  
tumorigenesis, tumour survival, growth and metastasis.  
XX  
SQ Sequence 1722 BP; 381 A; 541 C; 563 G; 237 T; 0 other;

Query Match 21.8%; Score 757; DB 21; Length 1722;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX	Homo sapiens.
OS	
XX	
XX	Key Location/Qualifiers
XX	CDS 1..1791
FT	/tag= a
FT	/product= "FEZ1"
FT	
XX	WO200005065-A2.
PN	
XX	
XX	31-AUG-2000.
XX	
XX	25-FEB-2000; 2000HO-US04950.
PF	
XX	
XX	25-FEB-1999; 99US-0121537.
PR	
XX	(UYJE-) UNIV JEFFERSON THOMAS.
PA	
XX	
XX	Croce CM, Ishii H;
PI	
XX	WFI; 2000-558396/51.
DR	
XX	P-PSDB; AAB08715.
DR	
XX	New polynucleotide homologous with a portion of one strand of the human FEZ1 gene, useful for alleviating abnormal cell proliferation such as cancer -
PT	
PT	
PT	
XX	Claim 7; Fig 5I; 255pp; English.
XX	
XX	The present sequence encodes a human FEZ1 polypeptide. FEZ1 is a tumour suppressor gene, located at chromosome location 8p22. Decreased or no expression of FEZ1 is detected in a variety of cancer cells.
CC	Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts with tubulin, with microtubules, and with protein EPI-gamma. Post-translational phosphorylation and dephosphorylation modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are useful for inducing cells to proliferate. Compounds which modulate FEZ1 association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility, rate and stage of cellular DNA replication, intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate FEZ1 binding and phosphorylation are also useful for alleviating a disorder, such as tumorigenesis, tumour survival, growth and metastasis.
CC	
XX	Sequence 1791 BP; 393 A; 561 C; 591 G; 246 T; 0 other;
SQ	
	Query Match 21.8%; Score 757; DB 21; Length 1791;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	776 GGCTCCGAGAGGGTGTCAGTGCAGGCCACAGCCTTTCAAGCCTGTGTGCCACCGTCAAG 835
Db	345 GGCTCCGAGAGGGTGTCAGTGCAGTGCAGGCCACAGCCTTCAAGCCTGTGTGCCACCGTCAAG 404
QY	836 AGCATCTTGCACTCTCTCCC CGAGAGTGCCAGCCACCAGTCGACCCGCCCTCCAGA 895
Db	405 AGCATCTTGCACTCTCTCCC CGAGAGTGCCAGCCACCAGTCGACCCGCCCTCCAGA 464
QY	896 CAAGCCCAAGGACGAGAGCTGAAGCCTTGGCGCTGTGCTCTGGGGCGCTGTCAACTCCGG 955
Db	465 CAAGCCCAAGGACGAGAGCTGAAGCCTTGGCGCTGTGCTCTGGGGCGCTGTCAACTCCGG 524
QY	956 CCAGAACTCCATGTCAGAGCTGCCACACACAGCACAGCAGCAGTAGTACCAGTGGACCC 1015
Db	525 CCAGAACTCCATGTCAGAGCTGCCACACACAGCACAGCAGCAGTAGTACCAGTGGACCC 584
QY	1016 GTGTGTCACACCCGTGGGACCCACAAGCGTTTTTGGGGGCTCCGCCCAACAATCACCCA 1075
Db	585 GTGTGTCACACCCGTGGGACCCACAAGCGTTTTTGGGGGCTCCGCCCAACAATCACCCA 644

RESULT: B  
AAA64509

ID	AAA6
yy	

AC AAA

DT 02-0

DE  
CDNA[illegible]KW  
tumorKW  
cellKW  
tumo





Db 1116 ACTGAGCTTCAGCAGGAGAGCGCAGCTCGGAGGAGTTCGAGACCTCATGAAGGA 1175  
QY 1496 GCAGGACCTGTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACGCTTCGGGCC 1555  
Db 1176 GCAGGACCTGTGGAGACCAAGCTCAGGTCTTACGAGAGGAGAGACGCTTCGGGCC 1235  
QY 1556 CGCGCTGGAGAGACCCAGTGGAGGTG 1583  
Db 1236 CGCGCTGGAGAGACCCAGTGGAGGTG 1263

RESULT 10

AAS30595  
ID AAS30595 standard; cDNA; 560 BP.

XX AC AAS30595;

XX DT 21-NOV-2001 (first entry)

XX DE DNA encoding novel lung cancer antigen, Seq ID No 17.

XX KW Human; lung cancer; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW nocropic; neuroprotective; antibacterial; virucide; fungicide;  
KW ophthalmological; autoimmune disease; rheumatoid arthritis; neoplasm;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; skin aging;  
KW ocular disorder; wound healing; organ transplantation; ss.

XX OS Homo sapiens.

XX PN WO200155300-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01238.

XX PR 31-JAN-2000; 2000US-0179065.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Barash SC, Ruben SM;

XX DR WPI; 2001-465565/50.

XX PS P-PSDB; AAU18935.

XX PT Isolated nucleic acid molecule encoding a lung cancer antigen is used

XX in preventing, treating or ameliorating a medical condition

XX Claim 1; SEQ ID No 17; 475pp; English.

XX CC The invention relates to novel isolated lung cancer antigen  
XX polynucleotides (I) and polypeptides (II). (I) and (II) are used to  
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
XX rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are  
XX also used in diagnosing a pathological condition or susceptibility to a  
XX pathological condition, in particular, lung cancer. The antibodies to  
XX (II) can also be used in alleviating symptoms associated with the  
XX disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
XX linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
XX treated include autoimmune diseases e.g. rheumatoid arthritis,  
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,  
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
XX e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
XX ocular disorders e.g. corneal infection. The polypeptides can also be  
XX used to aid wound healing and epithelial cell proliferation, to prevent  
XX skin aging due to sunburn, to maintain organs before transplantation, for  
XX supporting cell culture of primary tissues, to regenerate tissues and in  
XX chemotaxis. AAS30580-AAS30685 represent novel human lung cancer antigen  
XX coding sequences, PCR primers and related sequences of the invention.  
XX Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly  
CC from WIPO at: ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 560 BP; 120 A; 196 C; 161 G; 83 T; 0 other;

Query Match 13.7%; Score 475; DB 22; Length 560;

Best Local Similarity 99.8%; Pred. No. 6.5e-210;

Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCCTGTGCTGCCACGCTCAGG 835

Db 35 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCCTGTGCTGCCACGCTCAGG 94

QY 836 AGCCATCTGCACCTCTCCCGGAGAGTGCAGCCACACAGCTGCACCCCGCCCTCCAGA 895

Db 95 AGCCATCTGCACCTCTCCCGGAGAGTGCAGCCACACAGCTGCACCCCGCCCTCCAGA 154

QY 896 CAAGCCCAAGGAGGAGGAGCTGAAGCCTGCTCTGGGGGGCTGTGAGACTCCGG 955

Db 155 CAAGCCCAAGGAGGAGGAGCTGAAGCCTGCTCTGGGGGGCTGTGAGACTCCGG 214

QY 956 CCGGAATCCATGTCCAGCCTGCCACACACAGCAGCAGCAGCTACCACTGGACCC 1015

Db 215 CCGGAATCCATGTCCAGCCTGCCACACACAGCAGCAGCAGCTACCACTGGACCC 274

QY 1016 GCTGGTCCACACCCCGTGGGACCCCAAGCCGTTTTGGGGGCTCCGCCCAACATCACCCA 1075

Db 275 GCTGGTCCACACCCCGTGGGACCCCAAGCCGTTTTGGGGGCTCCGCCCAACATCACCCA 334

QY 1076 GGGCATGTCTCTCAGGACAGCAATGATGAGCCTGAAGGCTCTGCTCTTCGAGCG 1135

Db 335 GGGCATGTCTCTCAGGACAGCAATGATGAGCCTGAAGGCTCTGCTCTTCGAGCG 394

QY 1136 AGGTAGCAAGCTGGGCGCACTCGAACAGGAGCAAGGGCCCTCGTGTCCGCTCCCC 1195

Db 395 AGGTAGCAAGCTGGGCGCACTCGAACAGGAGCAAGGGCCCTCGTGTCCGCTCCCC 454

QY 1196 CATCTCCAGGACGAGTGCAGCATCCAGGAGCTCGAACAGAGCTGTTGGAGAGGGAGGG 1255

Db 455 CATCTCCAGGACGAGTGCAGCATCCAGGAGCTCGAACAGAGCTGTTGGAGAGGGAGGG 514

QY 1256 CGCCCTCAGAGCTGCAGCGCAGCTTTGAGGAGAGAGGCTTGC 1301

Db 515 CGCCCTCAGAGCTGCAGCGCAGCTTTGAGGAGAGAGGCTTGC 560

RESULT 11

AAS28127  
ID AAS28127 standard; cDNA; 560 BP.

XX AC AAS28127;

XX DT 07-NOV-2001 (first entry)

XX DE Novel cDNA encoding for human respiratory antigen #259.

XX KW Human; respiratory antigen; respiratory disorder; throat disorder;  
XX lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;  
XX anti allergic; anti aschmatic; anti inflammatory; oilyfactory;  
XX respiratory active; ss.

XX OS Homo sapiens.

XX PN WO200155448-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01333.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
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 PR 14-AUG-2000; 2000US-0224518.  
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 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
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 PR 06-SEP-2000; 2000US-0230438.  
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 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
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 PR 14-SEP-2000; 2000US-0232398.  
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 PR 21-SEP-2000; 2000US-0234274.  
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 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
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 PR 29-SEP-2000; 2000US-0236327.  
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 PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
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 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
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 PR 08-NOV-2000; 2000US-0246476.  
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 PR 08-NOV-2000; 2000US-0246528.  
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 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 PR Rosen CA, Barash SC, Ruben SM;  
 PR WPI; 2001-476224/51.  
 PR P-PSDB; AAU17943.  
 PR Isolated polypeptide for treating, preventing and/ or prognosing  
 PT disorders related to the respiratory system including respiratory  
 PT cancers and also for testing and detection e.g. diagnosis -  
 XX Claim 4; SED ID No 269; 546pp; English.  
 XX

CC The present invention relates to the isolation of novel human  
CC respiratory antigens (AAU17685-AAU17975), and cDNA and genomic  
CC sequences encoding for these polypeptides. The sequences of the  
CC invention are useful for preventing, treating and/or prognosing  
CC disorders related to the respiratory system including throat  
CC disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),  
CC lung disorders e.g. pneumonia, allergic disorders e.g. asthma,  
CC pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of  
CC the respiratory tissues e.g. lung cancer. The polynucleotide sequences  
CC of the invention are useful in gene therapy and antisense therapy.  
CC AAS27869-AAS28159 encode for novel human respiratory antigens.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 560 BP; 120 A; 196 C; 161 G; 83 T; 0 other;

Query Match 13.7%; Score 475; DB 22; Length 560;  
Best Local Similarity 99.8%; Pred. No. 6.5e-210;  
Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGCTGCCACGGTCAGG 835  
Db 35 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGCTGCCACGGTCAGG 94  
Qy 836 AGCCATCTGCACTCTCTCCCGGAGAGTGCAGCCACCAGCTGCACCCGCCCTCCAGA 895  
Db 95 AGCCATCTGCACTCTCTCCCGGAGAGTGCAGCCACCAGCTGCACCCGCCCTCCAGA 154  
Qy 896 CAAGCCCAAGAGGAGGCTGAGCCTGGCTGTGCTCTGGGGCGTGTGAGACTCCGG 955  
Db 155 CAAGCCCAAGAGGAGGAGTGAAGCCTGGCTGTGCTCTGGGGCGTGTGAGACTCCGG 214  
Qy 956 CCGGAATCTCCATGCTCCAGCCTGCCACACAGCAGCAGCAGCTACAGCTGGACCC 1015  
Db 215 CCGGAATCTCCATGCTCCAGCCTGCCACACAGCAGCAGCAGCTACAGCTGGACCC 274  
Qy 1016 GCTGGTCAACCCGTGGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACATCACCCA 1075  
Db 275 GCTGGTCAACCCGTGGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACATCACCCA 334  
Qy 1076 GGGATCGTCTCCAGGACAGCAATGATGAGCTGAGGCTGTGCTCTTCGAGCG 1135  
Db 335 GGGATCGTCTCCAGGACAGCAATGATGAGCTGAGGCTGTGCTCTTCGAGCG 394  
Qy 1136 AGGTAGCAAGCTGGGCCACTGCAACAGGCGAGCAAGGGCCCTGCTGTGCTCCCG 1195  
Db 395 AGGTAGCAAGCTGGGCCACTGCAACAGGCGAGCAAGGGCCCTGCTGTGCTCCCG 454  
Qy 1196 CATCTCCAGCAGGTGAGCTCCAGGAGCTGGAACAGAGAGCTTTGGAGAGGGAGGG 1255  
Db 455 CATCTCCAGCAGGTGAGCTCCAGGAGCTGGAACAGAGAGCTTTGGAGAGGGAGGG 514  
Qy 1256 CGCCCTCCAGAGCTGAGCCGAGCTTTGAGAGAGAGGAGCTGCC 1301  
Db 515 CGCCCTCCAGAGCTGAGCCGAGCTTTGAGAGAGAGGAGCTGCC 560

RESULT 12

AAA64511  
ID AAA64511 standard; cDNA; 633 BP.

XX AC  
XX AAA64511;

XX 02-JAN-2001 (first entry)

XX Nucleotide sequence of truncated FEZ1 transcript E264162.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein EF1-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 1..633  
FT /\*tag= a  
FT /product= "truncated FEZ1"  
XX  
XX WO200050565-A2.  
XX 31-AUG-2000.  
XX 25-FEB-2000; 2000WO-US04950.  
XX 25-FEB-1999; 99US-0121537.  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX Croce CM, Ishii H;  
XX WPI; 2000-558396/51.  
XX P-PSDB; AAB08718.  
XX New polynucleotide homologous with a portion of one strand of the human  
XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
XX cancer -  
XX Disclosure; Fig 5D; 255pp; English.  
XX  
XX The present sequence encodes a truncated human FEZ1 polypeptide. The  
XX encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour  
XX suppressor gene, located at chromosome location 8p22. Decreased  
XX or no expression of FEZ1 is detected in a variety of cancer cells.  
XX Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
XX also interacts with tubulin, with microtubules, and with protein  
XX EF1-gamma. Post-translational phosphorylation and dephosphorylation  
XX modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
XX expression are useful for inducing cells to proliferate. Compounds  
XX which modulate FEZ1 association with tubulin are useful for alleviating  
XX tubulin hyper- or hypo- polymerisation disorders, such as those  
XX associated with aberrant initiation of mitosis, modulation of the  
XX initiation and rate of cell proliferation and cell growth, modulation of  
XX cell shape, cell rigidity, cell motility, rate and stage of cellular  
XX DNA replication, intracellular distribution of organelles, metastatic  
XX potential of cell and cellular transformation from a non-cancerous to  
XX cancerous phenotype. Compounds which modulate FEZ1 binding and  
XX phosphorylation are also useful for alleviating a disorder, such as  
XX tumorigenesis, tumour survival, growth and metastasis.  
XX  
XX Sequence 633 BP; 136 A; 217 C; 175 G; 105 T; 0 other;

Query Match 6.2%; Score 214; DB 21; Length 633;  
Best Local Similarity 100.0%; Pred. No. 7.8e-89;  
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 776 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGCTGCCACGGTCAGG 835  
Db 345 GGGCTCCGAGAGGGTGCAGTGAGGCCACACAGCCTTCAAGCTGTGCTGCCACGGTCAGG 404  
Qy 836 AGCCATCTGCACTCTCTCCCGGAGAGTGCAGCCACAGCTGCACCCGCCCTCCAGA 895  
Db 405 AGCCATCTGCACTCTCTCCCGGAGAGTGCAGCCACAGCTGCACCCGCCCTCCAGA 464  
Qy 896 CAAGCCCAAGGAGCAGGAGCTGAGCCTGGCTGTGCTCTGGGGCGTGTGAGACTCCGG 955  
Db 465 CAAGCCCAAGGAGCAGGAGCTGAGCCTGGCTGTGCTCTGGGGCGTGTGAGACTCCGG 524  
Qy 956 CCGGAATCTCCATGCTCCAGCCTGCCACACAGCAGC 989  
Db 525 CCGGAATCTCCATGCTCCAGCCTGCCACACAGCAGC 558

RESULT 13



XX New prostate-specific polypeptide for detecting, diagnosing,  
PT monitoring, treating, staging and predicting cancers in humans having  
PT cancer and non-cancerous prostate disease  
XX  
PS Claim 1; Page 213; 255pp; English.  
XX  
CC ABN89000 to ABN89111 represent human prostate specific nucleic acid  
CC (PSNA) sequences which encode the human prostate specific proteins (PSP)  
CC given in ABB81341 to ABB81439. PSNA and PSP sequences have cytostatic  
CC activity, and can be used in gene therapy, antisense therapy and  
CC vaccines. PSNA and PSP sequences can be used for diagnosing and  
CC monitoring the presence and metastases of prostate cancer in a patient.  
CC PSNA and PSP sequences are also useful: (i) for determining non-cancerous  
CC prostate disease, by measuring their expression levels and/or structural  
CC alterations; (ii) for determining that the sample that has prostate  
CC tissue-like characteristics or is a prostate tissue; (iii) as elements  
CC in an array or a multi-analyte test to recognise expression patterns  
CC associated with prostate cancer and other prostate related disorders;  
CC and (iv) as elements in a computer program for pattern recognition of  
CC prostate disorders.  
XX  
SQ Sequence 881 BP; 353 A; 183 C; 217 G; 128 T; 0 other;

Query Match 0.9%; Score 32; DB 24; Length 881;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3215 TATATATATATATATATATATATATATAT 3246  
Db ||||||||||||||||||||||||||||  
132 TATATATATATATATATATATATATATAT 101

Search completed: June 16, 2003, 20:02:21  
Job time : 639.119 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 135.951 Seconds.  
(without alignments)

7834.381 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_871\_4343

Perfect score: 3473

Sequence: 1 agctgcgcctgggggcatct.....cgtggtggtcacgcctgca 3473

Scoring table: OLIGO NUC

Gapop 60.0., Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents\_NA.\*

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- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	32	0.9	6769	1	US-08-483-553-20
C 3	32	0.9	6769	1	US-08-487-002-20
C 4	32	0.9	6769	1	US-08-483-554B-20
C 5	32	0.9	6769	1	US-08-488-011B-20
C 6	32	0.9	6769	4	US-08-850-727-20
C 7	32	0.9	6769	5	PCT-US95-10202-20
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C 9	32	0.9	6769	5	PCT-US95-10220-20
C 10	28	0.8	19124	2	US-08-487-826B-13
C 11	26	0.7	1195	6	5240848-6
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C 21	24	0.7	790	6	5194596-8
C 22	24	0.7	961	6	5194596-16
C 23	24	0.7	961	6	5219739-16
C 24	24	0.7	1543	6	5332671-5
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C 38	22	0.6	2634	3	US-08-450-562-26
C 39	22	0.6	2634	4	US-08-984-709A-26
C 40	22	0.6	2634	4	US-08-450-272-26
C 41	22	0.6	2712	3	US-08-949-386-38
C 42	22	0.6	2712	3	US-08-450-562-38
C 43	22	0.6	2712	4	US-08-984-709A-38
C 44	22	0.6	2712	4	US-08-450-272-38
C 45	22	0.6	2970	3	US-08-949-386-37
C 46	22	0.6	2970	3	US-08-450-562-37
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C 68	21	0.6	1433	1	US-08-424-406-2
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C 77	21	0.6	1600	2	US-08-720-420A-117
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C 80	21	0.6	2551	2	US-08-482-279-70
C 81	21	0.6	2551	2	US-08-342-468-70
C 82	21	0.6	2551	3	US-09-015-968-70
C 83	21	0.6	2551	4	US-09-397-386-70
C 84	21	0.6	2775	4	US-09-053-871A-22
C 85	21	0.6	2781	3	US-08-749-522-4
C 86	21	0.6	2802	3	US-08-742-877-1
C 87	21	0.6	4673	1	US-07-638-431-1
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C 90	21	0.6	4946	3	US-08-817-188-1
C 91	21	0.6	5238	3	US-09-080-855-1
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C 93	21	0.6	5560	3	US-08-817-188-5
C 94	21	0.6	5864	3	US-08-894-440-4
C 95	21	0.6	5864	4	US-09-458-093-4
C 96	21	0.6	6769	1	US-08-480-784-20
C 97	21	0.6	6769	1	US-08-483-553-20
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C 100	21	0.6	6769	1	US-08-488-011B-20

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103	21	0.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	176	20	0.6	5319	2	US-09-323-433A-7	Sequence 7, Appl
104	21	0.6	6769	5	PCT-US95-10220-20	Sequence 20, Appl	177	20	0.6	6038	4	US-09-305-639-4	Sequence 4, Appl
105	21	0.6	12394	4	US-09-488-856A-10	Sequence 10, Appl	c 178	20	0.6	6124	4	US-08-213-419B-3	Sequence 3, Appl
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107	21	0.6	21234	4	US-09-810-671-3	Sequence 3, Appl	180	20	0.6	6350	4	US-09-647-826-1	Sequence 1, Appl
108	21	0.6	32042	4	US-09-245-281-44	Sequence 44, Appl	c 181	20	0.6	6678	3	US-08-816-617A-1	Sequence 1, Appl
109	21	0.6	35060	3	US-08-814-035-7	Sequence 7, Appl	c 182	20	0.6	7622	4	US-09-305-639-1	Sequence 1, Appl
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112	21	0.6	59065	4	US-09-813-197-3	Sequence 3, Appl	c 185	20	0.6	9432	2	US-08-473-750-4	Sequence 4, Appl
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116	21	0.6	111282	4	US-09-754-250-3	Sequence 3, Appl	189	20	0.6	10079	2	US-08-476-866-20	Sequence 20, Appl
117	21	0.6	112132	4	US-09-741-150-3	Sequence 3, Appl	190	20	0.6	11485	4	US-09-410-464-9	Sequence 9, Appl
118	21	0.6	162450	4	US-09-345-882-1	Sequence 1, Appl	191	20	0.6	11613	1	US-08-484-044-10	Sequence 10, Appl
119	21	0.6	168575	4	US-09-426-290-1	Sequence 1, Appl	192	20	0.6	12141	4	US-09-488-671-10	Sequence 10, Appl
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121	21	0.6	246240	2	US-08-724-394A-21	Sequence 21, Appl	c 194	20	0.6	15062	4	US-09-004-838-89	Sequence 89, Appl
122	21	0.6	246240	2	US-08-724-394A-22	Sequence 22, Appl	c 195	20	0.6	16063	4	US-09-801-052-3	Sequence 3, Appl
123	20	0.6	317	4	US-09-385-982-109	Sequence 109, App	c 196	20	0.6	17041	1	US-08-076-011-1	Sequence 1, Appl
124	20	0.6	341	4	US-09-404-879A-136	Sequence 136, App	197	20	0.6	17656	4	US-09-433-579-3	Sequence 3, Appl
125	20	0.6	461	4	US-09-404-879A-1	Sequence 1, Appl	198	20	0.6	19124	2	US-08-487-826B-13	Sequence 13, Appl
126	20	0.6	461	4	US-09-404-879A-3	Sequence 3, Appl	199	20	0.6	21234	4	US-09-810-671-3	Sequence 3, Appl
127	20	0.6	474	4	US-09-143-476-13	Sequence 13, Appl	200	20	0.6	29629	4	US-09-729-995-3	Sequence 3, Appl
128	20	0.6	602	1	US-08-764-100-8	Sequence 8, Appl	201	20	0.6	38682	4	US-08-943-731-2	Sequence 2, Appl
129	20	0.6	642	1	US-08-764-100-13	Sequence 13, Appl	202	20	0.6	38844	4	US-09-734-675-3	Sequence 3, Appl
130	20	0.6	643	1	US-08-764-100-7	Sequence 7, Appl	203	20	0.6	43676	3	US-09-356-952-12	Sequence 12, Appl
131	20	0.6	753	4	US-09-535-008-41	Sequence 41, Appl	c 204	20	0.6	50000	4	US-09-146-053-3	Sequence 3, Appl
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133	20	0.6	935	2	US-08-892-770-1	Sequence 1, Appl	206	20	0.6	53526	3	US-08-658-136-2	Sequence 2, Appl
134	20	0.6	1001	4	US-09-641-638-259	Sequence 259, App	207	20	0.6	53577	3	US-08-658-136-2	Sequence 2, Appl
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137	20	0.6	1181	2	US-08-632-598-2	Sequence 2, Appl	210	20	0.6	84495	4	US-09-797-906-3	Sequence 3, Appl
138	20	0.6	1181	4	US-09-231-240-2	Sequence 2, Appl	c 211	20	0.6	84495	4	US-09-797-906-3	Sequence 3, Appl
139	20	0.6	1278	4	US-08-943-731-63	Sequence 63, Appl	c 212	20	0.6	99500	4	US-09-798-096-10	Sequence 10, Appl
140	20	0.6	1368	3	US-08-874-563-5	Sequence 5, Appl	213	20	0.6	112132	4	US-09-741-150-3	Sequence 3, Appl
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146	20	0.6	1732	2	US-08-243-541-2	Sequence 2, Appl	219	19	0.5	634	1	US-08-450-065-1	Sequence 1, Appl
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152	20	0.6	1939	6	5198542-3	Patent No. 5198542	225	19	0.5	961	6	5194596-16	Patent No. 5194596
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154	20	0.6	2296	4	US-09-851-896-11	Sequence 11, Appl	227	19	0.5	1006	4	US-08-988-242-17	Sequence 17, Appl
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170	20	0.6	3950	4	US-09-398-398A-33	Sequence 33, Appl	243	19	0.5	1732	2	US-08-480-344-2	Sequence 2, Appl
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172	20	0.6	4253	3	US-08-577-483-7	Sequence 7, Appl	c 245	19	0.5	1763	6	5198542-1	Patent No. 5198542
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C 262	19	0.5	2551	4	US-09-397-386-70	Sequence 70, Appl	C 335	18	0.5	36	4	US-09-189-344-5	Sequence 5, Appli
C 263	19	0.5	2610	1	US-08-374-834-17	Sequence 17, Appl	C 336	18	0.5	36	4	US-09-189-344-5	Sequence 5, Appli
C 264	19	0.5	2610	1	US-08-644-271-28	Sequence 28, Appl	C 337	18	0.5	40	2	US-08-849-021-1	Sequence 1, Appli
C 265	19	0.5	2610	4	US-09-077-955-32	Sequence 32, Appl	C 338	18	0.5	40	2	US-08-849-021-1	Sequence 1, Appli
C 266	19	0.5	2975	1	US-08-368-281-1	Sequence 1, Appli	C 339	18	0.5	40	2	US-08-849-021-2	Sequence 2, Appli
C 267	19	0.5	2993	1	US-08-764-100-2	Sequence 2, Appli	C 340	18	0.5	40	2	US-08-849-021-2	Sequence 2, Appli
C 268	19	0.5	2993	1	US-08-764-100-10	Sequence 10, Appl	C 341	18	0.5	43	2	US-08-849-021-85	Sequence 85, Appl
C 269	19	0.5	3000	1	US-08-764-100-9	Sequence 9, Appli	C 342	18	0.5	43	2	US-08-849-021-85	Sequence 85, Appl
C 270	19	0.5	3001	1	US-08-764-100-1	Sequence 1, Appli	C 343	18	0.5	43	2	US-08-849-021-86	Sequence 86, Appl
C 271	19	0.5	3023	4	US-09-203-453-4	Sequence 4, Appli	C 344	18	0.5	43	2	US-08-849-021-86	Sequence 86, Appl
C 272	19	0.5	3240	1	US-08-368-281-3	Sequence 3, Appli	C 345	18	0.5	57	1	US-08-222-177A-163	Sequence 163, App
C 273	19	0.5	3300	3	US-08-913-842-4	Sequence 4, Appli	C 346	18	0.5	57	1	US-08-222-177A-163	Sequence 163, App
C 274	19	0.5	3312	1	US-08-049-473-1	Sequence 1, Appli	C 347	18	0.5	65	1	US-08-222-177A-301	Sequence 301, App
C 275	19	0.5	3312	1	US-08-312-648-1	Sequence 1, Appli	C 348	18	0.5	65	1	US-08-222-177A-301	Sequence 301, App
C 276	19	0.5	3312	5	PCT-US94-04190-1	Sequence 1, Appli	C 349	18	0.5	87	3	US-09-050-559C-36	Sequence 36, Appl
C 277	19	0.5	3319	1	US-08-006-676B-2	Sequence 2, Appli	C 350	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appli
C 278	19	0.5	3319	1	US-08-282-845-1	Sequence 1, Appli	C 351	18	0.5	128	1	US-07-922-723A-8	Sequence 8, Appli
C 279	19	0.5	3319	2	US-08-428-414A-4	Sequence 4, Appli	C 352	18	0.5	128	1	US-07-799-828C-8	Sequence 8, Appli
C 280	19	0.5	3319	5	PCT-US94-00324-2	Sequence 2, Appli	C 353	18	0.5	128	1	US-07-799-828C-8	Sequence 8, Appli
C 281	19	0.5	3387	1	US-08-261-822A-5	Sequence 5, Appli	C 354	18	0.5	128	1	US-07-799-828C-8	Sequence 8, Appli
C 282	19	0.5	3387	5	PCT-US95-07744A-5	Sequence 5, Appli	C 355	18	0.5	128	1	US-08-074-275-8	Sequence 8, Appli
C 283	19	0.5	3950	4	US-09-398-355A-33	Sequence 33, Appl	C 356	18	0.5	128	1	US-08-074-275-8	Sequence 8, Appli
C 284	19	0.5	4098	2	US-08-605-106-4	Sequence 4, Appli	C 357	18	0.5	128	1	US-08-480-366-8	Sequence 8, Appli
C 285	19	0.5	4253	3	US-08-577-483-7	Sequence 7, Appli	C 358	18	0.5	128	2	US-07-952-277A-8	Sequence 8, Appli
C 286	19	0.5	4254	2	US-08-443-639-7	Sequence 7, Appli	C 359	18	0.5	128	2	US-07-952-277A-8	Sequence 8, Appli
C 287	19	0.5	4853	4	US-08-881-450A-22	Sequence 22, Appl	C 360	18	0.5	129	1	US-08-616-368A-26	Sequence 26, Appl
C 288	19	0.5	5238	3	US-09-080-855-1	Sequence 1, Appli	C 361	18	0.5	129	1	US-08-616-368A-26	Sequence 26, Appl
C 289	19	0.5	5319	2	US-08-861-464-7	Sequence 7, Appli	C 362	18	0.5	129	3	US-09-054-298-26	Sequence 26, Appl
C 290	19	0.5	5319	2	US-08-396-001-7	Sequence 7, Appli	C 363	18	0.5	129	3	US-09-054-298-26	Sequence 26, Appl
C 291	19	0.5	5319	4	US-09-323-433A-7	Sequence 7, Appli	C 364	18	0.5	129	4	US-08-818-655-26	Sequence 26, Appl
C 292	19	0.5	5852	1	US-07-867-106-2	Sequence 2, Appli	C 365	18	0.5	129	4	US-08-818-655-26	Sequence 26, Appl
C 293	19	0.5	5923	4	US-09-064-922-3	Sequence 3, Appli	C 366	18	0.5	210	2	US-08-875-972-18	Sequence 18, Appl
C 294	19	0.5	6038	4	US-08-305-639-4	Sequence 4, Appli	C 367	18	0.5	258	1	US-07-711-615A-1	Sequence 1, Appli
C 295	19	0.5	6138	4	US-09-067-800-4	Sequence 4, Appli	C 368	18	0.5	258	5	PCT-US92-04833-1	Sequence 1, Appli
C 296	19	0.5	6138	4	US-09-067-800-4	Sequence 4, Appli	C 369	18	0.5	297	1	US-08-616-368A-17	Sequence 17, Appl
C 297	19	0.5	6138	4	US-09-349-677-4	Sequence 4, Appli	C 370	18	0.5	297	1	US-08-616-368A-17	Sequence 17, Appl
C 298	19	0.5	6138	4	US-09-349-677-4	Sequence 4, Appli	C 371	18	0.5	297	3	US-09-054-298-17	Sequence 17, Appl
C 299	19	0.5	6350	4	US-08-647-826-1	Sequence 1, Appli	C 372	18	0.5	297	3	US-09-054-298-17	Sequence 17, Appl
C 300	19	0.5	7622	4	US-08-305-639-1	Sequence 1, Appli	C 373	18	0.5	297	4	US-08-818-655-17	Sequence 17, Appl
C 301	19	0.5	8342	3	US-08-545-860D-63	Sequence 63, Appl	C 374	18	0.5	297	4	US-08-818-655-17	Sequence 17, Appl
C 302	19	0.5	8342	5	PCT-US94-04496-63	Sequence 63, Appl	C 375	18	0.5	353	4	US-09-366-887A-21	Sequence 21, Appl
C 303	19	0.5	8392	1	US-08-080-255-6	Sequence 6, Appli	C 376	18	0.5	406	4	US-08-868-452-35	Sequence 35, Appl
C 304	19	0.5	8392	3	US-08-465-713-6	Sequence 6, Appli	C 377	18	0.5	406	4	US-08-868-452-35	Sequence 35, Appl
C 305	19	0.5	8392	5	PCT-US93-05857-6	Sequence 6, Appli	C 378	18	0.5	473	1	US-08-868-452-35	Sequence 35, Appl
C 306	19	0.5	8453	4	US-08-167-681-45	Sequence 45, Appl	C 379	18	0.5	473	1	US-08-764-100-16	Sequence 16, Appl
C 307	19	0.5	8920	2	US-08-446-855A-1	Sequence 1, Appli	C 380	18	0.5	587	4	US-09-123-912-102	Sequence 102, App
C 308	19	0.5	8920	4	US-09-150-741-1	Sequence 1, Appli	C 381	18	0.5	587	4	US-09-643-597-102	Sequence 102, App
C 309	19	0.5	10007	4	US-09-410-464-13	Sequence 13, Appl	C 382	18	0.5	587	4	US-09-643-597-102	Sequence 102, App
C 310	19	0.5	10007	4	US-09-410-464-13	Sequence 13, Appl	C 383	18	0.5	605	4	US-09-366-887A-26	Sequence 26, App
C 311	19	0.5	11485	4	US-09-410-464-9	Sequence 9, Appli	C 384	18	0.5	615	4	US-09-385-982-240	Sequence 240, App
C 312	19	0.5	12793	4	US-09-004-838-124	Sequence 124, App	C 385	18	0.5	615	4	US-09-385-982-240	Sequence 240, App
C 313	19	0.5	15062	4	US-09-004-838-89	Sequence 89, Appl	C 386	18	0.5	618	4	US-08-961-810-17	Sequence 17, Appl
C 314	19	0.5	17041	1	US-08-076-011-1	Sequence 1, Appli	C 387	18	0.5	618	4	US-08-961-810-17	Sequence 17, Appl
C 315	19	0.5	17656	4	US-09-433-579-3	Sequence 3, Appli	C 388	18	0.5	618	4	US-08-352-902D-17	Sequence 17, Appl
C 316	19	0.5	17949	4	US-09-087-465-3	Sequence 3, Appli	C 389	18	0.5	618	4	US-08-352-902D-17	Sequence 17, Appl
C 317	19	0.5	38564	4	US-09-734-673-3	Sequence 3, Appli	C 390	18	0.5	684	1	US-08-577-463A-1	Sequence 1, Appli
C 318	19	0.5	38844	4	US-08-734-675-3	Sequence 3, Appli	C 391	18	0.5	684	1	US-08-577-463A-1	Sequence 1, Appli
C 319	19	0.5	43676	3	US-09-356-952-12	Sequence 12, Appl	C 392	18	0.5	713	4	US-09-149-476-72	Sequence 72, Appl

C 393	18	0.5	713	4	US-09-149-476-72	Sequence 72, Appl	466	18	0.5	1453	6	5194600-1	Patent No. 5194600
C 394	18	0.5	804	1	US-08-126-593A-3	Sequence 3, Appl	467	18	0.5	1468	6	5187075-4	Patent No. 5187075
C 395	18	0.5	804	1	US-08-126-593A-3	Sequence 3, Appl	C 468	18	0.5	1468	6	5187075-4	Patent No. 5187075
C 396	18	0.5	804	1	US-08-454-039A-3	Sequence 3, Appl	C 469	18	0.5	1499	4	US-09-484-970B-157	Sequence 157, App
C 397	18	0.5	804	1	US-08-454-039A-3	Sequence 3, Appl	C 470	18	0.5	1529	4	US-08-448-110-1	Sequence 1, Appl
C 398	18	0.5	828	4	US-08-998-416-360	Sequence 360, App	C 471	18	0.5	1529	6	5436393-2	Patent No. 5436393
C 399	18	0.5	828	4	US-08-998-416-360	Sequence 360, App	C 472	18	0.5	1570	3	US-08-617-860B-20	Sequence 20, Appl
C 400	18	0.5	830	4	US-09-149-476-236	Sequence 236, App	C 473	18	0.5	1570	3	US-08-617-860B-20	Sequence 20, Appl
C 401	18	0.5	830	4	US-09-149-476-236	Sequence 236, App	C 474	18	0.5	1601	3	US-08-817-188-3	Sequence 3, Appl
C 402	18	0.5	831	4	US-09-118-554-66	Sequence 66, Appl	C 475	18	0.5	1601	3	US-08-817-188-3	Sequence 3, Appl
C 403	18	0.5	831	4	US-09-118-554-66	Sequence 66, Appl	C 476	18	0.5	1607	1	US-07-679-451-1	Sequence 1, Appl
C 404	18	0.5	831	4	US-09-118-627-66	Sequence 66, Appl	C 477	18	0.5	1607	1	US-07-679-451-1	Sequence 1, Appl
C 405	18	0.5	831	4	US-09-118-627-66	Sequence 66, Appl	C 478	18	0.5	1607	2	US-07-989-847-1	Sequence 1, Appl
C 406	18	0.5	831	4	US-09-602-877A-66	Sequence 66, Appl	C 479	18	0.5	1607	2	US-07-989-847-1	Sequence 1, Appl
C 407	18	0.5	831	4	US-09-602-877A-66	Sequence 66, Appl	C 480	18	0.5	1607	3	US-07-721-847A-3	Sequence 3, Appl
C 408	18	0.5	883	4	US-09-171-209-25	Sequence 25, Appl	C 481	18	0.5	1607	3	US-07-721-847A-3	Sequence 3, Appl
C 409	18	0.5	883	4	US-09-171-209-25	Sequence 25, Appl	C 482	18	0.5	1607	4	US-08-469-411-1	Sequence 1, Appl
C 410	18	0.5	888	4	US-09-171-209-20	Sequence 20, Appl	C 483	18	0.5	1607	4	US-08-469-411-1	Sequence 1, Appl
C 411	18	0.5	888	4	US-09-171-209-20	Sequence 20, Appl	C 484	18	0.5	1607	4	US-08-925-779-3	Sequence 3, Appl
C 412	18	0.5	972	3	US-09-286-690-1	Sequence 1, Appl	C 485	18	0.5	1607	4	US-08-925-779-3	Sequence 3, Appl
C 413	18	0.5	1001	4	US-09-641-638-387	Sequence 387, App	C 486	18	0.5	1607	6	516058-3	Patent No. 516058
C 414	18	0.5	1001	4	US-09-641-638-387	Sequence 387, App	C 487	18	0.5	1607	6	516058-3	Patent No. 516058
C 415	18	0.5	1001	4	US-09-641-638-388	Sequence 388, App	C 488	18	0.5	1618	1	US-08-236-918A-3	Sequence 3, Appl
C 416	18	0.5	1001	4	US-09-641-638-388	Sequence 388, App	C 489	18	0.5	1618	4	US-09-150-864A-3	Sequence 3, Appl
C 417	18	0.5	1020	2	US-07-757-606B-3	Sequence 3, Appl	C 490	18	0.5	1646	1	US-07-995-950-2	Sequence 2, Appl
C 418	18	0.5	1020	2	US-07-757-606B-3	Sequence 3, Appl	C 491	18	0.5	1646	1	US-07-995-950-2	Sequence 2, Appl
C 419	18	0.5	1140	4	US-08-893-654B-3	Sequence 3, Appl	C 492	18	0.5	1646	1	US-08-300-582-2	Sequence 2, Appl
C 420	18	0.5	1140	4	US-08-893-654B-3	Sequence 3, Appl	C 493	18	0.5	1646	1	US-08-300-582-2	Sequence 2, Appl
C 421	18	0.5	1142	1	US-08-006-082A-5	Sequence 5, Appl	C 494	18	0.5	1690	4	US-08-943-731-166	Sequence 166, App
C 422	18	0.5	1142	1	US-08-006-082A-5	Sequence 5, Appl	C 495	18	0.5	1744	4	US-09-380-262B-3	Sequence 3, Appl
C 423	18	0.5	1160	1	US-08-006-082A-4	Sequence 4, Appl	C 496	18	0.5	1890	6	5312912-3	Patent No. 5312912
C 424	18	0.5	1160	1	US-08-006-082A-4	Sequence 4, Appl	C 497	18	0.5	1890	6	5312912-3	Patent No. 5312912
C 425	18	0.5	1172	4	US-08-969-046-5	Sequence 5, Appl	C 498	18	0.5	1906	1	US-08-207-904-18	Sequence 18, Appl
C 426	18	0.5	1260	1	US-07-841-646-4	Sequence 4, Appl	C 499	18	0.5	1906	1	US-08-207-904-18	Sequence 18, Appl
C 427	18	0.5	1260	1	US-07-841-646-4	Sequence 4, Appl	C 500	18	0.5	1934	1	US-07-941-651-1	Sequence 1, Appl
C 428	18	0.5	1260	1	US-07-901-703-14	Sequence 14, Appl	C 501	18	0.5	1934	1	US-07-941-651-1	Sequence 1, Appl
C 429	18	0.5	1260	1	US-07-901-703-14	Sequence 14, Appl	C 502	18	0.5	1934	1	US-08-279-996-1	Sequence 1, Appl
C 430	18	0.5	1260	1	US-08-147-023-4	Sequence 4, Appl	C 503	18	0.5	1934	1	US-08-279-996-1	Sequence 1, Appl
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C 433	18	0.5	1260	1	US-08-447-570-4	Sequence 4, Appl	C 506	18	0.5	1983	1	US-08-383-756-3	Sequence 3, Appl
C 434	18	0.5	1260	1	US-08-447-570-4	Sequence 4, Appl	C 507	18	0.5	1983	2	US-08-460-898-3	Sequence 3, Appl
C 435	18	0.5	1260	2	US-08-449-700-4	Sequence 4, Appl	C 508	18	0.5	1983	2	US-08-460-898-3	Sequence 3, Appl
C 436	18	0.5	1260	2	US-08-449-700-4	Sequence 4, Appl	C 509	18	0.5	2000	4	US-09-338-907-180	Sequence 180, App
C 437	18	0.5	1260	2	US-08-449-699A-4	Sequence 4, Appl	C 510	18	0.5	2000	4	US-09-338-907-180	Sequence 180, App
C 438	18	0.5	1260	5	PCT-US93-05446-14	Sequence 14, Appl	C 511	18	0.5	2000	4	US-09-218-207-180	Sequence 180, App
C 439	18	0.5	1260	5	PCT-US93-05446-14	Sequence 14, Appl	C 512	18	0.5	2073	4	US-09-134-001C-1731	Sequence 1731, App
C 440	18	0.5	1264	1	US-08-006-082A-1	Sequence 1, Appl	C 513	18	0.5	2076	2	US-08-617-101-1	Sequence 1, Appl
C 441	18	0.5	1264	1	US-08-006-082A-1	Sequence 1, Appl	C 514	18	0.5	2076	2	US-08-617-101-1	Sequence 1, Appl
C 442	18	0.5	1265	1	US-08-182-060A-5	Sequence 5, Appl	C 515	18	0.5	2251	4	US-08-991-677-11	Sequence 11, Appl
C 443	18	0.5	1265	1	US-08-182-060A-5	Sequence 5, Appl	C 516	18	0.5	2251	4	US-08-991-677-11	Sequence 11, Appl
C 444	18	0.5	1265	1	US-08-712-702A-5	Sequence 5, Appl	C 517	18	0.5	2267	4	US-09-142-569-5	Sequence 5, Appl
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C 446	18	0.5	1360	1	US-08-383-756-2	Sequence 2, Appl	C 519	18	0.5	2310	1	US-08-461-690B-1	Sequence 1, Appl
C 447	18	0.5	1360	1	US-08-383-756-2	Sequence 2, Appl	C 520	18	0.5	2310	1	US-08-461-690B-1	Sequence 1, Appl
C 448	18	0.5	1360	2	US-08-460-898-2	Sequence 2, Appl	C 521	18	0.5	2311	1	US-08-103-445-1	Sequence 1, Appl
C 449	18	0.5	1360	2	US-08-460-898-2	Sequence 2, Appl	C 522	18	0.5	2311	1	US-08-103-445-1	Sequence 1, Appl
C 450	18	0.5	1380	1	US-08-599-252-82	Sequence 82, Appl	C 523	18	0.5	2331	3	US-08-742-877-3	Sequence 3, Appl
C 451	18	0.5	1380	1	US-08-599-252-82	Sequence 82, Appl	C 524	18	0.5	2401	1	US-08-480-346-1	Sequence 1, Appl
C 452	18	0.5	1380	1	US-08-436-074-55	Sequence 55, Appl	C 525	18	0.5	2401	1	US-08-480-346-1	Sequence 1, Appl
C 453	18	0.5	1380	1	US-08-436-074-55	Sequence 55, Appl	C 526	18	0.5	2401	1	US-08-480-346-1	Sequence 1, Appl
C 454	18	0.5	1380	5	PCT-US96-06352-82	Sequence 82, Appl	C 527	18	0.5	2401	2	US-08-243-541-1	Sequence 1, Appl
C 455	18	0.5	1380	5	PCT-US96-06352-82	Sequence 82, Appl	C 528	18	0.5	2401	2	US-08-243-541-1	Sequence 1, Appl
C 456	18	0.5	1380	5	PCT-US96-06583-82	Sequence 82, Appl	C 529	18	0.5	2401	2	US-08-480-344-1	Sequence 1, Appl
C 457	18	0.5	1429	5	PCT-US96-06583-82	Sequence 82, Appl	C 530	18	0.5	2401	2	US-08-480-344-1	Sequence 1, Appl
C 458	18	0.5	1429	2	US-08-244-205-6	Sequence 6, Appl	C 531	18	0.5	2403	1	US-08-441-139-17	Sequence 17, Appl
C 459	18	0.5	1429	2	US-08-244-205-6	Sequence 6, Appl	C 532	18	0.5	2403	1	US-08-441-139-17	Sequence 17, Appl
C 460	18	0.5	1429	2	US-08-244-205-8	Sequence 8, Appl	C 533	18	0.5	2437	1	US-07-795-859B-5	Sequence 5, Appl
C 461	18	0.5	1429	2	US-08-244-205-8	Sequence 8, Appl	C 534	18	0.5	2437	1	US-07-795-859B-5	Sequence 5, Appl
C 462	18	0.5	1429	5	PCT-US92-10284-6	Sequence 6, Appl	C 535	18	0.5	2437	1	US-08-457-616-5	Sequence 5, Appl
C 463	18	0.5	1429	5	PCT-US92-10284-6	Sequence 6, Appl	C 536	18	0.5	2437	1	US-08-457-616-5	Sequence 5, Appl
C 464	18	0.5	1429	5	PCT-US92-10284-8	Sequence 8, Appl	C 537	18	0.5	2437	4	US-09-235-538-1	Sequence 1, Appl
C 465	18	0.5	1429	5	PCT-US92-10284-8	Sequence 8, Appl	C 538	18	0.5	2437	4	US-09-235-538-1	Sequence 1, Appl

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c 540	18	0.5	2473	2	US-08-540-804-3	Sequence 3, Appli	Sequence 3, Appli
541	18	0.5	2473	2	US-08-218-265-3	Sequence 3, Appli	Sequence 3, Appli
c 542	18	0.5	2473	2	US-08-218-265-3	Sequence 3, Appli	Sequence 3, Appli
543	18	0.5	2473	3	US-08-521-872-3	Sequence 3, Appli	Sequence 3, Appli
c 544	18	0.5	2473	3	US-08-521-872-3	Sequence 3, Appli	Sequence 3, Appli
545	18	0.5	2473	3	US-08-521-872-3	Sequence 3, Appli	Sequence 3, Appli
c 546	18	0.5	2473	4	US-08-590-399-3	Sequence 3, Appli	Sequence 3, Appli
547	18	0.5	2473	4	US-08-590-399-3	Sequence 3, Appli	Sequence 22, Appli
c 548	18	0.5	2612	4	US-09-105-390-7	Sequence 7, Appli	Sequence 1, Appli
549	18	0.5	2663	1	US-08-136-743B-3	Sequence 3, Appli	Sequence 14, Appli
c 550	18	0.5	2663	1	US-08-136-743B-3	Sequence 3, Appli	Sequence 14, Appli
551	18	0.5	2747	2	US-08-874-347-1	Sequence 1, Appli	Sequence 20, Appli
c 552	18	0.5	2747	3	US-09-093-522-1	Sequence 1, Appli	Sequence 20, Appli
553	18	0.5	2775	4	US-09-053-871A-22	Sequence 22, Appli	Sequence 1, Appli
c 554	18	0.5	2781	3	US-08-749-522-4	Sequence 4, Appli	Sequence 28, Appli
555	18	0.5	2802	3	US-08-743-877-1	Sequence 1, Appli	Sequence 28, Appli
c 556	18	0.5	3072	4	US-08-522-217-55	Sequence 55, Appli	Sequence 28, Appli
557	18	0.5	3072	4	US-08-522-217-55	Sequence 55, Appli	Sequence 5, Appli
c 558	18	0.5	3183	2	US-08-939-218A-1	Sequence 1, Appli	Sequence 1, Appli
559	18	0.5	3183	2	US-08-939-218A-1	Sequence 1, Appli	Sequence 1, Appli
c 560	18	0.5	3187	5	PCT-US95-06815-1	Sequence 1, Appli	Sequence 4, Appli
561	18	0.5	3187	5	PCT-US95-06815-1	Sequence 1, Appli	Sequence 4, Appli
c 562	18	0.5	3192	1	US-08-706-037-26	Sequence 26, Appli	Sequence 1, Appli
563	18	0.5	3192	1	US-08-706-037-26	Sequence 26, Appli	Sequence 1, Appli
c 564	18	0.5	3192	1	US-08-940-661A-1	Sequence 1, Appli	Sequence 1, Appli
565	18	0.5	3192	1	US-08-940-661A-1	Sequence 1, Appli	Sequence 1, Appli
c 566	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 1, Appli
567	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 1, Appli
c 568	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 1, Appli
569	18	0.5	3192	2	US-09-083-485-1	Sequence 1, Appli	Sequence 1, Appli
c 570	18	0.5	3387	1	US-08-261-822A-5	Sequence 5, Appli	Sequence 1, Appli
571	18	0.5	3387	5	PCT-US95-0774A-5	Sequence 5, Appli	Sequence 10, Appli
c 572	18	0.5	3395	4	US-09-103-478-3	Sequence 3, Appli	Sequence 5, Appli
573	18	0.5	3395	4	US-09-103-478-3	Sequence 3, Appli	Sequence 5, Appli
c 574	18	0.5	3395	4	US-09-193-931C-3	Sequence 3, Appli	Sequence 5, Appli
575	18	0.5	3395	4	US-09-193-931C-3	Sequence 3, Appli	Sequence 5, Appli
c 576	18	0.5	3511	4	US-09-380-262B-5	Sequence 5, Appli	Sequence 5, Appli
577	18	0.5	3528	4	US-08-984-320-2	Sequence 2, Appli	Sequence 2, Appli
c 578	18	0.5	3528	4	US-08-984-320-2	Sequence 2, Appli	Sequence 2, Appli
579	18	0.5	3528	4	US-08-487-087A-2	Sequence 2, Appli	Sequence 11, Appli
c 580	18	0.5	3528	4	US-08-487-087A-2	Sequence 2, Appli	Sequence 11, Appli
581	18	0.5	3623	2	US-07-989-847-13	Sequence 13, Appli	Sequence 11, Appli
c 582	18	0.5	3623	2	US-07-989-847-13	Sequence 13, Appli	Sequence 11, Appli
583	18	0.5	3623	4	US-08-469-411-13	Sequence 13, Appli	Sequence 11, Appli
c 584	18	0.5	3623	4	US-08-469-411-13	Sequence 13, Appli	Sequence 11, Appli
585	18	0.5	3627	1	US-08-104-072B-6	Sequence 6, Appli	Sequence 1, Appli
c 586	18	0.5	3627	1	US-08-104-072B-6	Sequence 6, Appli	Sequence 1, Appli
587	18	0.5	3627	1	US-08-351-413-7	Sequence 7, Appli	Sequence 1, Appli
c 588	18	0.5	3627	1	US-08-351-413-7	Sequence 7, Appli	Sequence 1, Appli
589	18	0.5	3627	2	US-09-025-583-7	Sequence 7, Appli	Sequence 2, Appli
c 590	18	0.5	3627	2	US-09-025-583-7	Sequence 7, Appli	Sequence 2, Appli
591	18	0.5	3697	1	US-08-571-758-1	Sequence 1, Appli	Sequence 5, Appli
c 592	18	0.5	3697	1	US-08-571-758-1	Sequence 1, Appli	Sequence 5, Appli
593	18	0.5	3697	1	US-08-909-984A-1	Sequence 1, Appli	Sequence 15, Appli
c 594	18	0.5	3697	1	US-08-909-984A-1	Sequence 1, Appli	Sequence 15, Appli
595	18	0.5	3697	1	US-08-909-983-1	Sequence 1, Appli	Sequence 16, Appli
c 596	18	0.5	3697	1	US-08-909-983-1	Sequence 1, Appli	Sequence 16, Appli
597	18	0.5	3744	4	US-08-961-527-263	Sequence 263, App	Sequence 1, Appli
c 598	18	0.5	3744	4	US-08-961-527-263	Sequence 263, App	Sequence 1, Appli
599	18	0.5	4084	3	US-08-866-340-1	Sequence 1, Appli	Sequence 3, Appli
c 600	18	0.5	4084	3	US-08-866-340-1	Sequence 1, Appli	Sequence 3, Appli
601	18	0.5	4383	4	US-08-397-653B-2	Sequence 2, Appli	Sequence 31, Appli
c 602	18	0.5	4383	4	US-08-397-653B-2	Sequence 2, Appli	Sequence 31, Appli
603	18	0.5	4383	6	5175095-4	Patent No. 5175095	Sequence 31, Appli
c 604	18	0.5	4383	6	5175095-4	Patent No. 5175095	Sequence 36, Appli
605	18	0.5	4383	6	5177307-1	Patent No. 5177307	Sequence 36, Appli
c 606	18	0.5	4383	6	5177307-1	Patent No. 5177307	Sequence 36, Appli
607	18	0.5	4456	3	US-08-321-686B-1	Sequence 1, Appli	Sequence 36, Appli
c 608	18	0.5	4456	3	US-08-321-686B-1	Sequence 1, Appli	Sequence 36, Appli
609	18	0.5	4460	4	US-09-103-875-4	Sequence 4, Appli	Sequence 36, Appli
c 610	18	0.5	4460	4	US-09-103-875-4	Sequence 4, Appli	Sequence 36, Appli
611	18	0.5	4507	2	US-08-568-459A-3	Sequence 3, Appli	Sequence 36, Appli

c 685	18	0.5	12124	1	US-08-456-265A-36	Sequence 36, Appl	c 758	17	0.5	24	2	US-08-849-021-70	Sequence 70, Appl
c 686	18	0.5	12124	1	US-08-455-416-36	Sequence 36, Appl	759	17	0.5	56	4	US-09-636-735A-4	Sequence 4, Appl
c 687	18	0.5	12124	1	US-08-455-416-36	Sequence 36, Appl	c 760	17	0.5	56	4	US-09-636-735A-4	Sequence 4, Appl
c 688	18	0.5	12124	1	US-08-455-244-36	Sequence 36, Appl	761	17	0.5	148	4	US-08-991-789A-229	Sequence 229, App
c 689	18	0.5	12124	1	US-08-455-244-36	Sequence 36, Appl	762	17	0.5	148	4	US-09-062-451-229	Sequence 229, App
c 690	18	0.5	12124	1	US-08-454-876-36	Sequence 36, Appl	763	17	0.5	148	4	US-09-598-326-229	Sequence 229, App
c 691	18	0.5	12124	1	US-08-454-876-36	Sequence 36, Appl	c 764	17	0.5	165	1	US-08-209-747-9	Sequence 9, Appl
c 692	18	0.5	12124	1	US-08-457-364-36	Sequence 36, Appl	c 765	17	0.5	165	1	US-08-458-298-9	Sequence 9, Appl
c 693	18	0.5	12124	2	US-08-457-364-36	Sequence 36, Appl	766	17	0.5	182	4	US-09-712-016-53	Sequence 53, Appl
c 694	18	0.5	12124	2	US-08-456-262-36	Sequence 36, Appl	c 767	17	0.5	221	4	US-08-943-731-12	Sequence 12, Appl
c 695	18	0.5	12124	2	US-08-456-262-36	Sequence 36, Appl	c 768	17	0.5	237	4	US-09-328-111-287	Sequence 287, App
c 696	18	0.5	12124	2	US-08-456-240-36	Sequence 36, Appl	769	17	0.5	232	4	US-08-971-188-7	Sequence 7, Appl
c 697	18	0.5	12124	2	US-08-456-240-36	Sequence 36, Appl	770	17	0.5	250	4	US-08-971-188-6	Sequence 6, Appl
c 698	18	0.5	12124	2	US-08-455-736-36	Sequence 36, Appl	771	17	0.5	306	4	US-09-605-785-650	Sequence 108, App
c 699	18	0.5	12124	2	US-08-455-736-36	Sequence 36, Appl	772	17	0.5	349	4	US-09-884-970B-108	Sequence 102, App
c 700	18	0.5	12124	2	US-08-971-217-36	Sequence 36, Appl	c 773	17	0.5	425	2	US-08-967-101-102	Sequence 102, App
c 701	18	0.5	12124	2	US-08-971-217-36	Sequence 36, Appl	c 774	17	0.5	425	2	US-08-524-541-102	Sequence 102, App
c 702	18	0.5	12124	4	US-09-350-600-36	Sequence 36, Appl	c 775	17	0.5	425	3	US-09-124-698-102	Sequence 102, App
c 703	18	0.5	12124	4	US-09-350-600-36	Sequence 36, Appl	c 776	17	0.5	425	4	US-09-127-480-102	Sequence 102, App
c 704	18	0.5	12730	4	US-09-004-838-91	Sequence 91, Appl	c 777	17	0.5	425	4	US-08-496-841C-102	Sequence 102, App
c 705	18	0.5	12730	4	US-09-004-838-91	Sequence 91, Appl	c 778	17	0.5	435	4	US-09-124-523-102	Sequence 102, App
c 706	18	0.5	13158	2	US-08-687-080-105	Sequence 105, App	779	17	0.5	484	6	5496550-5	Patent No. 5496550
c 707	18	0.5	15144	3	US-08-458-434A-6	Sequence 6, Appl	780	17	0.5	500	4	US-09-328-111-343	Sequence 343, App
c 708	18	0.5	15144	3	US-08-458-434A-6	Sequence 6, Appl	c 781	17	0.5	570	4	US-09-385-982-417	Sequence 417, App
c 709	18	0.5	17341	4	US-09-415-946-1	Sequence 1, Appl	782	17	0.5	575	3	US-08-726-807B-6	Sequence 6, Appl
c 710	18	0.5	17341	4	US-09-415-946-1	Sequence 1, Appl	c 783	17	0.5	575	3	US-08-726-807B-6	Sequence 6, Appl
c 711	18	0.5	17606	4	US-08-943-731-4	Sequence 4, Appl	784	17	0.5	575	3	US-09-258-367-6	Sequence 6, Appl
c 712	18	0.5	22846	2	US-08-469-461-3	Sequence 3, Appl	c 785	17	0.5	575	3	US-09-258-367-6	Sequence 6, Appl
c 713	18	0.5	22846	2	US-08-469-461-3	Sequence 3, Appl	786	17	0.5	575	4	US-09-546-550-6	Sequence 6, Appl
c 714	18	0.5	22846	3	US-07-890-609-3	Sequence 3, Appl	c 787	17	0.5	575	4	US-09-546-550-6	Sequence 6, Appl
c 715	18	0.5	22846	3	US-07-890-609-3	Sequence 3, Appl	788	17	0.5	575	4	US-09-431-414-6	Sequence 6, Appl
c 716	18	0.5	29604	3	US-08-781-891-207	Sequence 207, App	c 789	17	0.5	575	4	US-09-431-414-6	Sequence 6, Appl
c 717	18	0.5	29604	3	US-08-781-891-207	Sequence 207, App	790	17	0.5	575	4	US-09-225-670-6	Sequence 6, Appl
c 718	18	0.5	32207	2	US-08-770-379-20	Sequence 20, Appl	c 791	17	0.5	575	4	US-09-225-670-6	Sequence 6, Appl
c 719	18	0.5	32207	2	US-08-757-669A-20	Sequence 20, Appl	792	17	0.5	575	4	US-09-431-349C-6	Sequence 6, Appl
c 720	18	0.5	32207	4	US-09-230-371A-20	Sequence 20, Appl	c 793	17	0.5	575	4	US-09-431-349C-6	Sequence 6, Appl
c 721	18	0.5	35100	2	US-08-770-379-17	Sequence 17, Appl	794	17	0.5	592	3	US-07-721-847A-1	Sequence 1, Appl
c 722	18	0.5	35100	4	US-08-757-669A-17	Sequence 17, Appl	c 795	17	0.5	592	3	US-07-721-847A-1	Sequence 1, Appl
c 723	18	0.5	35100	4	US-09-230-371A-17	Sequence 3, Appl	796	17	0.5	592	4	US-08-925-779-1	Sequence 1, Appl
c 724	18	0.5	36651	4	US-09-738-894A-3	Sequence 3, Appl	c 797	17	0.5	592	4	US-08-925-779-1	Sequence 1, Appl
c 725	18	0.5	43795	3	US-08-742-185-101	Sequence 101, App	798	17	0.5	592	6	5166058-1	Patent No. 5166058
c 726	18	0.5	43795	3	US-08-742-185-101	Sequence 101, App	c 799	17	0.5	592	6	5166058-1	Patent No. 5166058
c 727	18	0.5	43950	4	US-09-735-934A-3	Sequence 3, Appl	800	17	0.5	631	4	US-08-991-789A-34	Sequence 34, Appl
c 728	18	0.5	44543	4	US-09-146-053-5	Sequence 5, Appl	c 801	17	0.5	631	4	US-08-991-789A-34	Sequence 34, Appl
c 729	18	0.5	45246	4	US-09-146-053-6	Sequence 6, Appl	802	17	0.5	631	4	US-09-062-451-34	Sequence 34, Appl
c 730	18	0.5	45246	4	US-09-146-053-6	Sequence 6, Appl	c 803	17	0.5	631	4	US-09-062-451-34	Sequence 34, Appl
c 731	18	0.5	45716	4	US-08-965-048-5	Sequence 5, Appl	804	17	0.5	631	4	US-09-598-326-34	Sequence 34, Appl
c 732	18	0.5	45716	4	US-08-965-048-5	Sequence 5, Appl	c 805	17	0.5	636	4	US-09-598-326-34	Sequence 34, Appl
c 733	18	0.5	45989	4	US-08-965-048-6	Sequence 6, Appl	c 806	17	0.5	636	4	US-09-221-017B-1004	Sequence 1004, Ap
c 734	18	0.5	45989	4	US-08-965-048-6	Sequence 6, Appl	c 807	17	0.5	645	4	US-09-328-111-106	Sequence 106, App
c 735	18	0.5	55516	2	US-08-996-306-1	Sequence 1, Appl	c 808	17	0.5	645	4	US-09-288-143-22	Sequence 22, Appl
c 736	18	0.5	55516	4	US-09-338-907-1	Sequence 1, Appl	c 809	17	0.5	646	4	US-09-288-143-22	Sequence 22, Appl
c 737	18	0.5	55516	4	US-09-218-207-1	Sequence 1, Appl	c 810	17	0.5	671	4	US-09-643-597-131	Sequence 131, App
c 738	18	0.5	55520	4	US-09-338-907-179	Sequence 179, App	c 811	17	0.5	676	4	US-09-490-818-1	Sequence 1, Appl
c 739	18	0.5	55520	4	US-09-218-207-179	Sequence 179, App	812	17	0.5	705	4	US-09-328-111-674	Sequence 674, App
c 740	18	0.5	65042	4	US-09-784-316-3	Sequence 3, Appl	c 813	17	0.5	705	4	US-09-328-111-674	Sequence 674, App
c 741	18	0.5	65042	4	US-09-784-316-3	Sequence 3, Appl	c 814	17	0.5	740	4	US-08-998-416-771	Sequence 771, App
c 742	18	0.5	72604	4	US-09-268-992-7	Sequence 7, Appl	c 815	17	0.5	741	4	US-09-149-476-202	Sequence 202, App
c 743	18	0.5	72604	4	US-09-657-474-7	Sequence 7, Appl	c 816	17	0.5	750	1	US-08-224-195-1	Sequence 1, Appl
c 744	18	0.5	87350	3	US-08-781-891-79	Sequence 79, Appl	c 817	17	0.5	773	4	US-09-149-476-20	Sequence 20, Appl
c 745	18	0.5	87350	3	US-08-781-891-79	Sequence 79, Appl	818	17	0.5	780	1	US-08-224-195-2	Sequence 2, Appl
c 746	18	0.5	87543	4	US-09-791-211-3	Sequence 3, Appl	819	17	0.5	842	2	US-08-820-170A-3	Sequence 3, Appl
c 747	18	0.5	87543	4	US-09-791-211-3	Sequence 3, Appl	c 820	17	0.5	842	3	US-09-055-699-3	Sequence 3, Appl
c 748	18	0.5	98844	4	US-09-791-211-10	Sequence 10, Appl	821	17	0.5	842	4	US-09-273-565-3	Sequence 3, Appl
c 749	18	0.5	98844	4	US-09-791-211-10	Sequence 10, Appl	822	17	0.5	842	4	US-09-565-538-3	Sequence 3, Appl
c 750	18	0.5	152331	3	US-09-128-155-16	Sequence 16, Appl	823	17	0.5	842	4	US-09-661-468-3	Sequence 3, Appl
c 751	18	0.5	152331	3	US-09-128-155-16	Sequence 16, Appl	824	17	0.5	852	2	US-09-069-330-1	Sequence 1, Appl
c 752	18	0.5	169998	4	US-09-676-610B-24	Sequence 24, Appl	c 825	17	0.5	860	1	US-08-310-416A-19	Sequence 19, Appl
c 753	18	0.5	169998	4	US-09-676-610B-24	Sequence 24, Appl	c 826	17	0.5	860	2	US-08-888-171-19	Sequence 19, Appl
c 754	18	0.5	176373	3	US-09-128-155-17	Sequence 17, Appl	c 827	17	0.5	901	4	US-09-475-316A-12	Sequence 12, Appl
c 755	17	0.5	22	2	US-08-849-021-84	Sequence 84, Appl	c 828	17	0.5	901	4	US-09-475-316A-12	Sequence 12, Appl
c 756	17	0.5	22	2	US-08-849-021-84	Sequence 84, Appl	829	17	0.5	917	2	US-08-924-759-17	Sequence 17, Appl
c 757	17	0.5	24	2	US-08-849-021-70	Sequence 70, Appl	c 830	17	0.5	917	2	US-08-924-759-17	Sequence 17, Appl

831	17	0.5	917	3	US-09-248-335-17	Sequence 17, Appl	904	17	0.5	1972	1	US-08-463-048-1	Sequence 1, Appl
C 832	17	0.5	917	3	US-09-248-335-17	Sequence 17, Appl	905	17	0.5	1972	1	US-08-463-229-1	Sequence 1, Appl
C 833	17	0.5	939	4	US-09-079-029-7	Sequence 7, Appl	906	17	0.5	1972	2	US-08-302-891-1	Sequence 1, Appl
C 834	17	0.5	1006	4	US-09-058-368-4	Sequence 4, Appl	C 907	17	0.5	1997	4	US-09-269-731-3	Sequence 3, Appl
C 835	17	0.5	1048	2	US-08-897-340-3	Sequence 3, Appl	C 908	17	0.5	2019	4	US-09-160-494-3	Sequence 3, Appl
C 836	17	0.5	1048	3	US-09-252-329-3	Sequence 3, Appl	C 909	17	0.5	2030	2	US-08-923-536A-1	Sequence 1, Appl
C 837	17	0.5	1068	4	US-09-235-103-3	Sequence 3, Appl	C 910	17	0.5	2030	2	US-08-923-536A-1	Sequence 1, Appl
C 838	17	0.5	1146	2	US-08-504-265B-74	Sequence 74, Appl	C 911	17	0.5	2065	2	US-08-968-751-1	Sequence 1, Appl
C 839	17	0.5	1195	6	5240848-6	Patent No. 5240848	C 912	17	0.5	2071	1	US-07-923-724-1	Sequence 1, Appl
C 840	17	0.5	1279	4	US-09-277-716-31	Sequence 31, Appl	C 913	17	0.5	2071	2	US-08-609-426A-1	Sequence 1, Appl
C 841	17	0.5	1279	4	US-09-277-716-31	Sequence 31, Appl	C 914	17	0.5	2071	2	US-08-374-652C-3	Sequence 3, Appl
C 842	17	0.5	1279	4	US-09-609-161B-31	Sequence 31, Appl	C 915	17	0.5	2075	1	US-08-167-628-1	Sequence 1, Appl
C 843	17	0.5	1279	4	US-09-609-161B-31	Sequence 31, Appl	C 916	17	0.5	2075	1	US-08-167-628-1	Sequence 1, Appl
C 844	17	0.5	1280	4	US-09-096-776B-4	Sequence 4, Appl	C 917	17	0.5	2075	1	US-08-386-680-1	Sequence 1, Appl
C 845	17	0.5	1320	4	US-09-370-838-22	Sequence 22, Appl	C 918	17	0.5	2075	1	US-08-386-680-1	Sequence 1, Appl
C 846	17	0.5	1328	4	US-09-370-838-24	Sequence 24, Appl	C 919	17	0.5	2075	1	US-08-459-717-1	Sequence 1, Appl
C 847	17	0.5	1330	2	US-09-036-582-33	Sequence 33, Appl	C 920	17	0.5	2075	1	US-08-459-717-1	Sequence 1, Appl
C 848	17	0.5	1330	2	US-09-036-582-33	Sequence 33, Appl	C 921	17	0.5	2075	1	US-08-712-302-1	Sequence 1, Appl
C 849	17	0.5	1331	4	US-09-370-838-27	Sequence 27, Appl	C 922	17	0.5	2075	1	US-08-712-302-1	Sequence 1, Appl
C 850	17	0.5	1333	4	US-09-370-838-28	Sequence 28, Appl	C 923	17	0.5	2075	2	US-08-880-031-1	Sequence 1, Appl
C 851	17	0.5	1347	4	US-09-286-529-18	Sequence 18, Appl	C 924	17	0.5	2075	2	US-08-880-031-1	Sequence 1, Appl
C 852	17	0.5	1355	4	US-09-370-838-31	Sequence 31, Appl	C 925	17	0.5	2075	3	US-09-097-179-1	Sequence 1, Appl
C 853	17	0.5	1356	1	US-08-592-936B-22	Sequence 22, Appl	C 926	17	0.5	2075	3	US-09-097-179-1	Sequence 1, Appl
C 854	17	0.5	1356	1	US-08-788-928A-2	Sequence 2, Appl	C 927	17	0.5	2075	4	US-09-080-715-1	Sequence 1, Appl
C 855	17	0.5	1356	2	US-09-111-573-22	Sequence 22, Appl	C 928	17	0.5	2075	4	US-09-080-715-1	Sequence 1, Appl
C 856	17	0.5	1362	4	US-08-979-608A-12	Sequence 12, Appl	C 929	17	0.5	2075	4	US-09-142-569-7	Sequence 7, Appl
C 857	17	0.5	1362	4	US-08-979-608A-12	Sequence 12, Appl	C 930	17	0.5	2075	5	US-09-142-569-7	Sequence 7, Appl
C 858	17	0.5	1407	4	US-09-134-001C-1162	Sequence 1162, Ap	C 931	17	0.5	2075	5	PCT-US96-08140-1	Sequence 1, Appl
C 859	17	0.5	1422	4	US-08-979-608A-13	Sequence 13, Appl	C 932	17	0.5	2075	5	PCT-US96-08140-1	Sequence 1, Appl
C 860	17	0.5	1422	4	US-08-979-608A-13	Sequence 13, Appl	C 933	17	0.5	2096	1	US-08-458-084-1	Sequence 1, Appl
C 861	17	0.5	1450	3	US-08-617-860B-22	Sequence 22, Appl	C 934	17	0.5	2096	1	US-08-205-508-1	Sequence 1, Appl
C 862	17	0.5	1450	3	US-08-617-860B-22	Sequence 22, Appl	C 935	17	0.5	2096	1	US-08-278-630A-10	Sequence 10, Appl
C 863	17	0.5	1494	4	US-09-255-502-1	Sequence 1, Appl	C 936	17	0.5	2096	5	PCT-US95-02945-1	Sequence 1, Appl
C 864	17	0.5	1496	6	RE34606-1	Patent No. RE34606	C 937	17	0.5	2099	4	US-09-643-597-158	Sequence 158, App
C 865	17	0.5	1497	1	US-08-322-677A-6	Sequence 6, Appl	C 938	17	0.5	2101	2	US-08-860-150-1	Sequence 1, Appl
C 866	17	0.5	1497	1	US-08-322-677A-6	Sequence 6, Appl	C 939	17	0.5	2101	3	US-09-338-132-1	Sequence 1, Appl
C 867	17	0.5	1497	3	US-08-898-218-6	Sequence 6, Appl	C 940	17	0.5	2116	1	US-07-811-048-9	Sequence 9, Appl
C 868	17	0.5	1497	3	US-08-848-793-6	Sequence 6, Appl	C 941	17	0.5	2145	2	US-08-592-936B-16	Sequence 16, Appl
C 869	17	0.5	1497	4	US-09-445-270-1	Sequence 1, Appl	C 942	17	0.5	2145	2	US-09-111-573-16	Sequence 16, Appl
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C 871	17	0.5	1499	4	US-09-484-970B-157	Sequence 157, App	C 944	17	0.5	2160	4	US-09-395-115-15	Sequence 15, Appl
C 872	17	0.5	1513	4	US-09-178-155-1	Sequence 1, Appl	C 945	17	0.5	2160	4	US-08-436-265-15	Sequence 15, Appl
C 873	17	0.5	1519	1	US-07-971-759-19	Sequence 19, Appl	C 946	17	0.5	2160	4	US-09-679-187-15	Sequence 15, Appl
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C 875	17	0.5	1524	4	US-08-840-767-3	Sequence 3, Appl	C 948	17	0.5	2190	4	US-09-729-995-1	Sequence 1, Appl
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C 877	17	0.5	1556	1	US-08-457-135-3	Sequence 3, Appl	C 950	17	0.5	2213	1	US-08-788-928A-1	Sequence 1, Appl
C 878	17	0.5	1573	1	US-08-597-545-4	Sequence 4, Appl	C 951	17	0.5	2213	2	US-09-111-573-12	Sequence 12, Appl
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C 881	17	0.5	1608	5	PCT-US94-02891-68	Sequence 1, Appl	C 954	17	0.5	2236	3	US-08-829-525-23	Sequence 23, Appl
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C 883	17	0.5	1617	4	US-08-979-608A-11	Sequence 11, Appl	C 956	17	0.5	2236	4	US-08-937-389-23	Sequence 23, Appl
C 884	17	0.5	1627	4	US-09-484-970B-19	Sequence 19, Appl	C 957	17	0.5	2236	4	US-09-310-367-23	Sequence 23, Appl
C 885	17	0.5	1670	3	US-08-709-839-1	Sequence 1, Appl	C 958	17	0.5	2236	3	US-09-032-337-23	Sequence 23, Appl
C 886	17	0.5	1670	4	US-08-829-838-1	Sequence 1, Appl	C 959	17	0.5	2238	3	US-08-617-860B-28	Sequence 28, Appl
C 887	17	0.5	1676	4	US-09-009-443-1	Sequence 1, Appl	C 960	17	0.5	2413	4	US-09-367-206-2	Sequence 2, Appl
C 888	17	0.5	1700	2	US-08-897-340-4	Sequence 4, Appl	C 961	17	0.5	2466	4	US-09-363-243-1	Sequence 1, Appl
C 889	17	0.5	1700	3	US-09-252-329-4	Sequence 4, Appl	C 962	17	0.5	2466	4	US-09-363-243-1	Sequence 1, Appl
C 890	17	0.5	1716	1	US-08-348-792-1	Sequence 1, Appl	C 963	17	0.5	2676	4	US-09-484-970B-41	Sequence 41, Appl
C 891	17	0.5	1716	2	US-08-462-738-1	Sequence 1, Appl	C 964	17	0.5	2747	2	US-08-874-347-1	Sequence 1, Appl
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C 893	17	0.5	1716	4	US-08-880-875-1	Sequence 1, Appl	C 966	17	0.5	2847	1	US-08-087-007-2	Sequence 2, Appl
C 894	17	0.5	1756	2	US-08-879-260-3	Sequence 3, Appl	C 967	17	0.5	2847	3	US-08-483-433-2	Sequence 2, Appl
C 895	17	0.5	1758	4	US-09-370-838-25	Sequence 25, Appl	C 968	17	0.5	2847	4	US-09-484-970B-22	Sequence 22, Appl
C 896	17	0.5	1811	3	US-09-231-529-5	Sequence 5, Appl	C 969	17	0.5	2847	5	PCT-US92-05920-2	Sequence 2, Appl
C 897	17	0.5	1811	4	US-08-577-816-5	Sequence 5, Appl	C 970	17	0.5	2877	4	US-09-235-103-1	Sequence 1, Appl
C 898	17	0.5	1868	1	US-08-069-863-1	Sequence 1, Appl	C 971	17	0.5	2917	1	US-08-592-936B-20	Sequence 20, Appl
C 899	17	0.5	1868	1	US-08-309-069-1	Sequence 1, Appl	C 972	17	0.5	2917	2	US-09-111-573-20	Sequence 20, Appl
C 900	17	0.5	1868	1	US-08-562-831-1	Sequence 1, Appl	C 973	17	0.5	2998	3	US-09-054-368-1	Sequence 1, Appl
C 901	17	0.5	1868	5	PCT-US95-05520-1	Sequence 1, Appl	C 974	17	0.5	2998	3	US-09-054-368-1	Sequence 1, Appl
C 902	17	0.5	1910	4	US-09-071-709-8	Sequence 8, Appl	C 975	17	0.5	2998	3	US-09-054-274-1	Sequence 1, Appl
C 903	17	0.5	1930	1	US-07-982-112-1	Sequence 1, Appl	C 976	17	0.5	2998	3	US-09-054-274-1	Sequence 1, Appl





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1  RESULT 3
2  US-08-487-002-20/c
3  ; Sequence 20, Application US/08487002
4  ; Patent No. 5710001
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Shattuck-Eidens, Donna M.
7  ; APPLICANT: Simard, Jacques
8  ; APPLICANT: Emi, Mitsuru
9  ; APPLICANT: Nakamura, Yusuke
10 ; APPLICANT: Durocher, Francine
11 ; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
12 ; TITLE OF INVENTION: Susceptibility Gene
13 ; NUMBER OF SEQUENCES: 85
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
16 ; STREET: 1201 New York Avenue, N.W., Suite 1000
17 ; CITY: Washington
18 ; STATE: DC
19 ; COUNTRY: USA
20 ; ZIP: 20005
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/487,002
28 ; FILING DATE:
29 ; CLASSIFICATION: 424
30 ; PRIORITY APPLICATION DATA:
31 ; APPLICATION NUMBER: US 08/409,305
32 ; FILING DATE: 24-MAR-1995
33 ; PRIORITY APPLICATION DATA:
34 ; APPLICATION NUMBER: US 08/348,824

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1  RESULT 4
2  US-08-483-554B-20/c
3  ; Sequence 20, Application US/08483554B
4  ; Patent No. 5747282
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Skolnick, Mark H.
7  ; APPLICANT: Goldgar, David E.
8  ; APPLICANT: Miki, Yoshio
9  ; APPLICANT: Swenson, Jeff
10 ; APPLICANT: Kamb, Alexander
11 ; APPLICANT: Harshman, Keith D.
12 ; APPLICANT: Shattuck-Eidens, Donna M.
13 ; APPLICANT: Tavtighian, Sean V.
14 ; APPLICANT: Wiseman, Roger W.
15 ; APPLICANT: Futreal, P. Andrew
16 ; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
17 ; TITLE OF INVENTION: Susceptibility Gene
18 ; NUMBER OF SEQUENCES: 85
19 ; CORRESPONDENCE ADDRESS:
20 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
21 ; STREET: 1201 New York Avenue, N.W., Suite 1000
22 ; CITY: Washington
23 ; STATE: DC
24 ; COUNTRY: USA
25 ; ZIP: 20005
26 ; COMPUTER READABLE FORM:
27 ; MEDIUM TYPE: Floppy disk
28 ; COMPUTER: IBM PC compatible
29 ; OPERATING SYSTEM: PC-DOS/MS-DOS
30 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
31 ; CURRENT APPLICATION DATA:
32 ; APPLICATION NUMBER: US/08/483,554B
33 ; FILING DATE: 07-JUN-1995
34 ; CLASSIFICATION: 514

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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/409,305  
;; FILING DATE: 24-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/348,824  
;; FILING DATE: 29-NOV-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/308,104  
;; FILING DATE: 16-SEP-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/300,266  
;; FILING DATE: 02-SEP-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/289,221  
;; FILING DATE: 12-AUG-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ihnen, Jeffrey L.  
;; REGISTRATION NUMBER: 28,957  
;; REFERENCE/DOCKET NUMBER: 24884-109347  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-962-4810  
;; TELEFAX: 202-962-8300  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6769 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;;  
US-08-483-554B-20

Query Match 0.9%; Score 32; DB 1; Length 6769;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3215 TATATATATATATATATATATATATATATAT 3246  
Db 1171 TATATATATATATATATATATATATATATAT 1140

RESULT 5  
US-08-488-011B-20/c  
; Sequence 20, Application US/08488011B  
; Patent No. 5753441  
; GENERAL INFORMATION:  
; APPLICANT: Skolnick, Mark H.  
; APPLICANT: Goldgar, David E.  
; APPLICANT: Miki, Yoshio  
; APPLICANT: Swenson, Jeff  
; APPLICANT: Kamb, Alexander  
; APPLICANT: Harshman, Keith D.  
; APPLICANT: Shattuck-Eidens, Donna M.  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Wiseman, Roger W.  
; APPLICANT: Futreal, P. Andrew  
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
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;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/409,305  
;; FILING DATE: 24-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/348,824  
;; FILING DATE: 29-NOV-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/308,104  
;; FILING DATE: 16-SEP-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/300,266  
;; FILING DATE: 02-SEP-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/289,221  
;; FILING DATE: 12-AUG-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ihnen, Jeffrey L.  
;; REGISTRATION NUMBER: 28,957  
;; REFERENCE/DOCKET NUMBER: 24884-109347-09  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-962-4810  
;; TELEFAX: 202-962-8300  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6769 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;;  
US-08-488-011B-20

Query Match 0.9%; Score 32; DB 1; Length 6769;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3215 TATATATATATATATATATATATATATATAT 3246  
Db 1171 TATATATATATATATATATATATATATATAT 1140

RESULT 6  
US-08-850-727-20/c  
; Sequence 20, Application US/08850727  
; Patent No. 6162897  
; GENERAL INFORMATION:  
; APPLICANT: Skolnick, Mark H.  
; APPLICANT: Goldgar, David E.  
; APPLICANT: Miki, Yoshio  
; APPLICANT: Swenson, Jeff  
; APPLICANT: Kamb, Alexander  
; APPLICANT: Harshman, Keith D.  
; APPLICANT: Shattuck-Eidens, Donna M.  
; APPLICANT: Tavtigian, Sean V.  
; APPLICANT: Wiseman, Roger W.  
; APPLICANT: Futreal, P. Andrew  
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
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APPLICATION NUMBER: US/08/850,727  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,554  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,824  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,104  
FILING DATE: 16-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,266  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,221  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6769 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-850-727-20

Query Match 0.9%; Score 32; DB 4; Length 6769;  
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3215 TATATATATATATATATATATATATATATAT 3246  
Db 1171 TATATATATATATATATATATATATATATAT 1140

RESULT 7  
PCT-US95-10202-20/c  
Sequence 20, Application PC/TUS9510202  
GENERAL INFORMATION:  
APPLICANT: Shattuck-Eidens, Donna M.  
APPLICANT: Simard, Jacques  
APPLICANT: Emi, Mitsuru  
APPLICANT: Nakamura, Yusuke  
APPLICANT: Durocher, Francine  
TITLE OF INVENTION: In Vivo Mutations and Polymorphisms  
TITLE OF INVENTION: in the 17q-linked Breast and Ovarian Cancer  
TITLE OF INVENTION: Susceptibility Gene  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10202  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/409,305  
FILING DATE: 24-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,824  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,104  
FILING DATE: 16-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,266  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,221  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6769 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-10202-20

Query Match 0.9%; Score 32; DB 5; Length 6769;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3215 TATATATATATATATATATATATATATATAT 3246  
Db 1171 TATATATATATATATATATATATATATATAT 1140

RESULT 8  
PCT-US95-10203-20/c  
Sequence 20, Application PC/TUS9510203  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Goldgar, David E.  
APPLICANT: Miki, Yoshio  
APPLICANT: Swenson, Jeff  
APPLICANT: Kamb, Alexander  
APPLICANT: Harshman, Keith D.  
APPLICANT: Shattuck-Eidens, Donna M.  
APPLICANT: Tavtigian, Sean V.  
APPLICANT: Wiseman, Roger W.  
APPLICANT: Futreal, P. Andrew  
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
TITLE OF INVENTION: Susceptibility Gene



Query Match      0.7%;    Score 26;    DB 6;    Length 1195;

RESULT 13  
US-09-150-864A-3/c  
; Sequence 3, Application US/09150864A

Patent No. 6355779  
GENERAL INFORMATION:  
APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor  
TITLE OF INVENTION: That Binds Thereto  
FILE REFERENCE: 2801-B  
CURRENT APPLICATION NUMBER: US/09/150,864A  
CURRENT FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 08/060,843  
PRIOR FILING DATE: 1993-05-07  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1618  
TYPE: DNA  
ORGANISM: Homo sapiens (clone: human4-1BB-L(7A))  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4)..(765)  
US-09-150-864A-3

Query Match 0.7%; Score 26; DB 4; Length 1618;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3216 ATATATATATATATATATATATATATA 3241  
Db 1005 ATATATATATATATATATATATATA 980

RESULT 14  
US-08-751-359-21  
Sequence 21, Application US/08751359  
Patent No. 6143559  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,359  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 510  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5526 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-751-359-21

Query Match 0.7%; Score 26; DB 3; Length 5526;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3395 TATATTTTATATATATATATATAA 3420

RESULT 15  
US-08-751-359-21/c  
Sequence 21, Application US/08751359  
Patent No. 6143559  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,359  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 510  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5526 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-751-359-21

Query Match 0.7%; Score 26; DB 3; Length 5526;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3208 TATATTTTATATATATATATATAA 3233  
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Job time : 165.951 secs



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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 367.156 Seconds  
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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	475	13.7	560	9	US-10-091-548-17
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11	32	0.9	5908	9	US-10-239-676-93
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15	29	0.8	148	10	US-09-969-373-172
16	29	0.8	158	9	US-09-754-853A-247
17	29	0.8	549	9	US-09-991-936-1786
18	29	0.8	2000	9	US-09-938-842A-5364
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Sequence 4, Appli  
Sequence 111, App  
Sequence 17, Appl  
Sequence 13, Appl  
Sequence 3281, Ap  
Sequence 164, App  
Sequence 154, App  
Sequence 154, App  
Sequence 185, App  
Sequence 559, App  
Sequence 579, App  
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Sequence 851, App  
Sequence 861, App  
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Sequence 1804, Ap  
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Sequence 38, Appl  
Sequence 7018, Ap  
Sequence 16649, A  
Sequence 108, App  
Sequence 8002, Ap  
Sequence 263, App  
Sequence 178, App  
Sequence 2430, Ap  
Sequence 385, App  
Sequence 385, App  
Sequence 3, Appli  
Sequence 36, Appl  
Sequence 9, Appli  
Sequence 20, Appl  
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Sequence 972, App  
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Sequence 514, App  
Sequence 339, App  
Sequence 333, App  
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244	21	0.6	485	9	US-09-918-995-689	Sequence 689, App	c 317	21	0.6	3961	9	US-09-764-891-6205	Sequence 6205, App
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246	21	0.6	487	9	US-09-918-995-1475	Sequence 1475, App	c 319	21	0.6	4171	10	US-09-764-877-2665	Sequence 2665, App
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249	21	0.6	496	10	US-09-867-701-9793	Sequence 9793, App	c 322	21	0.6	4946	10	US-09-733-151-1	Sequence 1, Appli
250	21	0.6	507	9	US-09-918-995-21781	Sequence 21781, A	c 323	21	0.6	5277	9	US-10-213-509-1	Sequence 1, Appli
251	21	0.6	550	9	US-09-991-936-1337	Sequence 1337, App	c 324	21	0.6	5345	9	US-09-764-868-1356	Sequence 1356, App
252	21	0.6	561	9	US-09-907-969-50	Sequence 50, Appli	c 325	21	0.6	5345	9	US-10-092-154-1729	Sequence 1729, App
253	21	0.6	561	10	US-09-884-441-50	Sequence 50, Appli	c 326	21	0.6	5345	10	US-09-764-847-1729	Sequence 1729, App
c 254	21	0.6	572	9	US-10-040-739-998	Sequence 998, App	c 327	21	0.6	5660	9	US-09-764-891-10170	Sequence 10170, A
c 255	21	0.6	575	9	US-10-092-154-1423	Sequence 1423, App	c 328	21	0.6	5660	9	US-09-764-891-10171	Sequence 10171, A
c 256	21	0.6	575	10	US-09-764-847-1841	Sequence 1841, App	c 329	21	0.6	5759	10	US-09-954-456-2001	Sequence 2001, App
257	21	0.6	592	10	US-09-864-761-8457	Sequence 8457, App	c 330	21	0.6	5821	9	US-10-071-766-52	Sequence 52, Appli
258	21	0.6	615	9	US-10-092-154-1423	Sequence 1423, App	c 331	21	0.6	5834	9	US-10-239-676-136	Sequence 136, App
259	21	0.6	615	10	US-09-764-847-1423	Sequence 1423, App	c 332	21	0.6	5908	9	US-10-239-676-94	Sequence 94, Appli
260	21	0.6	625	10	US-09-879-536-593	Sequence 593, App	c 333	21	0.6	5981	9	US-09-854-133-441	Sequence 441, App
c 261	21	0.6	632	9	US-10-198-846-9606	Sequence 9606, App	c 334	21	0.6	5981	10	US-09-738-973-441	Sequence 441, App
c 262	21	0.6	632	9	US-10-198-846-11154	Sequence 11154, App	c 335	21	0.6	5983	10	US-09-799-875-4	Sequence 4, Appli
263	21	0.6	650	10	US-09-263-959-369	Sequence 369, App	c 336	21	0.6	5983	10	US-09-799-875-4	Sequence 4, Appli
c 264	21	0.6	654	10	US-09-764-877-3472	Sequence 3472, App	c 337	21	0.6	6040	9	US-09-764-891-8765	Sequence 8765, App
265	21	0.6	672	10	US-09-764-877-3472	Sequence 3472, App	c 338	21	0.6	6044	9	US-09-764-891-8762	Sequence 8762, App
c 266	21	0.6	739	9	US-10-074-095-855	Sequence 855, App	c 339	21	0.6	6044	9	US-09-764-891-8764	Sequence 8764, App
c 267	21	0.6	739	9	US-10-074-095-856	Sequence 856, App	c 340	21	0.6	6045	9	US-10-239-676-16	Sequence 16, Appli
c 268	21	0.6	739	10	US-09-764-860-855	Sequence 855, App	c 341	21	0.6	6222	9	US-10-098-841-105	Sequence 105, App
c 269	21	0.6	739	10	US-09-764-860-856	Sequence 856, App	c 342	21	0.6	6327	9	US-10-239-676-151	Sequence 151, App
270	21	0.6	741	10	US-09-910-943-479	Sequence 479, App	c 343	21	0.6	6534	9	US-10-239-676-111	Sequence 111, App
c 271	21	0.6	780	9	US-10-198-846-7291	Sequence 7291, App	c 344	21	0.6	7260	9	US-10-136-639-4	Sequence 4, Appli
272	21	0.6	800	9	US-10-198-846-3900	Sequence 3900, App	c 345	21	0.6	7260	10	US-09-919-497-24	Sequence 24, Appli
273	21	0.6	832	9	US-09-974-879-37	Sequence 37, Appli	c 346	21	0.6	7260	10	US-09-880-107-3739	Sequence 3739, App
274	21	0.6	832	9	US-09-305-736-37	Sequence 37, Appli	c 347	21	0.6	7448	9	US-10-270-333-82	Sequence 82, Appli
c 275	21	0.6	839	8	US-08-927-939-51	Sequence 51, Appli	c 348	21	0.6	7606	9	US-10-074-095-800	Sequence 800, App
276	21	0.6	879	10	US-09-764-853-13	Sequence 13, Appli	c 349	21	0.6	7606	10	US-09-764-860-800	Sequence 801, App
c 277	21	0.6	925	9	US-10-198-846-4101	Sequence 4101, App	c 350	21	0.6	7608	9	US-10-074-095-801	Sequence 801, App
c 278	21	0.6	950	9	US-10-198-846-7276	Sequence 7276, App	c 351	21	0.6	7608	10	US-09-764-860-801	Sequence 801, App
c 279	21	0.6	955	9	US-10-037-270-228	Sequence 228, App	c 352	21	0.6	7739	10	US-09-764-877-3189	Sequence 3189, App
c 280	21	0.6	955	9	US-09-938-842A-3324	Sequence 3324, App	c 353	21	0.6	8205	9	US-09-860-670-276	Sequence 276, App
c 281	21	0.6	1232	9	US-10-198-846-7269	Sequence 7269, App	c 354	21	0.6	8701	9	US-10-052-154-1976	Sequence 1976, App
282	21	0.6	1261	9	US-10-198-846-10840	Sequence 10840, A	c 355	21	0.6	8701	10	US-09-764-847-1976	Sequence 1976, App
283	21	0.6	1453	10	US-09-764-877-2774	Sequence 2774, App	c 356	21	0.6	8794	9	US-09-764-891-8933	Sequence 8933, App
c 284	21	0.6	1503	9	US-10-198-846-14076	Sequence 14076, A	c 357	21	0.6	9496	9	US-09-764-891-5542	Sequence 5542, App
c 285	21	0.6	1524	9	US-09-922-405B-1	Sequence 1, Appli	c 358	21	0.6	9821	9	US-09-764-891-5933	Sequence 5933, App
c 286	21	0.6	1524	9	US-10-065-474-1	Sequence 1, Appli	c 359	21	0.6	9824	9	US-09-764-891-5934	Sequence 5934, App
287	21	0.6	1550	10	US-09-764-877-2178	Sequence 2178, App	c 360	21	0.6	9887	9	US-10-000-639-7	Sequence 7, Appli
288	21	0.6	1600	10	US-09-753-436-117	Sequence 117, App	c 361	21	0.6	10619	9	US-10-239-676-1	Sequence 1, Appli
289	21	0.6	1707	10	US-09-884-901-7	Sequence 7, Appli	c 362	21	0.6	10758	9	US-10-091-504-1647	Sequence 1647, App
c 290	21	0.6	1837	9	US-09-823-846-502	Sequence 502, App	c 363	21	0.6	10758	9	US-10-091-504-1650	Sequence 1650, App
c 291	21	0.6	1971	10	US-09-864-761-13921	Sequence 13921, A	c 364	21	0.6	10758	10	US-09-764-869-1647	Sequence 1647, App
292	21	0.6	1991	10	US-09-848-852A-4	Sequence 4, Appli	c 365	21	0.6	10758	10	US-09-764-869-1650	Sequence 1650, App
c 293	21	0.6	2000	9	US-09-938-842A-2717	Sequence 2717, App	c 366	21	0.6	10759	10	US-10-091-504-1649	Sequence 1649, App
c 294	21	0.6	2000	9	US-09-938-842A-3293	Sequence 3293, App	c 367	21	0.6	10759	10	US-09-764-869-1649	Sequence 1649, App
c 295	21	0.6	2000	9	US-09-938-842A-3384	Sequence 3384, App	c 368	21	0.6	11036	9	US-10-239-676-117	Sequence 117, App
c 296	21	0.6	2000	9	US-09-938-842A-3641	Sequence 3641, App	c 369	21	0.6	11036	9	US-10-239-676-118	Sequence 118, App
c 297	21	0.6	2000	9	US-09-938-842A-4474	Sequence 4474, App	c 370	21	0.6	11036	9	US-10-239-676-118	Sequence 118, App
c 298	21	0.6	2000	9	US-09-938-842A-4951	Sequence 4951, App	c 371	21	0.6	11809	9	US-09-764-891-10172	Sequence 10172, A
c 299	21	0.6	2000	9	US-09-938-842A-4998	Sequence 4998, App	c 372	21	0.6	11821	10	US-09-764-877-2857	Sequence 2857, App
300	21	0.6	2004	9	US-09-938-842A-5078	Sequence 5078, App	c 373	21	0.6	11870	9	US-09-764-891-10016	Sequence 10016, A
301	21	0.6	2004	10	US-09-887-576-159	Sequence 159, App	c 374	21	0.6	11870	9	US-09-764-891-10017	Sequence 10017, A
c 302	21	0.6	2012	10	US-09-887-576-242	Sequence 242, App	c 375	21	0.6	12192	9	US-10-074-095-629	Sequence 629, App
c 303	21	0.6	2027	9	US-10-132-652-1	Sequence 1, Appli	c 376	21	0.6	12192	10	US-09-764-860-629	Sequence 629, App
304	21	0.6	2029	9	US-10-037-270-306	Sequence 306, App	c 377	21	0.6	13606	9	US-10-239-676-166	Sequence 166, App
c 305	21	0.6	2029	9	US-10-037-270-306	Sequence 306, App	c 378	21	0.6	13743	9	US-09-764-872-615	Sequence 615, App
306	21	0.6	2080	9	US-10-037-270-305	Sequence 305, App	c 379	21	0.6	13996	9	US-10-125-540-602	Sequence 602, App
c 307	21	0.6	2080	9	US-10-037-270-305	Sequence 305, App	c 380	21	0.6	13996	9	US-10-125-540-602	Sequence 602, App
308	21	0.6	2297	9	US-09-764-891-8760	Sequence 8760, App	c 381	21	0.6	13996	10	US-09-764-870-602	Sequence 602, App
309	21	0.6	2297	9	US-09-764-891-8763	Sequence 8763, App	c 382	21	0.6	13996	10	US-09-764-870-602	Sequence 602, App
310	21	0.6	2563	9	US-09-764-891-8395	Sequence 8395, App	c 383	21	0.6	14001	9	US-10-125-540-601	Sequence 601, App
311	21	0.6	2613	10	US-09-822-830A-518	Sequence 518, App	c 384	21	0.6	14001	9	US-10-125-540-601	Sequence 601, App

385	21	0.6	14001	10	US-09-764-870-601	Sequence 601, App	c 458	21	0.6	80595	9	US-09-728-552-3	Sequence 3, Appli
386	21	0.6	14001	10	US-09-764-870-601	Sequence 601, App	c 459	21	0.6	81826	9	US-10-175-523-197	Sequence 157, App
387	21	0.6	14040	9	US-09-764-891-5478	Sequence 5078, A	c 460	21	0.6	82938	9	US-09-818-657-3	Sequence 36, Appli
388	21	0.6	14040	9	US-09-764-891-10205	Sequence 10205, A	c 461	21	0.6	84539	10	US-09-962-436-36	Sequence 3428, Ap
389	21	0.6	14093	10	US-10-092-154-1744	Sequence 1744, Ap	c 462	21	0.6	99014	10	US-09-880-107-3428	Sequence 3, Appli
390	21	0.6	14093	10	US-09-764-847-1744	Sequence 1744, Ap	c 463	21	0.6	108359	9	US-10-191-807-3	Sequence 96, Appli
391	21	0.6	15362	10	US-09-764-877-2856	Sequence 2856, Ap	c 464	21	0.6	110079	9	US-10-175-523-96	Sequence 3, Appli
392	21	0.6	15335	10	US-09-764-877-2855	Sequence 2855, Ap	c 465	21	0.6	111282	12	US-10-094-989-3	Sequence 3, Appli
393	21	0.6	15732	9	US-10-239-676-96	Sequence 96, Appli	c 466	21	0.6	116592	10	US-09-818-511-3	Sequence 3, Appli
394	21	0.6	17142	9	US-10-239-676-206	Sequence 206, App	c 467	21	0.6	116840	9	US-10-020-141-3	Sequence 11, Appli
395	21	0.6	17419	9	US-10-239-676-99	Sequence 99, Appli	c 468	21	0.6	118951	9	US-10-161-572-11	Sequence 3, Appli
396	21	0.6	17419	9	US-10-239-676-100	Sequence 100, App	c 469	21	0.6	126512	10	US-09-804-474A-3	Sequence 1, Appli
397	21	0.6	17450	9	US-09-764-891-8641	Sequence 8641, App	c 470	21	0.6	127197	9	US-09-754-853A-1	Sequence 3, Appli
398	21	0.6	17498	9	US-10-074-095-798	Sequence 798, App	c 471	21	0.6	148567	9	US-10-254-869-3	Sequence 3, Appli
399	21	0.6	17498	10	US-09-764-860-798	Sequence 798, App	c 472	21	0.6	148567	10	US-09-801-876B-3	Sequence 3, Appli
400	21	0.6	18408	9	US-09-764-891-7441	Sequence 7441, App	c 473	21	0.6	172637	10	US-09-805-458A-3	Sequence 314, App
401	21	0.6	18408	9	US-09-764-891-7442	Sequence 7442, App	c 474	21	0.6	174424	10	US-09-967-768A-314	Sequence 5, Appli
402	21	0.6	18409	9	US-09-764-868-1457	Sequence 1457, App	c 475	21	0.6	183337	9	US-10-020-141-5	Sequence 11, Appli
403	21	0.6	20268	9	US-10-072-349-173	Sequence 173, App	c 476	21	0.6	185695	9	US-10-020-141-11	Sequence 1, Appli
404	21	0.6	20268	10	US-09-764-855-173	Sequence 173, App	c 477	21	0.6	185695	9	US-10-017-721-1	Sequence 3, Appli
405	21	0.6	21234	12	US-10-109-854-3	Sequence 3, Appli	c 478	21	0.6	203654	10	US-09-820-905-3	Sequence 5, Appli
406	21	0.6	21936	9	US-09-764-891-8807	Sequence 8807, App	c 479	21	0.6	225883	9	US-10-175-523-57	Sequence 1, Appli
407	21	0.6	21936	9	US-09-764-891-9446	Sequence 9446, App	c 480	21	0.6	235033	9	US-10-301-844-1	Sequence 2, Appli
408	21	0.6	23603	9	US-09-860-670-264	Sequence 264, App	c 481	21	0.6	237326	9	US-09-301-844-2	Sequence 3, Appli
409	21	0.6	23613	9	US-09-860-670-258	Sequence 258, App	c 482	21	0.6	335913	9	US-09-754-853A-2	Sequence 3, Appli
410	21	0.6	24023	9	US-10-094-679-1	Sequence 1, Appli	c 483	21	0.6	335913	9	US-09-754-853A-3	Sequence 20, Appli
411	21	0.6	24218	9	US-09-860-670-263	Sequence 263, App	c 484	21	0.6	659158	9	US-09-771-208-20	Sequence 1, Appli
412	21	0.6	25423	9	US-10-072-349-193	Sequence 193, App	c 485	21	0.6	684973	10	US-09-263-959-1	Sequence 1247, App
413	21	0.6	25423	10	US-09-764-855-193	Sequence 193, App	c 486	21	0.6	89	10	US-09-969-373-1247	Sequence 1228, App
414	21	0.6	25424	9	US-10-072-349-194	Sequence 194, App	c 487	21	0.6	94	10	US-09-969-373-1228	Sequence 1338, Ap
415	21	0.6	25424	10	US-09-764-855-194	Sequence 194, App	c 488	21	0.6	108	10	US-09-969-373-1338	Sequence 1205, Ap
416	21	0.6	25701	9	US-09-764-891-9766	Sequence 9766, App	c 489	21	0.6	111	10	US-09-969-373-1205	Sequence 539, App
417	21	0.6	25758	9	US-09-764-891-9765	Sequence 9765, App	c 490	21	0.6	111	10	US-09-969-373-1205	Sequence 235, App
418	21	0.6	26320	9	US-10-166-221-3	Sequence 3, Appli	c 491	21	0.6	123	10	US-09-969-373-539	Sequence 747, App
419	21	0.6	27118	9	US-09-764-891-10230	Sequence 10230, A	c 492	21	0.6	129	10	US-09-969-373-235	Sequence 809, App
420	21	0.6	31168	9	US-09-764-891-8396	Sequence 8396, App	c 493	21	0.6	131	10	US-09-969-373-747	Sequence 868, App
421	21	0.6	31168	10	US-09-764-868-1464	Sequence 1464, Ap	c 494	21	0.6	131	10	US-09-969-373-809	Sequence 968, App
422	21	0.6	31314	10	US-09-764-877-3875	Sequence 3875, App	c 495	21	0.6	135	10	US-09-969-373-868	Sequence 1018, Ap
423	21	0.6	31474	9	US-09-764-891-8149	Sequence 8149, App	c 496	21	0.6	135	10	US-09-969-373-767	Sequence 1223, Ap
424	21	0.6	31994	9	US-09-764-904-71	Sequence 71, Appli	c 497	21	0.6	135	10	US-09-969-373-1018	Sequence 1071, App
425	21	0.6	31994	9	US-10-091-548-71	Sequence 71, Appli	c 498	21	0.6	137	10	US-09-969-373-1223	Sequence 177, App
426	21	0.6	31994	9	US-10-074-095-599	Sequence 599, App	c 499	21	0.6	138	10	US-09-864-864-101	Sequence 101, App
427	21	0.6	31994	10	US-09-764-860-599	Sequence 599, App	c 500	21	0.6	142	10	US-09-969-373-177	Sequence 177, App
428	21	0.6	32042	9	US-10-118-984-44	Sequence 44, Appli	c 501	21	0.6	142	10	US-09-969-373-210	Sequence 210, App
429	21	0.6	32042	10	US-09-728-721-63	Sequence 63, Appli	c 502	21	0.6	143	10	US-09-969-373-829	Sequence 829, App
430	21	0.6	32082	9	US-09-764-891-9679	Sequence 9679, App	c 503	21	0.6	143	10	US-09-969-373-1272	Sequence 1272, App
431	21	0.6	32146	9	US-10-074-095-797	Sequence 797, App	c 504	21	0.6	144	10	US-09-969-373-698	Sequence 698, App
432	21	0.6	32146	10	US-09-764-860-797	Sequence 797, App	c 505	21	0.6	147	9	US-09-754-853A-354	Sequence 43, Appli
433	21	0.6	32169	9	US-09-764-891-8605	Sequence 8605, Ap	c 506	21	0.6	148	10	US-09-969-373-429	Sequence 429, Appli
434	21	0.6	32185	10	US-09-764-877-3171	Sequence 3171, Ap	c 507	21	0.6	149	10	US-09-969-373-429	Sequence 94, Appli
435	21	0.6	32189	9	US-09-764-891-8604	Sequence 8604, Ap	c 508	21	0.6	150	10	US-09-969-373-94	Sequence 227, App
436	21	0.6	32190	9	US-09-860-670-255	Sequence 255, App	c 509	21	0.6	152	9	US-09-754-853A-227	Sequence 833, App
437	21	0.6	32195	9	US-10-102-627-92	Sequence 92, Appli	c 510	21	0.6	152	10	US-09-969-373-833	Sequence 1380, Ap
438	21	0.6	32220	10	US-09-764-877-3933	Sequence 3933, Ap	c 511	21	0.6	152	10	US-09-969-373-1380	Sequence 363, App
439	21	0.6	32248	9	US-10-074-095-802	Sequence 802, App	c 512	21	0.6	153	9	US-09-754-853A-363	Sequence 26437, A
440	21	0.6	32249	9	US-09-860-670-260	Sequence 260, App	c 513	21	0.6	153	10	US-09-969-373-173	Sequence 173, App
441	21	0.6	32249	10	US-09-860-670-260	Sequence 260, App	c 514	21	0.6	153	10	US-09-969-373-173	Sequence 1194, Ap
442	21	0.6	32249	9	US-09-764-891-7364	Sequence 7364, Ap	c 515	21	0.6	153	10	US-09-969-373-1194	Sequence 533, App
443	21	0.6	38059	10	US-09-880-107-2125	Sequence 2125, Ap	c 516	21	0.6	158	10	US-09-969-373-533	Sequence 203, App
444	21	0.6	38186	9	US-09-373-658-38	Sequence 38, Appli	c 517	21	0.6	168	10	US-09-969-373-203	Sequence 82, Appli
445	21	0.6	40090	10	US-09-820-004-3	Sequence 3, Appli	c 518	21	0.6	170	10	US-09-969-373-82	Sequence 1083, Ap
446	21	0.6	43950	12	US-10-060-332-3	Sequence 3, Appli	c 519	21	0.6	173	10	US-09-969-373-1083	Sequence 276, App
447	21	0.6	46050	10	US-09-820-003A-3	Sequence 3, Appli	c 520	21	0.6	174	9	US-09-754-853A-276	Sequence 972, App
448	21	0.6	48436	10	US-09-927-602-38	Sequence 38, Appli	c 521	21	0.6	178	10	US-09-969-373-972	Sequence 1248, Ap
449	21	0.6	49984	10	US-09-739-457-5	Sequence 5, Appli	c 522	21	0.6	180	10	US-09-969-373-1248	Sequence 292, App
450	21	0.6	50000	9	US-10-060-763-4	Sequence 4, Appli	c 523	21	0.6	184	9	US-09-754-853A-292	Sequence 1464, Ap
451	21	0.6	50000	12	US-10-063-763-4	Sequence 4, Appli	c 524	21	0.6	186	10	US-09-969-373-1464	Sequence 4244, Ap
452	21	0.6	52354	10	US-09-742-311-3	Sequence 3, Appli	c 525	21	0.6	190	9	US-09-796-692-4244	Sequence 4244, Ap
453	21	0.6	53542	10	US-09-801-574-61	Sequence 61, Appli	c 526	21	0.6	190	9	US-10-040-862-4244	Sequence 253, App
454	21	0.6	57130	10	US-09-835-081-3	Sequence 1, Appli	c 527	21	0.6	193	10	US-09-969-373-253	Sequence 1113, Ap
455	21	0.6	66479	9	US-10-041-856-1	Sequence 86, Appli	c 528	21	0.6	194	10	US-09-969-373-1113	Sequence 1217, Ap
456	21	0.6	66686	10	US-09-736-960-86	Sequence 4, Appli	c 529	21	0.6	194	10	US-09-969-373-1217	
457	21	0.6	80246	9	US-09-728-552-4	Sequence 4, Appli	c 530	21	0.6	194	10	US-09-969-373-1217	

531	20	0.6	197	10	US-09-369-373-1022	Sequence 1022, Ap	604	20	0.6	403	10	US-09-878-574-3960	Sequence 3960, Ap
532	20	0.6	199	10	US-09-369-373-931	Sequence 931, Ap	c 605	20	0.6	407	10	US-09-864-761-3134	Sequence 3134, Ap
533	20	0.6	199	10	US-09-369-373-1193	Sequence 1193, Ap	c 606	20	0.6	407	10	US-09-969-373-1315	Sequence 1315, Ap
534	20	0.6	203	10	US-09-369-373-961	Sequence 961, Ap	c 607	20	0.6	408	9	US-09-946-807-1477	Sequence 1477, Ap
535	20	0.6	205	9	US-09-754-853A-310	Sequence 310, App	c 608	20	0.6	408	9	US-09-918-995-5372	Sequence 5372, Ap
536	20	0.6	209	10	US-09-369-373-1107	Sequence 1107, Ap	c 609	20	0.6	408	10	US-09-795-668-1477	Sequence 1477, Ap
537	20	0.6	212	10	US-09-369-373-1097	Sequence 1097, Ap	c 610	20	0.6	408	10	US-09-795-686-1477	Sequence 1477, Ap
538	20	0.6	217	9	US-10-060-036-2965	Sequence 2965, Ap	c 611	20	0.6	411	10	US-09-969-373-236	Sequence 236, App
539	20	0.6	219	10	US-09-369-373-246	Sequence 246, App	c 612	20	0.6	416	9	US-09-918-995-33135	Sequence 33135, A
540	20	0.6	230	10	US-09-369-373-110	Sequence 110, App	c 613	20	0.6	416	9	US-09-803-719-1868	Sequence 1868, Ap
541	20	0.6	230	10	US-09-369-373-111	Sequence 111, App	c 614	20	0.6	419	10	US-09-969-373-237	Sequence 237, App
542	20	0.6	234	10	US-09-369-373-1527	Sequence 1527, Ap	c 615	20	0.6	420	9	US-09-918-995-3758	Sequence 3758, Ap
543	20	0.6	238	9	US-09-754-853A-155	Sequence 155, App	c 616	20	0.6	421	10	US-09-925-297-370	Sequence 370, App
544	20	0.6	240	10	US-09-369-373-572	Sequence 572, App	c 617	20	0.6	427	10	US-09-867-701-10528	Sequence 10528, A
545	20	0.6	241	9	US-10-091-504-188	Sequence 188, App	c 618	20	0.6	430	9	US-09-918-995-34767	Sequence 34767, A
546	20	0.6	241	10	US-09-764-869-188	Sequence 188, App	c 619	20	0.6	431	9	US-09-918-995-17488	Sequence 17488, A
547	20	0.6	241	10	US-09-369-373-396	Sequence 396, App	c 620	20	0.6	433	9	US-09-918-995-16881	Sequence 16881, A
548	20	0.6	243	10	US-09-369-373-874	Sequence 874, App	c 621	20	0.6	436	10	US-09-867-701-7782	Sequence 7782, Ap
549	20	0.6	243	10	US-09-369-373-874	Sequence 874, App	c 622	20	0.6	437	9	US-09-918-995-17116	Sequence 17116, A
550	20	0.6	252	10	US-09-369-373-1061	Sequence 1061, Ap	c 623	20	0.6	443	9	US-09-918-995-27709	Sequence 27709, A
551	20	0.6	256	10	US-09-369-373-1312	Sequence 1312, Ap	c 624	20	0.6	448	10	US-09-969-708-377	Sequence 377, App
552	20	0.6	262	10	US-09-954-456-1999	Sequence 1999, Ap	c 625	20	0.6	453	9	US-09-918-995-2177	Sequence 2177, Ap
553	20	0.6	262	10	US-09-880-107-827	Sequence 827, App	c 626	20	0.6	454	10	US-09-867-701-9387	Sequence 9387, Ap
554	20	0.6	263	10	US-09-867-701-9223	Sequence 9223, Ap	c 627	20	0.6	455	10	US-09-864-761-14466	Sequence 14466, A
555	20	0.6	265	10	US-09-369-373-1074	Sequence 1074, Ap	c 628	20	0.6	458	10	US-09-864-761-3800	Sequence 3800, Ap
556	20	0.6	266	9	US-09-754-853A-161	Sequence 161, App	c 629	20	0.6	461	9	US-09-907-969-3	Sequence 1, Appli
557	20	0.6	266	9	US-09-754-853A-161	Sequence 161, App	c 630	20	0.6	461	9	US-09-884-441-1	Sequence 1, Appli
558	20	0.6	275	10	US-09-867-701-8770	Sequence 8770, Ap	c 631	20	0.6	461	10	US-09-884-441-3	Sequence 3, Appli
559	20	0.6	275	10	US-09-867-701-8897	Sequence 8897, Ap	c 632	20	0.6	461	10	US-09-867-701-10022	Sequence 1869, Ap
560	20	0.6	276	10	US-09-369-373-630	Sequence 630, App	c 633	20	0.6	469	10	US-09-864-761-1869	Sequence 34582, Ap
561	20	0.6	276	10	US-09-369-373-1465	Sequence 1465, Ap	c 634	20	0.6	470	9	US-09-918-995-34582	Sequence 24980, A
562	20	0.6	280	9	US-10-037-598-21	Sequence 21, Appl	c 635	20	0.6	471	9	US-09-918-995-24980	Sequence 26052, A
563	20	0.6	291	9	US-09-803-719-1252	Sequence 1252, Ap	c 636	20	0.6	473	9	US-09-918-995-26052	Sequence 34501, A
564	20	0.6	291	9	US-09-803-719-1453	Sequence 1453, Ap	c 637	20	0.6	473	9	US-09-918-995-34501	Sequence 13, Appl
565	20	0.6	293	10	US-09-764-877-2750	Sequence 2750, Ap	c 638	20	0.6	474	9	US-09-809-391-13	Sequence 27039, A
566	20	0.6	294	10	US-09-867-701-9509	Sequence 9509, Ap	c 639	20	0.6	478	9	US-09-918-995-27039	Sequence 21585, A
567	20	0.6	296	10	US-09-369-373-974	Sequence 974, App	c 640	20	0.6	480	9	US-09-918-995-21585	Sequence 19161, A
568	20	0.6	297	9	US-10-091-504-2400	Sequence 2400, Ap	c 641	20	0.6	481	9	US-09-918-995-19161	Sequence 25363, A
569	20	0.6	297	9	US-09-991-936-1002	Sequence 1002, Ap	c 642	20	0.6	481	9	US-09-918-995-25363	Sequence 4334, Ap
570	20	0.6	297	10	US-09-764-869-2400	Sequence 2400, Ap	c 643	20	0.6	484	9	US-09-918-995-4434	Sequence 10125, A
571	20	0.6	300	9	US-10-013-329-3	Sequence 3, Appli	c 644	20	0.6	485	10	US-09-864-761-10125	Sequence 30715, A
572	20	0.6	304	9	US-10-091-504-2406	Sequence 2406, Ap	c 645	20	0.6	489	9	US-09-918-995-30715	Sequence 26874, A
573	20	0.6	304	10	US-09-764-869-2406	Sequence 2406, Ap	c 646	20	0.6	489	9	US-09-918-995-26874	Sequence 17588, A
574	20	0.6	313	10	US-09-369-373-1463	Sequence 1463, Ap	c 647	20	0.6	490	9	US-09-918-995-17588	Sequence 28954, A
575	20	0.6	317	10	US-09-871-161-109	Sequence 109, App	c 648	20	0.6	492	9	US-09-918-995-28954	Sequence 1325, Ap
576	20	0.6	317	10	US-09-960-352-3366	Sequence 3366, Ap	c 649	20	0.6	501	9	US-10-198-846-1525	Sequence 14033, A
577	20	0.6	318	9	US-09-764-891-7651	Sequence 7651, Ap	c 650	20	0.6	505	9	US-09-918-995-14033	Sequence 2115, Ap
578	20	0.6	322	10	US-09-369-373-1065	Sequence 1065, Ap	c 651	20	0.6	509	10	US-09-764-869-2115	Sequence 2115, Ap
579	20	0.6	325	10	US-09-369-373-1339	Sequence 1339, Ap	c 652	20	0.6	508	9	US-09-918-995-24201	Sequence 3963, Ap
580	20	0.6	332	10	US-09-803-719-1292	Sequence 1292, Ap	c 653	20	0.6	509	10	US-09-764-877-3964	Sequence 3964, Ap
581	20	0.6	334	10	US-09-867-701-9936	Sequence 9936, Ap	c 654	20	0.6	509	10	US-09-764-877-3964	Sequence 3965, Ap
582	20	0.6	337	10	US-09-764-877-3785	Sequence 3785, Ap	c 655	20	0.6	512	10	US-09-783-590-2879	Sequence 2879, Ap
583	20	0.6	341	9	US-09-907-969-136	Sequence 136, App	c 656	20	0.6	521	9	US-09-918-995-25752	Sequence 25752, A
584	20	0.6	341	10	US-09-884-441-136	Sequence 136, App	c 657	20	0.6	524	9	US-09-764-891-7075	Sequence 7075, Ap
585	20	0.6	356	10	US-09-369-373-825	Sequence 825, App	c 658	20	0.6	531	9	US-09-764-891-7076	Sequence 7076, Ap
586	20	0.6	356	10	US-09-369-373-825	Sequence 825, App	c 659	20	0.6	532	9	US-09-918-995-3769	Sequence 3769, Ap
587	20	0.6	356	10	US-09-369-373-827	Sequence 827, App	c 660	20	0.6	549	9	US-09-991-936-1786	Sequence 1786, Ap
588	20	0.6	369	10	US-09-369-373-1006	Sequence 1006, Ap	c 661	20	0.6	550	10	US-09-263-959-396	Sequence 396, App
589	20	0.6	373	10	US-09-962-436-492	Sequence 492, App	c 662	20	0.6	563	10	US-09-864-761-9392	Sequence 9392, Ap
590	20	0.6	375	10	US-09-369-373-1369	Sequence 1369, Ap	c 663	20	0.6	567	10	US-09-864-761-9781	Sequence 9781, Ap
591	20	0.6	377	9	US-09-918-995-29856	Sequence 29856, A	c 664	20	0.6	577	9	US-09-918-995-29443	Sequence 29443, A
592	20	0.6	388	9	US-09-918-995-27277	Sequence 27277, A	c 665	20	0.6	583	10	US-09-864-761-15417	Sequence 15417, A
593	20	0.6	399	9	US-09-918-995-16899	Sequence 16899, A	c 666	20	0.6	589	10	US-09-917-800A-332	Sequence 332, App
594	20	0.6	400	9	US-09-918-995-33367	Sequence 33367, A	c 667	20	0.6	599	9	US-09-864-761-11964	Sequence 11964, A
595	20	0.6	401	9	US-09-946-807-274	Sequence 274, App	c 668	20	0.6	628	9	US-09-764-891-7935	Sequence 7935, Ap
596	20	0.6	401	9	US-09-946-807-274	Sequence 274, App	c 669	20	0.6	632	10	US-09-772-134B-57	Sequence 57, Appl
597	20	0.6	401	9	US-09-946-807-1090	Sequence 1090, Ap	c 670	20	0.6	640	10	US-09-854-133-431	Sequence 431, App
598	20	0.6	401	10	US-09-795-668-275	Sequence 275, App	c 671	20	0.6	640	10	US-09-738-973-431	Sequence 431, App
599	20	0.6	401	10	US-09-795-668-275	Sequence 275, App	c 672	20	0.6				
600	20	0.6	401	10	US-09-795-668-1090	Sequence 1090, Ap	c 673	20	0.6				
601	20	0.6	401	10	US-09-795-668-274	Sequence 274, App	c 674	20	0.6				
602	20	0.6	401	10	US-09-795-668-275	Sequence 275, App	c 675	20	0.6				
603	20	0.6	401	10	US-09-795-668-1090	Sequence 1090, Ap	c 676	20	0.6				

677	20	0.6	650	10	US-09-263-959-385	Sequence 385, App	c 750	20	0.6	2000	9	US-09-938-842A-4888	Sequence 4888, Ap
678	20	0.6	656	9	US-09-986-480-84	Sequence 84, Appl	751	20	0.6	2000	9	US-09-938-842A-4951	Sequence 4951, Ap
c 679	20	0.6	658	9	US-09-893-519A-143	Sequence 143, App	752	20	0.6	2000	9	US-09-938-842A-4963	Sequence 4963, Ap
c 680	20	0.6	659	10	US-09-764-877-2785	Sequence 2785, Ap	753	20	0.6	2000	9	US-09-938-842A-4994	Sequence 4994, Ap
c 681	20	0.6	679	10	US-10-073-961-633	Sequence 633, App	c 754	20	0.6	2000	9	US-09-938-842A-5057	Sequence 5057, Ap
c 682	20	0.6	679	10	US-09-764-887-633	Sequence 633, App	c 755	20	0.6	2000	9	US-09-938-842A-5099	Sequence 5099, Ap
c 683	20	0.6	683	10	US-09-764-877-2393	Sequence 2393, Ap	c 756	20	0.6	2000	9	US-09-938-842A-5122	Sequence 5122, Ap
c 684	20	0.6	696	10	US-09-910-943-288	Sequence 288, App	c 757	20	0.6	2000	9	US-09-938-842A-5287	Sequence 5287, Ap
c 685	20	0.6	714	9	US-10-198-846-6487	Sequence 6487, App	c 758	20	0.6	2002	10	US-09-887-576-324	Sequence 324, App
c 686	20	0.6	725	9	US-10-202-193-295	Sequence 295, App	c 759	20	0.6	2003	10	US-09-887-576-15	Sequence 15, Appl
c 687	20	0.6	736	9	US-10-202-193-294	Sequence 294, App	c 760	20	0.6	2018	9	US-10-091-504-1568	Sequence 1568, Ap
c 688	20	0.6	736	10	US-09-772-134B-53	Sequence 53, Appl	c 761	20	0.6	2018	10	US-09-764-869-1568	Sequence 1568, Ap
c 689	20	0.6	803	9	US-10-091-504-2437	Sequence 2437, Ap	c 762	20	0.6	2009	9	US-10-244-633-5	Sequence 5, Appl
c 690	20	0.6	803	10	US-09-764-869-2437	Sequence 2437, Ap	c 763	20	0.6	2119	9	US-10-091-504-2439	Sequence 2439, Ap
c 691	20	0.6	867	9	US-09-764-891-8794	Sequence 8794, Ap	c 764	20	0.6	2119	10	US-09-764-869-2439	Sequence 2439, Ap
c 692	20	0.6	875	9	US-10-198-846-3516	Sequence 3516, Ap	c 765	20	0.6	2142	9	US-10-091-504-2440	Sequence 2440, Ap
c 693	20	0.6	884	9	US-10-198-846-3350	Sequence 3350, Ap	c 766	20	0.6	2142	10	US-09-764-869-2440	Sequence 2440, Ap
c 694	20	0.6	921	9	US-10-198-846-7263	Sequence 7263, Ap	c 767	20	0.6	2172	9	US-09-966-880A-15	Sequence 15, Appl
c 695	20	0.6	942	9	US-09-764-891-9845	Sequence 9845, Ap	c 768	20	0.6	2241	10	US-09-822-849A-290	Sequence 290, App
c 696	20	0.6	988	9	US-10-195-781A-1	Sequence 1, Appl	c 769	20	0.6	2390	9	US-09-374-046A-91	Sequence 91, Appl
c 697	20	0.6	997	10	US-09-764-877-2210	Sequence 2210, Ap	c 770	20	0.6	2410	10	US-09-771-161A-66	Sequence 66, Appl
c 698	20	0.6	1005	9	US-10-079-854-102	Sequence 102, App	c 771	20	0.6	2437	9	US-09-764-904-102	Sequence 102, App
c 699	20	0.6	1005	9	US-10-074-095-301	Sequence 301, App	c 772	20	0.6	2437	9	US-10-091-548-102	Sequence 102, App
c 700	20	0.6	1005	10	US-09-764-878-102	Sequence 102, App	c 773	20	0.6	2437	9	US-10-074-095-1157	Sequence 1157, Ap
c 701	20	0.6	1005	10	US-09-764-860-301	Sequence 301, App	c 774	20	0.6	2437	10	US-09-764-860-1157	Sequence 1157, Ap
c 702	20	0.6	1060	10	US-09-764-877-2730	Sequence 2730, Ap	c 775	20	0.6	2460	9	US-10-198-846-11526	Sequence 11526, A
c 703	20	0.6	1086	10	US-09-529-063-6	Sequence 6, Appl	c 776	20	0.6	2547	10	US-09-764-877-2582	Sequence 2582, Ap
c 704	20	0.6	1149	9	US-10-198-846-4399	Sequence 4399, Ap	c 777	20	0.6	2550	10	US-09-764-864-318	Sequence 318, App
c 705	20	0.6	1151	9	US-09-974-879-105	Sequence 105, App	c 778	20	0.6	2567	9	US-09-510-332-146	Sequence 146, App
c 706	20	0.6	1151	9	US-09-305-736-105	Sequence 105, App	c 779	20	0.6	2600	9	US-10-073-961-526	Sequence 526, App
c 707	20	0.6	1360	9	US-10-198-846-12833	Sequence 12833, A	c 780	20	0.6	2600	10	US-09-764-887-526	Sequence 526, App
c 708	20	0.6	1382	9	US-10-092-154-1253	Sequence 1253, Ap	c 781	20	0.6	2750	9	US-09-822-846-63	Sequence 63, Appl
c 709	20	0.6	1382	10	US-09-764-847-1253	Sequence 1253, Ap	c 782	20	0.6	2769	9	US-10-119-926-105	Sequence 105, App
c 710	20	0.6	1442	9	US-10-146-130-1	Sequence 1, Appl	c 783	20	0.6	2818	9	US-09-966-880A-7	Sequence 7, Appl
c 711	20	0.6	1442	9	US-09-964-667-1	Sequence 1, Appl	c 784	20	0.6	2831	9	US-09-764-891-6097	Sequence 6097, Ap
c 712	20	0.6	1442	9	US-09-872-968-1	Sequence 1, Appl	c 785	20	0.6	2998	9	US-10-195-781A-3	Sequence 3, Appl
c 713	20	0.6	1442	9	US-10-092-934-1	Sequence 1, Appl	c 786	20	0.6	3023	9	US-10-066-443-4	Sequence 4, Appl
c 714	20	0.6	1442	9	US-10-153-334-53	Sequence 53, Appl	c 787	20	0.6	3023	9	US-10-256-889-4	Sequence 4, Appl
c 715	20	0.6	1442	9	US-10-198-089-48	Sequence 48, Appl	c 788	20	0.6	3023	10	US-09-900-236-4	Sequence 4, Appl
c 716	20	0.6	1442	10	US-09-964-666-1	Sequence 1, Appl	c 789	20	0.6	3190	9	US-10-153-668-165	Sequence 165, App
c 717	20	0.6	1442	10	US-09-964-412-1	Sequence 1, Appl	c 790	20	0.6	3381	9	US-09-764-891-5397	Sequence 5397, Ap
c 718	20	0.6	1491	9	US-09-938-842A-4918	Sequence 4918, Ap	c 791	20	0.6	3425	10	US-09-764-877-3888	Sequence 3888, Ap
c 719	20	0.6	1506	10	US-09-815-242-7845	Sequence 7845, Ap	c 792	20	0.6	3536	10	US-09-880-107-3271	Sequence 3271, Ap
c 720	20	0.6	1544	10	US-09-880-107-2122	Sequence 2122, Ap	c 793	20	0.6	3631	10	US-09-764-864-7378	Sequence 738, App
c 721	20	0.6	1547	9	US-10-073-961-525	Sequence 525, App	c 794	20	0.6	3813	10	US-09-764-877-3325	Sequence 3325, Ap
c 722	20	0.6	1625	10	US-09-764-887-525	Sequence 525, App	c 795	20	0.6	3830	9	US-10-037-598-26	Sequence 26, Appl
c 723	20	0.6	1625	9	US-10-198-846-13305	Sequence 13305, A	c 796	20	0.6	3950	9	US-09-900-797-33	Sequence 33, Appl
c 724	20	0.6	1635	9	US-10-092-154-1075	Sequence 1075, Ap	c 797	20	0.6	3950	10	US-09-887-586A-33	Sequence 33, Appl
c 725	20	0.6	1635	10	US-09-764-847-1075	Sequence 1075, Ap	c 798	20	0.6	3950	10	US-09-903-012-33	Sequence 33, Appl
c 726	20	0.6	1681	9	US-09-986-480-40	Sequence 40, Appl	c 799	20	0.6	3971	9	US-09-764-891-5821	Sequence 5821, Ap
c 727	20	0.6	1704	9	US-10-198-846-10761	Sequence 10761, A	c 800	20	0.6	4071	9	US-10-091-504-2040	Sequence 2040, Ap
c 728	20	0.6	1764	10	US-09-947-027-3	Sequence 3, Appl	c 801	20	0.6	4071	10	US-09-764-869-2040	Sequence 2040, Ap
c 729	20	0.6	1764	12	US-10-091-009-3	Sequence 3, Appl	c 802	20	0.6	4394	10	US-09-764-877-2127	Sequence 2127, Ap
c 730	20	0.6	1803	10	US-09-887-576-268	Sequence 268, App	c 803	20	0.6	4400	10	US-09-764-877-2128	Sequence 2128, Ap
c 731	20	0.6	1823	9	US-09-938-842A-4744	Sequence 4744, Ap	c 804	20	0.6	4535	9	US-10-175-523-24	Sequence 24, Appl
c 732	20	0.6	1881	9	US-09-938-842A-3346	Sequence 3346, Ap	c 805	20	0.6	4589	9	US-09-764-891-8845	Sequence 8845, Ap
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826	20	0.6	5605	9	US-09-943-388-3	Sequence 3, Appli	899	20	0.6	10859	9	US-09-764-891-7408	Sequence 7408, Ap
827	20	0.6	5605	9	US-10-196-437A-7	Sequence 7, Appli	c 900	20	0.6	11071	10	US-09-764-877-2793	Sequence 2793, Ap
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843	20	0.6	6544	10	US-09-764-847-1544	Sequence 1544, Ap	c 916	20	0.6	12989	10	US-09-764-847-1489	Sequence 1489, Ap
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## ALIGNMENTS

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RESULT 1
US-09-764-904-89
; Sequence 89, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764,904
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-904-89

Query Match      48.3%; Score 1677; DB 9; Length 2411;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
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; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
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; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
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; PRIOR APPLICATION NUMBER: 60/215,135  
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; PRIOR FILING DATE: 2000-11-17  
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; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
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; PRIOR APPLICATION NUMBER: 60/249,245  
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; PRIOR APPLICATION NUMBER: 60/249,244  
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; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
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; PRIOR APPLICATION NUMBER: 60/232,400  
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; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
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; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
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; PRIOR FILING DATE: 2000-10-20  
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; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08

Query Match 48.3%; Score 1677; DB 9; Length 2411;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 61 CTAGGGCAAGAGGGCCCGAGGCACTGAGAAATCCAGCCCTCACACCAGCTCAAGCCCTCG 120  
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Qy 121 TGGTCCCGACGAGTGGACACTGAAATCAATTTTCTATTTCAGTCTCTGCCCCCTTGCCCT 180  
Db 651 TGGTCCCGACGAGTGGACACTGAAATCAATTTTCTATTTCAGTCTCTGCCCCCTTGCCCT 710  
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QY 541 GCTATTTTCATAGAACAAAGTCGCCAATGCGCATTTAGGGTTTTTCCCTCCCTAAGAGAGAT 600  
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US-09-764-860-1133  
; Sequence 1133, Application US/09764860  
; Patent No. US20020094953A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et. al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT APPLICATION NUMBER: US/09/764,860  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1133  
; LENGTH: 2411  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-860-1133

Query Match 48.3%; Score 1677; DB 10; Length 2411;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1877; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCTGCCCTGGGGCATCTTGAATACAGGCTGGAGTTTGTCTCATCTTACAGAGA 60  
Db 531 AGCTGCCCTGGGGCATCTTGAATACAGGCTGGAGTTTGTCTCATCTTACAGAGA 590  
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1441	AGCTTTCAGCAGGGAAGCGGCAGCTCCGCGCAGGAGCTTCGAGAGCCTCATGAAGGAGCAGG	1500	
1971	AGCTTTCAGCAGGGAAGCGGCAGCTCCGCGCAGGAGCTTCGAGAGCCTCATGAAGGAGCAGG	2030	
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## RESULT 5

RESULTS  
US-09-764-904-17

; Sequence 17, Application US/09764904

; Patent No. US20020173454A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA122

; CURRENT APPLICATION NUMBER: US/09/764,904

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 137

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; SOFTWARE: PatentIn Ver. 2.0
; GEO ID NO 17

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; SEQ ID NO 17

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; LENGTH: 560
; TYPE: DNA

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TYPE: DNA  
ORGANISM: Homo sapiens

ORGANISM: Homo sapiens  
IIS-09-764-904-17

US-09-164-904-17

Query Match 13.7%: Score 475: DB 9: Length 560:

Query Match 13.7%, Score 475, DS 3,  
Best Local Similarity 99.8%: Pred. No. 1.7e-240:

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: Matches 525: Conservative      0: Mismatches 1: Indels 0: Gaps 0:
: Best Local Similarity 33.8%, Freq: NO: 1.7E-240,

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Db 95 AGCCATCCTGCACTCCTCCCCGGAGAGTGCAGCCACCAGCTGCACCCCGCCCTCCAGA 154

QY 896 CAAGCCCAAGGAGCAGGAGCTGAAGCCTGGCCTGTGCTCTGGGGCGCTGTCAGACTCCGG 955

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Qy 455 CATCTCCACGACGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAGGGAGGG 514  
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Qy 1256 CGCCTCCAGAGCTGCAGCGCAGCTTTGAGAGAGAGGAGCTTGCC 1301  
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RESULT 6

US-10-091-548-17  
; Sequence 17, Application US/10091548  
; Publication No. US20030049703A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA122C1  
; CURRENT APPLICATION NUMBER: US/10/091.548  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 137  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-548-17

Query Match 13.7%; Score 475; DB 9; Length 560;  
Best Local Similarity 99.8%; Pred. No. 1.7e-240;  
Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 776 GGGCTCCAGAGGGTGCAGTGAGGCCACAGCCTTCAAGCTGTGCTGCCACGGTCAGG 835  
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Qy 155 CAAGCCCAAGGAGGAGGAGTGAAGCTGCGCTGTGGGGGCTGTGAGACTCCGG 214  
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Qy 215 CCGGAATCCATGTCTCAGCTGCCACACAGCAGCAGCAGCAGCTACAGCTGAGCCC 274  
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;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/251,856  
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;; PRIOR APPLICATION NUMBER: 60/251,868  
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;; PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/249,213  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,212  
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;; PRIOR APPLICATION NUMBER: 60/249,214  
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;; PRIOR APPLICATION NUMBER: 60/249,297  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/232,400  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/231,242  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,081  
;; PRIOR FILING DATE: 2000-09-08  
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;; PRIOR FILING DATE: 2000-09-08  
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;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,244  
;; PRIOR FILING DATE: 2000-09-08  
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;; PRIOR FILING DATE: 2000-09-14  
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;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,397  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,399  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,401  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/241,808  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,826  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,786  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,221  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08

Query Match 13.7%; Score 475; DB 9; Length 560;

Best Local Similarity 99.8%; Pred No. 1.7e-240; Mismatches 0; Indels 0; Gaps 0;

Matches 525; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 776 GGGCTCCGAGAAGGGTGCAGTGAGCGCCACAGCCTTCAAGCTGTGTGTCGCCACGGTCAGG 835

Db 35 GGGCTCCGAGAAGGGTGCAGTGAGCGCCACAGCCTTCAAGCTGTGTGTCGCCACGGTCAGG 94

Qy 836 AGCCATCCTGCATCTCTCCCGGAGAGTGCCAGCACAGCTGCACCCGCCCTCCAGA 895

Db 95 AGCCATCCTGCATCTCTCCCGGAGAGTGCCAGCACAGCTGCACCCGCCCTCCAGA 154

Qy 896 CAAGCCCAAGGAGCAGGAGCTGAGCCTGGCCTGTGCTCTGGGGCGGTGTGAGACTCCGG 955

Db 155 CAAGCCCAAGGAGCAGGAGCTGAGCCTGGCCTGTGCTCTGGGGCGGTGTGAGACTCCGG 214



Query Match 0.9%; Score 32; DB 9; Length 32203;  
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
US-09-969-373-172/c  
; Sequence 172, Application US/09969373  
; Patent No. US2002013952A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A



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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 3946.59 Seconds  
(without alignments)  
14252.028 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_871\_4343

Perfect score: 3473

Sequence: 1 agcgcgcctgggggcatct.....cggtggtgcacgcctgca 3473

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

- 1: em\_estba:\*
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- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
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- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	396	11.4	447	9 A1042490	A1042490 ox62e04.x
C 3	381	11.0	668	12 BF058214	BF058214 7k28d05.x
C 4	333	9.6	547	12 BF50813	BF50813 7n42e07.x
C 5	287	8.3	531	10 BE276168	BE276168 601144424
C 6	283	8.1	743	10 BE410921	BE410921 601303579

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AW016544	UI-H-B10P	344	10	AW016544
AA644373	af64c10.s	153	9	AA644373
AW028197	wv84a01.x	397	10	AW028197
BF725320	bxi4ell.y	714	12	BF725320
AV663617	AV663617	407	10	AV663617
AV663618	AV663618	596	10	AV663618
BH105255	RPCI-24-3	305	17	BH105255
BQ739770	PFCSToab4	355	14	BQ739770
BF506858	BB170024B	570	13	BF506858
BF505681	BB170032B	717	13	BF505681
AU087623	AU087623	308	9	AU087623
BH259700	CH230-113	491	17	BH259700
BM273468	PFCSToaa5	434	13	BM273468
AU086378	AU086378	500	9	AU086378
AU086887	AU086887	500	9	AU086887
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AU088256	AU088256	500	9	AU088256
BI814790	PFCSToaa0	501	13	BI814790
BM273468	PFCSToaa5	523	13	BM273468
AL737380	Danio rer	94	17	AL737380
AL779579	AL779579	227	9	AL779579
BM274140	PFCSToaa6	262	13	BM274140
BH043946	RPCI-24-2	264	17	BH043946
AI979395	fd36c12.y	278	9	AI979395
BQ633211	PFCSToab3	279	14	BQ633211
AL747474	Danio rer	285	17	AL747474
BH248597	BOGAT28TF	310	17	BH248597
AZ737672	RPCI-24-1	335	17	AZ737672
C06416	C06416	343	14	C06416
BH130332	G-604.r M	343	17	BH130332
AA278229	z877e10.r	356	9	AA278229
AA287156	z658a01.r	356	9	AA287156
BM336936	MEST201-B	362	13	BM336936
AI184894	oo07h01.x	368	9	AI184894
AZ761382	IM0555K10	398	17	AZ761382
BH098661	RPCI-24-2	407	17	BH098661
AU086295	AU086295	420	9	AU086295
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AZ284683	RPCI-23-1	437	17	AZ284683
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AQ857354	nbeb0005F	463	17	AQ857354
BH025607	RPCI-24-3	469	17	BH025607
AQ984657	RPCI-23-3	474	17	AQ984657
AQ671827	HS_5462.A	480	17	AQ671827
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AU087072	AU087072	500	9	AU087072
AU087803	AU087803	500	9	AU087803
AU088525	AU088525	500	9	AU088525
BM276433	PFCSToaa8	503	13	BM276433
AZ158617	SP_0061.A	506	17	AZ158617
AQ485382	RPCI-11-2	508	17	AQ485382
AQ838282	HS_5175.B	518	17	AQ838282
BH043278	RPCI-24-3	528	17	BH043278
AZ063844	RPCI-23-4	533	17	AZ063844
AZ262626	RPCI-23-1	533	17	AZ262626
B84300	RPCI11-23E3	533	17	B84300
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AQ890220	HS_3215.B	556	17	AQ890220
BM274622	PFCSToaa4	571	13	BM274622
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BH264269	CH230-161	590	17	BH264269
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AQ271706	nbxb00026H	625	17	AQ271706
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BH093402	RPCI-24-2	650	17	BH093402

80	32	0.9	667	17	AZ387690	IM0147K18	AZ387690	IM0147K18	c	153	31	0.9	792	17	AQ854864	CPG2091A	AQ854864	CPG2091A
81	32	0.9	675	17	BH678140	BOM0126TR	BH678140	BOM0126TR	c	154	31	0.9	792	17	BH471987	BOGX59TR	BH471987	BOGX59TR
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83	32	0.9	679	14	BM969053	UI-CF-DUI	BM969053	UI-CF-DUI	c	156	31	0.9	1421	13	BM395139	50072-2-7	BM395139	50072-2-7
84	32	0.9	686	17	BH102976	RPCI-24-2	BH102976	RPCI-24-2	c	157	31	0.9	2053	13	BM416466	OP21561 M	BM416466	OP21561 M
85	32	0.9	740	14	BQ769435	UI-M-FIO	BQ769435	UI-M-FIO	c	158	30	0.9	208	17	AZ936694	2M0193F04	AZ936694	2M0193F04
86	32	0.9	746	17	BH097849	RPCI-24-2	BH097849	RPCI-24-2	c	159	30	0.9	246	14	BQ452254	PFEStoa9	BQ452254	PFEStoa9
87	32	0.9	764	17	BH092650	RPCI-24-2	BH092650	RPCI-24-2	c	160	30	0.9	247	13	B1477599	da144d02	AQ352313	CITBI-E1-
88	32	0.9	823	17	BH462945	BOGWA81TR	BH462945	BOGWA81TR	c	161	30	0.9	285	17	AQ352313	CITBI-E1-	AQ352313	CITBI-E1-
89	32	0.9	830	17	BH044595	RPCI-24-2	BH044595	RPCI-24-2	c	162	30	0.9	342	17	AQ071549	HS 2174-A	AQ071549	HS 2174-A
90	32	0.9	832	12	BF065040	HV_CEB002	BF065040	HV_CEB002	c	163	30	0.9	344	9	AU087185	AU087185_	AU087185	AU087185_
91	32	0.9	847	17	AZ046234	nbeb00910	AZ046234	nbeb00910	c	164	30	0.9	364	17	B90998	CIT-HSP-217	B90998	CIT-HSP-217
92	32	0.9	886	14	BQ436964	AGENCOURT	BQ436964	AGENCOURT	c	165	30	0.9	368	13	B1814405	PFEStoa2	B1814405	PFEStoa2
93	32	0.9	899	17	AZ157626	SP 0057 A	AZ157626	SP 0057 A	c	166	30	0.9	370	10	AW432763	sh82f05-Y	AW432763	sh82f05-Y
94	32	0.9	999	14	BQ888876	AGENCOURT	BQ888876	AGENCOURT	c	167	30	0.9	370	13	B1815364	PFEStoa1	B1815364	PFEStoa1
95	32	0.9	1005	9	AL542351	AL542351	AL542351	AL542351	c	168	30	0.9	384	9	AU086846	AU086846	AU086846	AU086846
96	32	0.9	1038	17	CNS06L7M	T3 end of	BM394571	50072-2-4	c	169	30	0.9	396	17	AQ087312	HS 2191-B	AQ087312	HS 2191-B
97	32	0.9	1379	13	BM394571	50072-2-4	BM394571	50072-2-4	c	170	30	0.9	399	14	N82155	TGESTZY480	N82155	TGESTZY480
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99	32	0.9	1621	12	BE963462	601657243	BE963462	601657243	c	172	30	0.9	419	13	B1815213	PFEStoa1	B1815213	PFEStoa1
100	31	0.9	170	14	BQ596981	PFEStoa2	BQ596981	PFEStoa2	c	173	30	0.9	426	17	AZ239309	RPCI-23-3	AZ239309	RPCI-23-3
101	31	0.9	188	17	BH342108	CH230-130	BH342108	CH230-130	c	174	30	0.9	428	13	B1815693	PFEStoa3	B1815693	PFEStoa3
102	31	0.9	205	14	N97804	1287C3 czap	N97804	1287C3 czap	c	175	30	0.9	439	17	AQ085243	HS 2163-A	AQ085243	HS 2163-A
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C 226	29	0.8	375	17	AA550636	1825m3 gm	299	28	0.8	209	13	BJ326632	BJ326632
C 227	29	0.8	380	13	BM273809	PFEStoaas	300	28	0.8	214	13	BI512093	BI512093
C 228	29	0.8	389	17	AZ191638	SP 1019 B	301	28	0.8	227	14	BQ597041	PFEStoaab2
C 229	29	0.8	395	13	BI813774	P001807_O	C 302	28	0.8	257	17	AZ720781	RPCI-24-1
C 230	29	0.8	398	17	AQ910006	G8STC0799	303	28	0.8	277	9	AA565869	nj32f02.8
C 231	29	0.8	411	14	BQ739764	PFEStoaab4	304	28	0.8	294	14	BQ451988	PFEStoaas
C 232	29	0.8	418	14	BQ596480	PFEStoaab1	305	28	0.8	317	13	BI304099	UI-R-DR0-
C 233	29	0.8	418	17	AZ232526	1M0045C04	C 306	28	0.8	347	17	AZ888252	RPCI-24-1
C 234	29	0.8	419	9	A1248345	qh70902.x	C 307	28	0.8	377	13	BI815704	PFEStoaas
C 235	29	0.8	420	17	AZ118427	RPCI-23-4	C 308	28	0.8	381	9	AU086168	AU086168
C 236	29	0.8	423	12	BE947346	UI-M-BH3-	C 309	28	0.8	394	17	AQ787345	HS 3215 B
C 237	29	0.8	426	9	AA343271	EST48951	C 310	28	0.8	396	12	EG662775	DRAC03C02
C 238	29	0.8	428	17	AQ664753	HS 5238 B	C 311	28	0.8	402	13	BM274703	PFEStoaas
C 239	29	0.8	437	17	AZ357913	1M0099L15	C 312	28	0.8	405	12	EG663591	DRAC03C02
C 240	29	0.8	439	14	BQ739598	PFEStoaab4	C 313	28	0.8	416	17	AQ404029	HS 5050 B
C 241	29	0.8	449	13	BM275174	PFEStoaas	C 314	28	0.8	438	10	AW912988	u47e08-y
C 242	29	0.8	451	13	BM274221	PFEStoaas	C 315	28	0.8	440	9	AU086933	AU086933
C 243	29	0.8	452	10	BB744976	BB744976	C 316	28	0.8	444	13	BM274222	PFEStoaas
C 244	29	0.8	456	17	AQ887281	HS 5555 A	C 317	28	0.8	446	17	AZ470114	1M0284101
C 245	29	0.8	460	17	AQ530955	RPCI-11-3	C 318	28	0.8	448	14	BQ739635	PFEStoaab4
C 246	29	0.8	463	13	BM276265	PFEStoaas	C 319	28	0.8	473	13	BI535370	398844 MA
C 247	29	0.8	464	13	BM275642	PFEStoaas	C 320	28	0.8	483	17	AZ085963	RPCI-23-2
C 248	29	0.8	469	13	BI441797	da140d01.	C 321	28	0.8	490	13	BI815797	PFEStoaas
C 249	29	0.8	473	13	BI815248	PFEStoaas	C 322	28	0.8	495	17	AQ734028	HS 2151 A
C 250	29	0.8	475	10	AA490399	UI-M-BH3-	C 323	28	0.8	496	9	AU087508	AU087508
C 251	29	0.8	480	14	BQ031488	UI-1-CF0-	C 324	28	0.8	497	9	AU087925	AU087925
C 252	29	0.8	482	13	BI514115	BI160014A	C 325	28	0.8	500	9	AU086245	AU086245
C 253	29	0.8	485	9	A1592975	vu89e05.x	C 326	28	0.8	500	9	AU086610	AU086610
C 254	29	0.8	488	17	AZ276717	RPCI-23-1	C 327	28	0.8	500	9	AU086968	AU086968
C 255	29	0.8	490	9	AA900490	UI-R-EO-d	C 328	28	0.8	500	9	AU087101	AU087101
C 256	29	0.8	491	17	AQ827720	HS 5314 A	C 329	28	0.8	500	9	AU087396	AU087396
C 257	29	0.8	494	13	BI514340	BI160015A	C 330	28	0.8	500	9	AU087439	AU087439
C 258	29	0.8	496	17	AZ262758	RPCI-23-4	C 331	28	0.8	500	9	AU087906	AU087906
C 259	29	0.8	500	9	AU086241	AU086241	C 332	28	0.8	500	9	AU088403	AU088403
C 260	29	0.8	500	9	AU086696	AU086696	C 333	28	0.8	500	9	AU088512	AU088512
C 261	29	0.8	500	9	AU086915	AU086915	C 334	28	0.8	505	17	B88548	B88548
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C 264	29	0.8	500	9	AU087525	AU087525	C 337	28	0.8	515	13	BM275967	PFEStoaas
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C 266	29	0.8	502	14	BQ596846	PFEStoaab2	C 339	28	0.8	517	13	BI515191	BI160017B
C 267	29	0.8	503	17	AZ562204	RPCI-23-2	C 340	28	0.8	517	13	BM273805	PFEStoaas
C 268	29	0.8	511	17	AQ136687	HS 2195 A	C 341	28	0.8	518	13	BI515362	BI160019A
C 269	29	0.8	523	17	AZ179400	SP 0165 A	C 342	28	0.8	525	13	BI515428	BI160019A
C 270	29	0.8	528	13	BI815829	PFEStoaas	C 343	28	0.8	542	9	AL773742	AL773742
C 271	29	0.8	534	13	BI815829	PFEStoaas	C 344	28	0.8	542	13	BM275372	PFEStoaas
C 272	29	0.8	540	17	AZ840395	2M0136L20	C 345	28	0.8	542	17	AZ157517	SP 0016 A
C 273	29	0.8	559	17	AZ018307	RPCI-23-3	C 346	28	0.8	550	13	BI509694	BI170018B
C 274	29	0.8	567	17	AZ878663	RPCI-23-1	C 347	28	0.8	556	17	AZ016474	RPCI-23-3
C 275	29	0.8	570	17	AZ358044	1M0100101	C 348	28	0.8	560	13	BJ330230	BJ330230
C 276	29	0.8	572	14	BQ526359	NTSC no15	C 349	28	0.8	562	17	AZ148286	SP 0029 B
C 277	29	0.8	574	14	BQ629497	saq02h01.	C 350	28	0.8	568	17	AZ886000	RPCI-23-1
C 278	29	0.8	577	9	AL804911	AL804911	C 351	28	0.8	578	13	BJ389811	BJ389811
C 279	29	0.8	582	13	BM273686	PFEStoaas	C 352	28	0.8	589	13	BM273878	PFEStoaas
C 280	29	0.8	583	13	BI514020	BI160014A	C 353	28	0.8	593	14	AQ196700	UI-R-EAO-
C 281	29	0.8	588	13	BM275713	PFEStoaas	C 354	28	0.8	596	17	AZ362080	1M0107J02
C 282	29	0.8	606	14	BQ524785	NTSC no07	C 355	28	0.8	604	14	BQ596870	PFEStoaab2
C 283	29	0.8	609	10	AV356181	AV356181	C 356	28	0.8	610	17	AZ742705	RPCI-24-1
C 284	29	0.8	635	12	BF472183	BF472183	C 357	28	0.8	618	13	BJ366505	BJ366505
C 285	29	0.8	641	17	BH522233	BOGSS22TR	C 358	28	0.8	645	10	AW950684	EST362754
C 286	29	0.8	658	14	BQ526360	NTSC no15	C 359	28	0.8	647	17	AQ450221	50009C09
C 287	29	0.8	659	12	BF294157	BF294157	C 360	28	0.8	654	17	BH269435	CH230-19H
C 288	29	0.8	666	9	AV273793	AV273793	C 361	28	0.8	654	17	BH269435	CH230-19H
C 289	29	0.8	719	14	BQ176374	UI-M-DJ2-	C 362	28	0.8	681	17	AZ335818	1M0065L03
C 290	29	0.8	744	17	AZ893146	RPCI-24-1	C 363	28	0.8	698	17	AZ556974	RPCI-23-2
C 291	29	0.8	765	17	BH607521	BOHFJ96TF	C 364	28	0.8	698	17	AZ728396	RPCI-24-1
C 292	29	0.8	832	17	BH061170	RPCI-24-3	C 365	28	0.8	713	17	AZ176266	SP 0141 A
C 293	29	0.8	895	14	BQ220502	AGENCOURT	C 366	28	0.8	725	10	AV692815	AV692815
C 294	29	0.8	2265	12	BF128485	601810323	C 367	28	0.8	727	17	BH086698	RPCI-24-9
C 295	29	0.8	3565	11	AK004556	MuB muSCU	C 368	28	0.8	732	10	AV691728	AV691728
C 296	28	0.8	142	17	AZ43486	1M0239H03	C 369	28	0.8	738	10	AV692816	AV692816
C 297	28	0.8	147	17	AZ747291	RPCI-24-1	C 370	28	0.8	740	10	AV691729	AV691729
C 298	28	0.8	167	17	AZ602391	1M0421E09	C 371	28	0.8	743	17	BH031136	RPCI-24-3



C 372	28	0.8	775	17	AQ854767	CG21388	445	27	0.8	511	12	BG555169	BG555169	de95e07.x
C 373	28	0.8	783	17	BH522424	BOHJL07TR	C 446	27	0.8	511	13	BM338181	BM338181	MEST222-H
C 374	28	0.8	812	17	BH178455	011_J_02-	C 447	27	0.8	516	12	BQ603144	BQ603144	MI-P-NA-A
C 375	28	0.8	812	17	BH178455	011_J_02-	C 448	27	0.8	516	12	BQ603144	BQ603144	MI-P-NA-A
C 376	28	0.8	815	17	BH352602	CH230-175	C 449	27	0.8	524	13	BH128940	BH128940	U7-R-DKO-
C 377	28	0.8	835	17	AZ695866	RPCI-23-2	C 450	27	0.8	525	17	BH121510	BH121510	RPCI-24-3
C 378	28	0.8	1299	13	BM394791	50072-2-6	C 451	27	0.8	527	17	AQ172252	AQ172252	HS_3179-B
C 379	28	0.8	1652	13	BM395003	50072-2-7	C 452	27	0.8	528	17	AQ800724	AQ800724	HS_5315-B
C 380	27	0.8	200	14	BQ596826	PfESToaab2	C 453	27	0.8	528	17	BH10462	BH10462	CH230-193
C 381	27	0.8	200	14	BQ596826	PfESToaab2	C 454	27	0.8	530	17	AZ886419	AZ886419	RPCI-23-1
C 382	27	0.8	236	14	N98064	011-11-3	C 455	27	0.8	533	17	AQ591933	AQ591933	HS_5414-A
C 383	27	0.8	250	14	N98016	2150C3 czap	C 456	27	0.8	536	17	AQ211941	AQ211941	HS_3241-B
C 384	27	0.8	266	17	AZ583402	1M0378M23	C 457	27	0.8	537	17	BH323914	BH323914	CH230-104
C 385	27	0.8	273	13	BM268056	MEST376-B	C 458	27	0.8	541	13	BM273797	BM273797	PfESToaab5
C 386	27	0.8	274	13	BM274634	PfESToaab4	C 459	27	0.8	543	13	BM273797	BM273797	PfESToaab5
C 387	27	0.8	280	9	AU087647	AU087647	C 460	27	0.8	546	10	AW538015	AW538015	B1650014B
C 388	27	0.8	281	14	BQ596510	PfESToaab1	C 461	27	0.8	550	13	BH14182	BH14182	B160014B
C 389	27	0.8	286	9	AU087673	AU087673	C 462	27	0.8	552	17	AQ538004	AQ538004	RPCI-11-3
C 390	27	0.8	294	14	N97597	1030C3 czap	C 463	27	0.8	553	13	BH1670695	BH1670695	PfESToaab0
C 391	27	0.8	318	13	BH157121	1M0150018	C 464	27	0.8	554	9	AU149369	AU149369	AU149369
C 392	27	0.8	320	17	AZ928031	1M0150018	C 465	27	0.8	554	13	BM274761	BM274761	PfESToaab7
C 393	27	0.8	321	13	BH157121	1M0150018	C 466	27	0.8	561	17	BH078344	BH078344	RPCI-24-3
C 394	27	0.8	328	17	AQ017800	CT-HSP-2	C 467	27	0.8	563	13	BH1670535	BH1670535	PfESToaab0
C 395	27	0.8	342	10	AV691884	AV691884	C 468	27	0.8	563	13	BM275212	BM275212	PfESToaab6
C 396	27	0.8	343	9	AU086817	AU086817	C 469	27	0.8	563	17	AQ561057	AQ561057	HS_5342-B
C 397	27	0.8	347	17	AZ389560	1M0150018	C 470	27	0.8	565	17	AQ079015	AQ079015	CT-HSP-2
C 398	27	0.8	348	17	CNS045F8	1M0150018	C 471	27	0.8	572	17	BH313000	BH313000	CH230-12D
C 399	27	0.8	354	17	AQ246404	HS_2064-B	C 472	27	0.8	573	13	BM275162	BM275162	PfESToaab8
C 400	27	0.8	361	9	AI133217	zm35a01.I	C 473	27	0.8	583	17	AQ774291	AQ774291	HS_3086-A
C 401	27	0.8	366	14	BQ452441	PfESToaab9	C 474	27	0.8	588	9	AL632384	AL632384	AL632384
C 402	27	0.8	376	13	BH14954	PfESToaab0	C 475	27	0.8	592	17	CNS02U7F	CNS02U7F	Tetraodon
C 403	27	0.8	377	13	BM273826	PfESToaab6	C 476	27	0.8	602	13	BH16270	BH16270	B160021B
C 404	27	0.8	381	13	BM273527	PfESToaab5	C 477	27	0.8	608	13	BM161711	BM161711	EST564234
C 405	27	0.8	390	9	AU086299	AU086299	C 478	27	0.8	615	9	AL712274	AL712274	DKF2P6860
C 406	27	0.8	396	17	BH358845	CH230-126	C 479	27	0.8	615	12	BE806160	BE806160	s954h10.Y
C 407	27	0.8	403	14	N97876	1432C3 czap	C 480	27	0.8	617	17	AZ095059	AZ095059	RPCI-23-1
C 408	27	0.8	416	17	AZ928053	479_dif04	C 481	27	0.8	623	17	BH363698	BH363698	CH230-60A
C 409	27	0.8	420	12	BF770455	RC2-IT004	C 482	27	0.8	627	10	AW222691	AW222691	EST299502
C 410	27	0.8	421	9	AU087621	AU087621	C 483	27	0.8	631	13	BM276345	BM276345	PfESToaab8
C 411	27	0.8	423	13	BH136135	PfESToaab2	C 484	27	0.8	642	13	BM267903	BM267903	MEST373-G
C 412	27	0.8	424	14	BQ633388	PfESToaab4	C 485	27	0.8	649	14	BQ192058	BQ192058	UI-R-RD13-
C 413	27	0.8	426	9	AU087549	AU087549	C 486	27	0.8	652	9	AU134513	AU134513	AU134513
C 414	27	0.8	427	17	AQ022939	HS_2185-A	C 487	27	0.8	653	17	AA550371	AA550371	1517m3 gm
C 415	27	0.8	440	17	AQ513779	HS_5152-A	C 488	27	0.8	656	12	BF296492	BF296492	037PB611
C 416	27	0.8	450	13	BM275482	PfESToaab5	C 489	27	0.8	664	17	AZ316496	AZ316496	1M0034J08
C 417	27	0.8	450	17	AZ199756	SP_1040-A	C 490	27	0.8	681	17	BH207155	BH207155	Sml-51M13
C 418	27	0.8	453	9	AU087959	AU087959	C 491	27	0.8	704	17	AZ230276	AZ230276	RPCI-23-6
C 419	27	0.8	456	13	BH14644	PfESToaab4	C 492	27	0.8	713	17	AQ650488	AQ650488	1M0538A08
C 420	27	0.8	460	17	AQ530955	RPCI-11-3	C 493	27	0.8	716	17	AQ574273	AQ574273	nbxb0083P
C 421	27	0.8	469	13	BH15280	PfESToaab1	C 494	27	0.8	717	13	BH045445	BH045445	BJ045445
C 422	27	0.8	469	13	BH15280	PfESToaab1	C 495	27	0.8	719	13	BH045445	BH045445	BJ045445
C 423	27	0.8	473	13	BM274148	PfESToaab6	C 496	27	0.8	725	17	AZ561119	AZ561119	RPCI-23-2
C 424	27	0.8	475	17	AZ262310	RPCI-23-4	C 497	27	0.8	729	17	CNS04MGW	CNS04MGW	1M0538A06
C 425	27	0.8	489	17	AZ060178	PfESToaab6	C 498	27	0.8	737	17	BM028532	BM028532	Ipskn0078
C 426	27	0.8	491	13	BM274073	PfESToaab6	C 499	27	0.8	741	13	BM028532	BM028532	Ipskn0078
C 427	27	0.8	498	10	AW232842	fj32d12.x	C 500	27	0.8	748	14	BQ103768	BQ103768	ESTB1700
C 428	27	0.8	500	9	AU086152	AU086152	C 501	27	0.8	753	17	BH314212	BH314212	CH230-63A
C 429	27	0.8	500	9	AU086589	AU086589	C 502	27	0.8	767	17	BH314212	BH314212	CH230-63A
C 430	27	0.8	500	9	AU086643	AU086643	C 503	27	0.8	767	17	BH314212	BH314212	CH230-63A
C 431	27	0.8	500	9	AU087045	AU087045	C 504	27	0.8	830	17	BH044595	BH044595	RPCI-24-2
C 432	27	0.8	500	9	AU087082	AU087082	C 505	27	0.8	845	17	BH491488	BH491488	BOGJY56TR
C 433	27	0.8	500	9	AU087328	AU087328	C 506	27	0.8	848	17	CNS03N06	CNS03N06	Tetraodon
C 434	27	0.8	500	9	AU087403	AU087403	C 507	27	0.8	853	17	AQ750271	AQ750271	HS_5576-A
C 435	27	0.8	500	9	AU087483	AU087483	C 508	27	0.8	869	12	EG697230	EG697230	602660466
C 436	27	0.8	500	9	AU087584	AU087584	C 509	27	0.8	911	17	CNS07375	CNS07375	clone BA0
C 437	27	0.8	500	9	AU087888	AU087888	C 510	27	0.8	949	17	CNS06J08	CNS06J08	T7 end of
C 438	27	0.8	500	9	AU087971	AU087971	C 511	27	0.8	1038	17	CNS06L7M	CNS06L7M	AL403832
C 439	27	0.8	500	9	AU088109	AU088109	C 512	27	0.8	1101	17	CNS00KON	CNS00KON	T3 end of
C 440	27	0.8	500	9	AU088345	AU088345	C 513	27	0.8	1101	17	CNS05P80	CNS05P80	AL078112
C 441	27	0.8	500	9	AU088346	AU088346	C 514	27	0.8	1707	13	BM394561	BM394561	Trosophila
C 442	27	0.8	500	9	AU088390	AU088390	C 515	27	0.8	1878	12	BG845876	BG845876	50072-2-4
C 443	27	0.8	500	9	AU088502	AU088502	C 516	26	0.7	118	9	AI409071	AI409071	EST237363
C 444	27	0.8	505	9	AI492378	t127c12.x	C 517	26	0.7	161	14	BQ633588	BQ633588	PfESToaab4

C 518	26	0.7	167	17	AZ267916	A2267916	RPIC-23-1	C 591	26	0.7	478	10	BE018440
C 519	26	0.7	214	14	BQ596558	BQ596558	RPIC-23-1	592	26	0.7	482	14	BQ633203
C 520	26	0.7	218	14	H82340	H82340	YU9H08.r1	593	26	0.7	484	12	BF001607
C 521	26	0.7	234	17	AZ882914	AZ882914	RPIC-23-1	C 594	26	0.7	486	13	BJ365318
C 522	26	0.7	236	14	BQ596706	BQ596706	PFEStoa2	595	26	0.7	486	14	BQ739708
C 523	26	0.7	247	13	BI815521	BI815521	PFEStoa2	C 596	26	0.7	487	10	BE458384
C 524	26	0.7	257	9	AU086678	AU086678	AU086678	C 597	26	0.7	488	17	AQ120663
525	26	0.7	259	9	AI157086	AI157086	ud16a05.r	598	26	0.7	489	12	BF513548
C 526	26	0.7	265	13	BM275053	BM275053	PFEStoa7	599	26	0.7	489	17	AQ2060178
C 527	26	0.7	278	10	AV726570	AV726570	AV726570	C 600	26	0.7	490	9	AA800486
C 528	26	0.7	301	14	BQ451048	BQ451048	PFEStoa0	601	26	0.7	490	13	BM275231
C 529	26	0.7	301	14	N98106	N98106	2192C3 czap	C 602	26	0.7	490	17	AQ203615
C 530	26	0.7	312	14	N98005	N98005	2026C3 czap	C 603	26	0.7	491	13	BI675562
531	26	0.7	312	17	BI812237	BI812237	O20_D_14-	C 604	26	0.7	497	13	BM491430
532	26	0.7	312	17	CNS07NOH	AL619187	T2 end of	605	26	0.7	497	17	AQ922217
C 533	26	0.7	313	9	AU087609	AU087609	AU087609	C 606	26	0.7	499	17	AQ139954
534	26	0.7	319	14	N98074	N98074	2229C3 czap	607	26	0.7	500	9	AU086136
C 535	26	0.7	321	14	W16536	W16536	2b10409.r1	C 608	26	0.7	500	9	AU086425
C 536	26	0.7	325	13	BI814312	BI814312	PFEStoa2	C 609	26	0.7	500	9	AU086748
C 537	26	0.7	325	14	T28727	T28727	EST53404 Hu	C 610	26	0.7	500	9	AU086812
C 538	26	0.7	327	17	AZ257566	AZ257566	RPIC-23-1	611	26	0.7	500	9	AU086874
C 539	26	0.7	329	14	BQ392379	BQ392379	NISC mq24	C 612	26	0.7	500	9	AU087021
540	26	0.7	330	17	AQ584397	AQ584397	RPIC-11-4	C 613	26	0.7	500	9	AU087155
C 541	26	0.7	342	14	BQ596883	BQ596883	PFEStoa2	614	26	0.7	500	9	AU087218
C 542	26	0.7	344	14	BQ451468	BQ451468	PFEStoa9	615	26	0.7	500	9	AU087273
C 543	26	0.7	344	14	BQ452333	BQ452333	PFEStoa9	616	26	0.7	500	9	AU087456
C 544	26	0.7	353	10	AW936480	AW936480	QV4-DT002	617	26	0.7	500	9	AU087837
C 545	26	0.7	354	13	BI936191	BI936191	PFEStoa2	618	26	0.7	500	9	AU088026
546	26	0.7	358	13	BI936075	BI936075	PFEStoa2	619	26	0.7	500	9	AU088135
C 547	26	0.7	361	9	A409080	A409080	EST237372	620	26	0.7	500	9	AU088483
548	26	0.7	361	13	BI814037	BI814037	PFEStoa0	621	26	0.7	500	9	AU088490
C 549	26	0.7	362	10	AV725187	AV725187	AV725187	C 622	26	0.7	501	13	BI814790
C 550	26	0.7	368	13	BI814405	BI814405	PFEStoa2	623	26	0.7	501	13	BI478245
551	26	0.7	375	13	BI670658	BI670658	PFEStoa0	624	26	0.7	504	13	BI478245
C 552	26	0.7	378	17	AQ031304	AQ031304	HS-2213_B	C 625	26	0.7	505	13	BI123500
553	26	0.7	378	17	AQ106231	AQ106231	HS-3051_B	C 626	26	0.7	508	13	BI514335
554	26	0.7	381	10	BB802930	BB802930	BB802930	C 627	26	0.7	510	9	AA893265
555	26	0.7	382	13	BI162652	BI162652	PFEStoa3	628	26	0.7	513	10	BE328150
556	26	0.7	383	14	N97976	N97976	1739C3 czap	629	26	0.7	516	17	BI197671
C 557	26	0.7	388	14	BM854400	BM854400	K-EST0136	C 630	26	0.7	518	13	BM274067
C 558	26	0.7	397	13	BJ078187	BJ078187	BJ078187	631	26	0.7	519	17	AZ928055
C 559	26	0.7	398	13	BJ394065	BJ394065	BJ394065	C 632	26	0.7	519	9	A1409079
560	26	0.7	398	17	AZ761382	AZ761382	IM0555K10	633	26	0.7	520	17	BH843091
561	26	0.7	399	14	N97593	N97593	1024C3 czap	C 634	26	0.7	523	13	BM167768
C 562	26	0.7	401	9	BQ739562	BQ739562	PFEStoa4	C 635	26	0.7	524	17	AQ974493
C 563	26	0.7	413	14	AQ702923	AY702923	zi76d04.s	C 636	26	0.7	525	13	BJ426469
564	26	0.7	414	13	BI511680	BI511680	BB160006B	C 637	26	0.7	529	17	BI195369
565	26	0.7	415	17	AQ150727	AQ150727	HS-3203_A	638	26	0.7	529	17	AQ502749
566	26	0.7	418	17	AQ216606	AQ216606	HS-2139_A	639	26	0.7	530	17	AZ886419
C 567	26	0.7	420	17	AQ533464	AQ533464	RPIC-11-3	640	26	0.7	530	17	BI199135
568	26	0.7	424	13	BI204186	BI204186	EST522226	C 641	26	0.7	534	17	BI764621
569	26	0.7	427	10	AW048128	AW048128	UI-M-BH1-	642	26	0.7	535	10	AW638825
C 570	26	0.7	429	17	AQ914351	AQ914351	nbeb00480	C 643	26	0.7	536	17	AQ830438
571	26	0.7	429	17	BI195089	BI195089	TC3-68L23	C 644	26	0.7	537	10	AW933537
572	26	0.7	431	13	BM275996	BM275996	PFEStoa8	645	26	0.7	537	13	BM275514
573	26	0.7	432	14	W37510	W37510	zc12d04.s1	C 646	26	0.7	537	13	BM275927
C 574	26	0.7	436	10	AW932771	AW932771	EST358614	647	26	0.7	537	17	AZ873884
575	26	0.7	439	10	AW627569	AW627569	hb87h03.x	C 648	26	0.7	538	13	BJ397063
576	26	0.7	447	14	BQ452354	BQ452354	PFEStoa9	C 649	26	0.7	538	13	BJ422055
C 577	26	0.7	453	13	BM411835	BM411835	EST586162	650	26	0.7	539	13	BJ396971
C 578	26	0.7	457	13	BI936194	BI936194	PFEStoa2	C 651	26	0.7	540	13	BI502940
C 579	26	0.7	458	13	BI815758	BI815758	PFEStoa3	C 652	26	0.7	540	13	BI816073
C 580	26	0.7	460	13	BI675535	BI675535	dac62e06	C 653	26	0.7	543	13	BM275916
C 581	26	0.7	460	17	AQ198638	AQ198638	RPIC11-59	C 654	26	0.7	544	9	AL658903
582	26	0.7	461	17	AZ902609	AZ902609	RPIC-24-1	655	26	0.7	544	13	BJ392332
583	26	0.7	463	9	A1918803	A1918803	ts86g05.x	C 656	26	0.7	545	9	AL781236
C 584	26	0.7	464	13	BM275506	BM275506	PFEStoa5	657	26	0.7	547	13	BJ392160
C 585	26	0.7	465	9	AF244983	AF244983	AF244983	658	26	0.7	548	13	BM274922
C 586	26	0.7	465	9	A1410242	A1410242	EST238535	C 589	26	0.7	554	12	EG512900
587	26	0.7	465	9	AU087511	AU087511	AU087511	660	26	0.7	556	12	EG512900
C 588	26	0.7	466	17	AQ611982	AQ611982	HS-5072_B	C 661	26	0.7	556	12	EG512900
C 589	26	0.7	467	14	BQ451839	BQ451839	PFEStoa50	C 662	26	0.7	556	13	BI166831
C 590	26	0.7	473	9	AU087951	AU087951	AU087951	663	26	0.7	559	13	BI815150

664	BM653101	13	560	0.7	26	BM553101	170006873	C 737	26	0.7	716	13	BM167270
665	AQ998129	17	562	0.7	26	AQ998129	RPCI-23-2	C 738	26	0.7	729	17	AZ660406
666	BM275442	13	566	0.7	26	BM275442	PfESToa86	C 739	26	0.7	731	10	AV693920
667	BM782490	14	566	0.7	26	BM782490	K-EST0059	C 740	26	0.7	733	17	AZ617011
668	BI936160	13	568	0.7	26	BI936160	PfESToa2	C 741	26	0.7	737	13	BM170282
669	BM273626	13	569	0.7	26	BM273626	PfESToa5	C 742	26	0.7	739	17	BH424268
670	BM314725	13	570	0.7	26	BM314725	1954c05.y	C 743	26	0.7	742	13	BM163235
671	AZ005004	17	571	0.7	26	AZ005004	RPCI-23-3	C 744	26	0.7	747	13	BM165966
672	AQ504035	17	571	0.7	26	AQ504035	RPCI-11-2	C 745	26	0.7	748	10	AV725838
673	BI503579	13	575	0.7	26	BI503579	BB170014B	C 746	26	0.7	755	17	B92121
674	BM160696	13	579	0.7	26	BM160696	EST563219	C 747	26	0.7	782	13	BM413222
675	BM171338	13	579	0.7	26	BM171338	EST573861	C 748	26	0.7	783	13	BM159742
676	AZ875478	17	579	0.7	26	AZ875478	2M0190107	C 749	26	0.7	796	10	AV693921
677	BM275358	13	582	0.7	26	BM275358	PfESToa86	C 750	26	0.7	799	13	BM413307
678	BM757101	14	582	0.7	26	BM757101	K-EST0035	C 751	26	0.7	812	17	BH257903
679	BM273375	13	585	0.7	26	BM273375	PfESToa4	C 752	26	0.7	828	17	CNS05202
680	BH205894	17	585	0.7	26	BH205894	SM1-42C16	C 753	26	0.7	829	17	AZ690899
681	BM165613	13	587	0.7	26	BM165613	EST568136	C 754	26	0.7	917	14	BQ880667
682	BM709585	14	589	0.7	26	BM709585	UI-E-CQ1-	C 755	26	0.7	946	17	BH158562
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688	BJ332936	13	594	0.7	26	BJ332936	BJ332936	C 761	25	0.7	132	14	N98177
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690	AZ991190	17	597	0.7	26	AZ991190	2M0275D18	C 763	25	0.7	158	14	N97710
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692	AL802987	9	601	0.7	26	AL802987	AL802987	C 765	25	0.7	168	9	AA025815
693	BH841619	17	602	0.7	26	BH841619	TC3-53N23	C 766	25	0.7	178	12	BF784097
694	AZ750977	17	603	0.7	26	AZ750977	RPCI-24-1	C 767	25	0.7	211	17	AZ923814
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696	AV649639	10	604	0.7	26	AV649639	AV649639	C 769	25	0.7	221	14	T18153
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C 860	25	0.7	425	10	BB812256	BB812256	BB812256	C 933	25	0.7	500	9	AU086761	AU086761	AU086761
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C 877	25	0.7	449	17	AA550472	1626m3 9m	AA550472	C 950	25	0.7	506	9	AA527066	ni06h01.s	AA527066
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C 879	25	0.7	451	17	BI670614	PfESToa0	BI670614	C 952	25	0.7	507	17	AZ739889	RPCI-24-7	AZ739889
C 880	25	0.7	452	13	BI670614	PfESToa0	BI670614	C 953	25	0.7	508	10	AW493888	UI-M-BH3-	AW493888
C 881	25	0.7	454	9	AA687640	nv07e02.s	AA687640	C 954	25	0.7	508	17	AZ644043	IM0507N16	AZ644043
C 882	25	0.7	456	13	BI512109	BB160008A	BI512109	C 955	25	0.7	509	17	AQ341248	RPCI11-12	AQ341248



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 447)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 656 Std Error: 0.00  
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NbHPU, and fetal heart NBHH19W) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

BASE COUNT 62 a 133 c 156 g 96 t  
ORIGIN

Query Match 11.4%; Score 396; DB 9; Length 447;  
Best Local Similarity 99.8%; Pred. No. 2.6e-184;  
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 855 CCGAGAGTGCAGCCAGCAGTGACCCCGCCCTCCAGACAAGCCCAAGAGCAGGAG 914  
DB 447 CCGGAGAGTGCAGCCAGCAGTGACCCCGCCCTCCAGACAAGCCCAAGAGCAGGAG 388

QY 915 CTGAAGCTTGGCTGTCTGTGGGCGCTGTACAGCTCCGCGCGAACTCCATGTCCAGC 974  
DB 387 CTGAAGCTTGGCTGTCTGTGGGCGCTGTACAGCTCCGCGCGAACTCCATGTCCAGC 328

QY 975 CTGCCCCACACAGCAGCAGCAGCTACAGCTGGACCCCGCTGGTCACACCCCGTGGGA 1034  
DB 327 CTGCCCCACACAGCAGCAGCAGCTACAGCTGGACCCCGCTGGTCACACCCCGTGGGA 268

QY 1035 CCCACAAGCCGTTTGGGGGTCGCCCCACACATCACCCAGGGCATCGTCTCCAGGAC 1094  
DB 267 CCCACAAGCCGTTTGGGGGTCGCCCCACACATCACCCAGGGCATCGTCTCCAGGAC 208

QY 1095 AGCAACATGATGAGCTCAAGGCTGTCTTCTCCGACGAGGTAGCAAGCTGGGCCAC 1154  
DB 207 AGCAACATGATGAGCTCAAGGCTGTCTTCTCCGACGAGGTAGCAAGCTGGGCCAC 148

QY 1155 TCGAACAAAGGACAGCAAGGGCCCTCGTGTGTGTCGCTCCCATCTCCACGAGCAGTGC 1214  
DB 147 TCGAACAAAGGACAGCAAGGGCCCTCGTGTGTGTCGCTCCCATCTCCACGAGCAGTGC 88

QY 1215 AGCATCCAGGAGCTGGAAACAGAACTGTGGAGAGGGAGGGCGCCCTCCAGAACTGCAG 1274  
DB 87 AGCATCCAGGAGCTGGAGCAGAACTGTGGAGAGGGAGGGCGCCCTCCAGAACTGCAG 28

QY 1275 CGCAGCTTTGAGGAGAGGAGCTTGCC 1301  
DB 27 CGCAGCTTTGAGGAGAGGAGCTTGCC 1

RESULT 3  
LOCUS BF058214/c  
DEFINITION 7k28d05.x1 NCI CGAP Ovl8 Homo sapiens cDNA clone IMAGE:3476769 3'  
similar to TR:Q9Y5W1 Q9Y5W1 FEZ1. [5] TR:Q9Y5W0 TR:Q9Y5V9 TR:Q9Y5V8  
TR:Q9Y5V7 ; contains MER22.t3 TAR1 repetitive element ;, mRNA  
sequence.  
ACCESSION BF058214  
VERSION BF058214.1 GI:10812110  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 668)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D.; Ph.D.; Michael  
R. Emmert-Buck, M.D.; Ph.D. cDNA Library Preparation: M. Bento  
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 441.

FEATURES  
Location/Qualifiers  
1..668  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3476769"  
/clone\_lib="NCI CGAP Ovl8"  
/tissue\_type="fibroheoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pTT3D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCGACATTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pTT3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 185 c 226 g 150 t 2 others  
ORIGIN

Query Match 11.0%; Score 381; DB 12; Length 668;  
Best Local Similarity 99.8%; Pred. No. 7.5e-177;  
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 GGGCTCCGAGAGGTCAGTGAGGCCACAGCCTTCAAGCCTGTGTCACCGTCAGG 835  
DB 514 GGGCTCCGAGAGGTCAGTGAGGCCACAGCCTTCAAGCCTGTGTCACCGTCAGG 455

QY 836 AGCCATCTGCATCTCTCCCGGAGAGTGCAGCCACCCAGCTGCACCCCGCTCCAGA 895  
DB 454 AGCCATCTGCATCTCTCCCGGAGAGTGCAGCCACCCAGCTGCACCCCGCTCCAGA 395

QY 896 CAAGCCCAAGAGCAGAGCTGAAGCTGGCCTGTGCTCTGGGGCGCTGTGAGACTCCGG 955  
DB 394 CAAGCCCAAGAGCAGAGCTGAAGCTGGCCTGTGCTCTGGGGCGCTGTGAGACTCCGG 335

QY 956 CCGGAATCCATGTCAGCCTGCCACACAGCAGCAGCAGCTACAGCTGGAGCC 1015  
DB 334 CCGGAATCCATGTCAGCCTGCCACACAGCAGCAGCAGCTACAGCTGGAGCC 275

QY 1016 GCTGTCACACCGTGGGACCAAGCCGTTTGGGGCTCCGCCACACATCACCA 1075  
 |||||  
 Db 274 GCTGTCACACCGTGGGACCAAGCCGTTTGGGGCTCCGCCACACATCACCA 215  
 |||||  
 QY 1076 GGGATCTCTCTCCAGGACAGCAACATGATGAGCTTGAAGCTCTGTCTTCTCCGACGG 1135  
 |||||  
 Db 214 GGGATCTCTCTCCAGGACAGCAACATGATGAGCTTGAAGCTCTGTCTTCTCCGACGG 155  
 |||||  
 QY 1136 AGGTAGCAAGCTGGGCCACTGCAACAGGACAGCAAGGGCCCTCTGTGTCTCCGTCGCC 1195  
 |||||  
 Db 154 AGGTAGCAAGCTGGGCCACTGCAACAGGACAGCAAGGGCCCTCTGTGTCTCCGTCGCC 95  
 |||||  
 QY 1196 CATCTCCACGGA 1207  
 |||||  
 Db 94 CATCTCCACGGA 83  
 |||||

RESULT 4  
 BF590813/c  
 LOCUS BF590813 547 bp mRNA linear EST 12-DEC-2000  
 DEFINITION 7h42e07.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:3318660 3'  
 similar to TR:Q9Y5W1 FEZ1. [5] TR:Q9Y5W0 TR:Q9Y5V9 TR:Q9Y5V8  
 TR:Q9Y5V7 ; contains MER22.t3 TAR1 repetitive element ;, mRNA  
 sequence.

ACCESSION BF590813  
 VERSION BF590813.1 GI:11683137  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 547)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 434.  
 Location/Qualifiers  
 1..547  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3318660"  
 /clone\_lib="NCI CGAP Col6"  
 /tissue\_type="colon tumor, RER+"  
 /lab\_host="DH10B"  
 /note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI CGAP Col6 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (cloneIDs 1057416-1061255, and 1144584-1145351).  
 Subtraction by Bento Soares and M. Fatima Ronaldo. "

BASE COUNT 83 a 156 c 189 g 119 t  
 ORIGIN  
 Query Match 9.6%; Score 333; DB 12; Length 547;  
 Best Local Similarity 99.5%; Pred. No. 4.1e-153;  
 Matches 433; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 877 TGCACCCCGCCCTCCAGACAGCCCAAGGACGAGCTGAAGCCTGGCTGTGCTCTG 936

Db 435 TGACACCCCGCCCTCCAGACAAGCCCAAGAGAGGAGCTGAAGCCTGGCTGTGCTGTG 376  
 |||||  
 QY 937 GGGCGCTGTTCAGACTCCGGCCGGAATCTCCATGTCTCCAGCTGCCACACACAGCACAGCA 996  
 |||||  
 Db 375 GGGCGCTGTTCAGACTCCGGCCGGAATCTCCATGTCTCCAGCTGCCACACACAGCACAGCA 316  
 |||||  
 QY 997 GCAGCTACCAAGCTGGAGCCCGCTGGTTCACACCGCTGGGACCCCAAGCCGCTTTTGGGGGCT 1056  
 |||||  
 Db 315 GCAGCTACCAAGCTGGAGCCCGCTGGTTCACACCGCTGGGACCCCAAGCCGCTTTTGGGGGCT 256  
 |||||  
 QY 1057 CCGGCCACAACATCACCACGAGGATCTCTCTCCAGGACAGCAACATGATGAGCTTGAAGG 1116  
 |||||  
 Db 255 CCGGCCACAACATCACCACGAGGATCTCTCTCCAGGACAGCAACATGATGAGCTTGAAGG 196  
 |||||  
 QY 1117 CTCTGTCTCTTCGACGAGGAGTAGCAAGCTGGGCCACTCGAACAAAGGACAGCAAGGGCC 1176  
 |||||  
 Db 195 CTCTGTCTCTTCGACGAGGAGTAGCAAGCTGGGCCACTCGAACAAAGGACAGCAAGGGCC 136  
 |||||  
 QY 1177 CTTCTGTCTCTTCGACGAGGAGTAGCAAGCTGGGCCACTCGAACAAAGGACAGCAAGGGCC 1236  
 |||||  
 Db 135 CTTCTGTCTCTTCGACGAGGAGTAGCAAGCTGGGCCACTCGAACAAAGGACAGCAAGGGCC 76  
 |||||  
 QY 1237 AGCTGTCTTCGACGAGGAGGAGGCGCCCTCCAGAGCTTGCAGCGCAGCTTTGAGGAGAGGAGC 1296  
 |||||  
 Db 75 AGCTGTCTTCGACGAGGAGGAGGCGCCCTCCAGAGCTTGCAGCGCAGCTTTGAGGAGAGGAGC 16  
 |||||  
 QY 1297 TTGCCTCCAGCCTGG 1311  
 |||||  
 Db 15 TTGCCTCCAGCCTGG 1

RESULT 5  
 BE276168/c  
 LOCUS BE276168 531 bp mRNA linear EST 13-JUL-2000  
 DEFINITION 60114424P1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3050716 5',  
 mRNA sequence.

ACCESSION BE276168  
 VERSION BE276168.1 GI:9151131  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 531)  
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](mailto:image.llnl.gov)  
 Plate: L1CM96 row: 0 column: 05  
 High quality sequence stop: 531.  
 Location/Qualifiers  
 1..531  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3050716"  
 /clone\_lib="NIH MGC 20"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit

FEATURES  
 source  
 1..531  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3050716"  
 /clone\_lib="NIH MGC 20"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit



(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 87 a 173 c 156 g 115 t

Query Match 8.3%; Score 287; DB 10; Length 531;  
Best Local Similarity 99.7%; Pred. No. 2.4e-130;  
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1523 GTCTTACGAGGGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 1582  
DB GTCTTACGAGGGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 299  
OY 1583 GAGGCCACACAGGGCTCATGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 1642  
DB GAGGCCACACAGGGCTCATGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 239  
OY 1643 CTCTCTGTGTGTCGCAATAGCGTGCACAAACACAGACCGCGAGGCAAGCGGGCTTAATGT 1702  
DB CTCTCTGTGTGTCGCAATAGCGTGCACAAACACAGACCGCGAGGCAAGCGGGCTTAATGT 179  
OY 1703 GCTGCTTTATCACCACAAAGAGGGCTCCCTGCACAAACCATGTTGGGGGATCGACTTACA 1762  
DB GCTGCTTTATCACCACAAAGAGGGCTCCCTGCACAAACCATGTTGGGGGATCGACTTACA 119  
OY 1763 TCTGAGCTTCCTCTGTGTCACCAACATACCTCATGGCTCTAGATTTTCAGTTTCCCAAG 1822  
DB TCTGAGCTTCCTCTGTGTCACCAACATACCTCATGGCTCTAGATTTTCAGTTTCCCAAG 59  
OY 1823 TGAGCCATTAATCATGAAGCGGAGCCAGATGACCA 1860  
DB TGAGCCATTAATCATGAAGCGGAGCCAGATGACCA 21

RESULT 6  
LOCUS BE410921/c 743 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601303579F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3638203 5',  
mRNA sequence.

ACCESSION BE410921  
VERSION BE410921.1 GI:9347371  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 743)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
plate: LLCW338 row: m column: 20  
High quality sequence start: 49  
High quality sequence stop: 688.  
Location/Qualifiers

FEATURES  
source  
1. .743  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3638203"  
/clone\_lib="NIH\_MGC\_21"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 119 a 229 c 226 g 168 t 1 others

Query Match 8.1%; Score 283; DB 10; Length 743;  
Best Local Similarity 99.7%; Pred. No. 2.4e-128;  
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1523 GTCTTACGAGGGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 1582  
DB GTCTTACGAGGGGAGAACAGCAGCTTCGGCCCGCGCTGGAGGAGAGACCCAGTGGAGGT 322  
OY 1583 GAGGCCACACAGGGCTCATGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 1642  
DB GAGGCCACACAGGGCTCATGGTTTGGGTGTCAGCGGTTTGGCCCGCAGTACCCCTCT 262  
OY 1643 CTCTCTGTGTGTCGCAATAGCGTGCACAAACACAGACCGCGAGGCAAGCGGGCTTAATGT 1702  
DB CTCTCTGTGTGTCGCAATAGCGTGCACAAACACAGACCGCGAGGCAAGCGGGCTTAATGT 202  
OY 1703 GCTGCTTTATCACCACAAAGAGGGCTCCCTGCACAAACCATGTTGGGGGATCGACTTACA 1762  
DB GCTGCTTTATCACCACAAAGAGGGCTCCCTGCACAAACCATGTTGGGGGATCGACTTACA 142  
OY 1763 TCTGAGCTTCCTCTGTGTCACCAACATACCTCATGGCTCTAGATTTTCAGTTTCCCAAG 1822  
DB TCTGAGCTTCCTCTGTGTCACCAACATACCTCATGGCTCTAGATTTTCAGTTTCCCAAG 82  
OY 1823 TGAGCCATTAATCATGAAGCGGAGCCAGATG 1856  
DB TGAGCCATTAATCATGAAGCGGAGCCAGATG 48

RESULT 7  
LOCUS AI984777/c 817 bp mRNA linear EST 08-MAR-2000  
DEFINITION wr85b07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2494453 3',  
similar to TR:O60299 O60299 KIAA0552 PROTEIN. ; mRNA sequence.

ACCESSION AI984777  
VERSION AI984777.1 GI:5812054  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 817)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 1307 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 428.  
Location/Qualifiers

FEATURES  
source  
1. .817  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2494453"  
/clone\_lib="NCI-CGAP\_Kid11"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Donaldo.

BASE COUNT 133 a 235 c 266 g 180 t 3 others  
ORIGIN

Query Match 6.9%; Score 241; DB 9; Length 817;  
Best Local Similarity 99.7%; Pred. No. 1.5e-107; Indels 0; Gaps 0;  
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1010 GGACCCGCTGTGCACACCGTGGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACAT 1069  
Db 292 GGACCCGCTGTGCACACCGTGGGACCCACAAAGCCGTTTGGGGGCTCCGCCCAACAT 233

Qy 1070 CACCAGGGGATCGTCTCCAGGACAGCAATGATGAGCCTGAAGGCTCTGTCTTCTC 1129  
Db 232 CACCAGGGGATCGTCTCCAGGACAGCAATGATGAGCCTGAAGGCTCTGTCTTCTC 173

Qy 1130 CGACGGAGGTAGCAGCTGGGCCACTCGAACAGGCACAGAGGCCCTCTGTGTCCG 1189  
Db 172 CGACGGAGGTAGCAGCTGGGCCACTCGAACAGGCACAGAGGCCCTCTGTGTCCG 113

Qy 1190 CTCCCCATCTCCACGCGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAG 1249  
Db 112 CTCCCCATCTCCACGCGAGTGCAGCATCCAGGAGCTGGAACAGAGCTGTTGGAGAG 53

Qy 1250 GGAGGGCCCTCCAGAGCTGCAGCGAGCTTTCAGGAGAGGAGCTTGCC 1301  
Db 52 GGAGGGCCCTCCAGAGCTGCAGCGAGCTTTCAGGAGAGGAGCTTGCC 1

RESULT 8  
BE384131/c  
LOCUS BE384131 673 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601272956F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3614076 5', mRNA sequence.

ACCESSION BE384131  
VERSION BE384131.1 GI:9329496  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 673)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LLCM275 row: P column: 13  
High quality sequence stop: 670.  
Location/Qualifiers  
1. .673  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3614076"  
/clone\_lib="NIH\_MGC\_20"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally

FEATURES  
source

cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 110 a 211 c 208 g 144 t  
ORIGIN

Query Match 4.8%; Score 165; DB 10; Length 673;  
Best Local Similarity 99.5%; Pred. No. 6e-70; Indels 0; Gaps 0;  
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1523 GTCTTACGAGGGAGAGACCCAGCTTCGGCCCGCTGGAGGAGACCCAGTGGAGGT 1582  
Db 357 GTCTTACGAGGGAGAGACCCAGCTTCGGCCCGCTGGAGGAGACCCAGTGGAGGT 298

Qy 1583 GAGGCCACACAGGGCTCATGGGTTTGGGTGTTCAGCGGTTTGGCGCCAGTACCCCTCT 1642  
Db 297 GAGGCCACACAGGGCTCATGGGTTTGGGTGTTCAGCGGTTTGGCGCCAGTACCCCTCT 238

Qy 1643 CTTTCTGGTGTGCCAATAGCGTGAACACAGACCGCGCAGGAGCGGGGCTAATGT 1702  
Db 237 CTTTCTGGTGTGCCAATAGCGTGAACACAGACCGCGCAGGAGCGGGGCTAATGT 178

Qy 1703 GCTGGCTTTATCACCACCAAGAGGGGCTCCCTGCAA 1738  
Db 177 GCTGGCTTTATCACCACCAAGAGGGGCTCCCTGCAA 142

RESULT 9  
AW016544/c  
LOCUS AW016544 344 bp mRNA linear EST 10-SEP-1999  
DEFINITION UI-H-BiOp-abg-g-04-0-UI.s1 NCI\_CGAP\_Sub2 Homo sapiens cDNA clone IMAGE:2711982 3', mRNA sequence.

ACCESSION AW016544  
VERSION AW016544.1 GI:5865301  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 344)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Oligo-dT track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLYA-No.

JOURNAL  
COMMENT

FEATURES  
source

Location/Qualifiers  
1. .344  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2711982"  
/clone\_lib="NCI\_CGAP\_Sub2"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pVT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NCI CGAP Sub2 library is a subtracted library derived from BI. Bi constitutes a mixture of 21 normalized or subtracted NCI CGAP libraries: NCI\_CGAP\_Co4, NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_Co10, NCI\_CGAP\_Co16, NCI\_CGAP\_Kid5, NCI\_CGAP\_Kid12, NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2, NCI\_CGAP\_Br2, NCI\_CGAP\_Co8, NCI\_CGAP\_Co11, NCI\_CGAP\_Le12, NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24, NCI\_CGAP\_Lu19, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6

```

Email: est@watson.wustl.edu
This clone is available royalty-free through LILNL; contact the
IMAGE Consortium (info@image.lilnl.gov) for further information.
Insert Length: 698 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 146.
Location/Qualifiers
1. .153
./organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1046802"
/clone_lib="Soares NbHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/notice="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1 M A G clones 260232-265233

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BASE COUNT      24 a    50 c    48 g    31 t
ORIGIN
Query Match      3.5%; Score 122; DB 9; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1110 CTGAAGGCTCTGTCTCTTCTCGACGGAGGTAGCAAGCTGGGCCACTCGAACCAAGGCAGAC 1169
1153 CTGAAGGCTCTGTCTCTTCTCGACGGAGGTAGCAAGCTGGGCCACTCGAACCAAGGCAGAC 94
1170 AAGGCCCTCGTGTGTCTGGCTCCCCCATCTCCACGGACGAGTGCAGCATCCAGGAGCTG 1229
93 AAGGCCCTCGTGTGTCTGGCTCCCCCATCTCCACGGACGAGTGCAGCATCCAGGAGCTG 34
1230 GA 1231
||
33 GA 32
db
RESULT 11

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LOCUS	W028197.1	397 bp	linear	EST 09-MAR-2000
DEFINITION	wv94a01.x1 Soares thymus_NHFT Homo sapiens CDNA clone			
IMAGE	IMAGE:2536200 3' similar to TR:O60299 O60299 KIAA0552 PROTEIN. i, mRNA sequence.			
ACCESSION	AW028197			
VERSION	AW028197.1			
KEYWORDS	GI:5886953			
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 397)			
JOURNAL	NCI-CCGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .			
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-r@mail.nih.gov			
	This clone is available royalty-free through LNL; contact the			
	IMAGE Consortium ( <a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a> ) for further information.			
	Insert Length: 1067 Std Error: 0.00			
	Seq primer: -40UP from Gibco			
	High quality sequence stop: 139.			
FEATURES	Location/Qualifiers			
	1..397			





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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 101.346 Seconds  
(without alignments)  
15794.017 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_4365\_4419

Perfect score: 55

Sequence: 1 gagcgaggcagcagcacttga.....atcagctggccaacatgag 55

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9108	9	AF123653 Homo sapi
2	55	100.0	173264	2	AC025853 Homo sapi
C 3	40	72.7	5321	9	AB037741 Homo sapi
C 4	40	72.7	49999	6	AX015917 Sequence
5	40	72.7	70328	9	AL513472 Human DNA
C 6	40	72.7	100020	9	AC092165 Homo sapi
C 7	40	72.7	105051	2	AC009449 Homo sapi
C 8	40	72.7	124000	9	AP002498 Homo sapi
9	40	72.7	143034	9	AC104184 Homo sapi
C 10	40	72.7	146224	9	AC005883 Homo sapi
C 11	40	72.7	152591	2	AC068081 Homo sapi
12	40	72.7	158276	2	AC012033 Homo sapi
C 13	40	72.7	158608	9	CNS05TDJ Human chr
C 14	40	72.7	162190	2	AC020592 Homo sapi
C 15	40	72.7	170330	9	AC097638 Homo sapi
16	40	72.7	172033	9	AL136131 Human DNA
-17	40	72.7	173836	9	AC027125 Homo sapi
18	40	72.7	173889	2	AC013691 Homo sapi
C 19	40	72.7	175250	2	AC069521 Homo sapi
20	40	72.7	179816	2	AC074188 Homo sapi
21	40	72.7	179871	2	AC024602 Homo sapi
22	40	72.7	188126	9	AC087590 Homo sapi
23	40	72.7	190648	9	CNS01DXI Human chr
24	40	72.7	193332	2	AL355349 Homo sapi
C 25	40	72.7	210301	9	AF307337 Homo sapi
26	40	72.7	262951	2	AC124848 Homo sapi
27	39	70.9	129272	9	AL451125 Human DNA
28	39	70.9	167386	2	AL159993 Homo sapi
C 29	39	70.9	180859	2	AC025553 Homo sapi
C 30	38	69.1	78941	9	AC005591 Homo sapi
31	38	69.1	162329	2	AC069225 Homo sapi
32	38	69.1	171123	9	AC020779 Homo sapi
33	38	69.1	174384	2	AC009524 Homo sapi
C 34	38	69.1	179680	9	AC016138 Homo sapi
C 35	38	69.1	196860	2	AC091121 Homo sapi
C 36	37	67.3	95801	9	AC078776 Homo sapi
C 37	37	67.3	149304	9	AC090763 Homo sapi
C 38	37	67.3	150877	2	AC021095 Homo sapi
39	37	67.3	162786	2	AC010783 Homo sapi
40	37	67.3	181777	2	AC068866 Homo sapi
C 41	37	67.3	181980	2	AC011827 Homo sapi
42	37	67.3	187621	2	AC079060 Homo sapi
43	36	65.5	1524	9	AK021770 Homo sapi
44	36	65.5	2901	9	HS0804309
C 45	36	65.5	10206	9	AL354664 Human DNA
46	36	65.5	72602	2	AC090541 Homo sapi
C 47	36	65.5	79223	9	AL391114 Human DNA
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52	36	65.5	100000	9	AP000166 Homo sapi
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57	36	65.5	132777	2	AC116376 Homo sapi
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C 64	36	65.5	166532	2	AC022279 Homo sapi
65	36	65.5	168602	2	AF271406 Homo sapi

Pred. No. is the number of results predicted by chance to have a



66	36	65.5	169633	9	AC023235	AC023235 Homo sapi	139	31	56.4	151933	2	AC073199	AC073199 Homo sapi
67	36	65.5	174751	9	AC009137	AC009137 Homo sapi	c 140	31	56.4	159870	9	AC010333	AC010333 Homo sapi
68	36	65.5	183146	9	AP003778	AP003778 Homo sapi	141	31	56.4	160039	9	AC106804	AC106804 Homo sapi
69	36	65.5	189994	9	AP002762	AP002762 Homo sapi	142	31	56.4	163846	2	AL513126	AL513126 Homo sapi
70	36	65.5	193332	2	AL355349	AL355349 Homo sapi	c 143	31	56.4	165653	9	AL138725	AL138725 Human DNA
71	36	65.5	193389	9	AC015743	AC015743 Homo sapi	c 144	31	56.4	167667	2	AL449064	AL449064 Homo sapi
72	36	65.5	194799	9	AC006430	AC006430 Homo sapi	145	31	56.4	167671	2	AC090081	AC090081 Homo sapi
73	36	65.5	195007	2	CNS06C81	AL391749 Human chr	146	31	56.4	173786	2	AC024472	AC024472 Homo sapi
74	36	65.5	202760	9	AC021987	AC021987 Homo sapi	c 147	31	56.4	174470	2	AC021888	AC021888 Homo sapi
75	36	65.5	211403	2	AC019093	AC019093 Homo sapi	c 148	31	56.4	179641	9	AC098591	AC098591 Homo sapi
76	36	65.5	225940	2	AC078799	AC078799 Homo sapi	c 149	31	56.4	180165	9	AC022017	AC022017 Homo sapi
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78	36	65.5	340000	9	AP001719	AP001719 Homo sapi	151	31	56.4	181510	2	AC026338	AC026338 Homo sapi
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82	35	63.6	168513	2	AC011982	AC011982 Homo sapi	c 155	30	54.5	9449	2	AC106848	AC106848 Homo sapi
83	35	63.6	173117	2	AL157885	AL157885 Homo sapi	c 156	30	54.5	29759	9	AL133392	AL133392 Human DNA
84	35	63.6	183491	9	CNS01DU4	AL131163 Human chr	c 157	30	54.5	86825	9	AC006967	AC006967 Homo sapi
85	35	63.6	186294	2	AC021108	AC021108 Homo sapi	c 158	30	54.5	96978	9	AC024075	AC024075 Homo sapi
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87	35	63.6	211980	9	AC010735	AC010735 Homo sapi	160	30	54.5	133439	9	AC084438	AC084438 Homo sapi
88	35	63.6	251124	9	AB000660	AB000660 Homo sapi	161	30	54.5	142933	9	AL513102	AL513102 Human DNA
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90	34	61.8	73845	2	AL356478	AL356478 Homo sapi	163	30	54.5	148521	9	HS1111N9	AL022574 Human DNA
91	34	61.8	128728	9	AL136179	AL136179 Human DNA	164	30	54.5	159082	9	AC025947	AC025947 Homo sapi
92	34	61.8	148648	9	AC021713	AC021713 Homo sapi	c 165	30	54.5	168193	9	CNS05TE2	AL359397 Human chr
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95	34	61.8	174992	2	AC025422	AC025422 Homo sapi	c 168	30	54.5	184027	2	AL691506	AL691506 Homo sapi
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97	34	61.8	181823	2	AC040167	AC040167 Homo sapi	c 170	30	54.5	233461	2	AC092978	AC092978 Homo sapi
98	34	61.8	185886	2	AC092122	AC092122 Homo sapi	c 171	30	54.5	293933	2	AC090040	AC090040 Homo sapi
99	34	61.8	196247	2	HS651N20	AL117346 Homo sapi	172	29	52.7	38046	2	AC092566	AC092566 Homo sapi
100	34	61.8	340000	9	HS21C082	AL163282 Homo sapi	c 173	29	52.7	40146	2	AC092307	AC092307 Homo sapi
101	33	60.0	38565	9	HS433G19	AL008735 Human DNA	c 174	29	52.7	46127	2	AC093230	AC093230 Homo sapi
102	33	60.0	184989	2	AC113392	AC113392 Homo sapi	c 175	29	52.7	68420	2	AC130285	AC130285 Homo sapi
103	33	60.0	191035	9	AC093527	AC093527 Homo sapi	c 176	29	52.7	68420	2	AC090804	AC090804 Homo sapi
104	33	60.0	217328	2	AC007513	AC007513 Homo sapi	c 177	29	52.7	140151	9	AC068334	AC068334 Homo sapi
105	33	60.0	223606	2	AC013479	AC013479 Homo sapi	c 178	29	52.7	144046	2	AC068334	AC068334 Homo sapi
106	32	58.2	77702	9	AC034241	AC034241 Homo sapi	c 179	29	52.7	163167	9	AC011347	AC011347 Homo sapi
107	32	58.2	80506	9	AC098857	AC098857 Homo sapi	c 180	29	52.7	166016	9	AL591378	AL591378 Human DNA
108	32	58.2	106465	9	HSJ765F13	AL109853 Human DNA	c 181	29	52.7	179056	2	AC068936	AC068936 Homo sapi
109	32	58.2	113778	2	AC109438	AC109438 Homo sapi	c 182	29	52.7	182051	9	AC007638	AC007638 Homo sapi
110	32	58.2	133042	9	AC011354	AC011354 Homo sapi	c 183	29	52.7	184896	2	AC012616	AC012616 Homo sapi
111	32	58.2	135545	2	AC025184	AC025184 Homo sapi	184	29	52.7	189312	2	AC126406	AC126406 Homo sapi
112	32	58.2	140628	2	AC016468	AC016468 Homo sapi	185	29	52.7	198141	9	AL355499	AL355499 Human DNA
113	32	58.2	145161	2	AC012640	AC012640 Homo sapi	186	29	52.7	296483	2	AC069258	AC069258 Homo sapi
114	32	58.2	151262	9	AC093824	AC093824 Homo sapi	c 187	28	50.9	3337	9	AB038344	AB038344 Homo sapi
115	32	58.2	160822	2	AC020920	AC020920 Homo sapi	188	28	50.9	35414	9	AC005328	AC005328 Homo sapi
116	32	58.2	161777	2	AC119056	AC119056 Papio cyn	c 189	28	50.9	70851	9	AC002540	AC002540 Human BAC
117	32	58.2	162739	9	AL353788	AL353788 Human DNA	190	28	50.9	71123	2	AC130350	AC130350 Homo sapi
118	32	58.2	169921	2	AC008913	AC008913 Homo sapi	c 191	28	50.9	73565	9	AC067962	AC067962 Homo sapi
119	32	58.2	171148	9	AL359195	AL359195 Human DNA	c 192	28	50.9	97749	9	AC004906	AC004906 Homo sapi
120	32	58.2	172309	9	AC018553	AC018553 Homo sapi	193	28	50.9	98069	9	AL136446	AL136446 Human DNA
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122	32	58.2	182902	9	AC092405	AC092405 Papio cyn	195	28	50.9	119395	9	AL139189	AL139189 Human DNA
123	32	58.2	184012	9	AC017080	AC017080 Homo sapi	196	28	50.9	119760	2	AC025458	AC025458 Homo sapi
124	32	58.2	184092	2	AC124858	AC124858 Homo sapi	c 197	28	50.9	121460	2	AC027330	AC027330 Homo sapi
125	32	58.2	186740	9	AC007343	AC007343 Homo sapi	c 198	28	50.9	126929	9	AC093801	AC093801 Homo sapi
126	32	58.2	210230	9	AC103409	AC103409 Homo sapi	199	28	50.9	128289	9	AC007972	AC007972 Homo sapi
127	32	58.2	218444	2	AL365256	AL365256 Homo sapi	c 200	28	50.9	131839	9	AC112166	AC112166 Homo sapi
128	32	58.2	231490	9	CNS01DU3	AL131353 Human chr	201	28	50.9	131841	9	HSJ881L22	AL117382 Human DNA
129	31	56.4	32926	2	AL354742	AL354742 Homo sapi	202	28	50.9	138021	9	AC090820	AC090820 Homo sapi
130	31	56.4	51479	9	AL596137	AL596137 Human DNA	c 203	28	50.9	144165	9	AC002127	AC002127 Human BAC
131	31	56.4	72245	9	HS93C23	AL008713 Human DNA	c 204	28	50.9	146741	9	AC011452	AC011452 Homo sapi
132	31	56.4	79111	2	AC010257	Continuation (4 of	205	28	50.9	150728	2	AL158034	AL158034 Homo sapi
133	31	56.4	79555	9	AL583856	AL583856 Human DNA	206	28	50.9	158560	9	AC098969	AC098969 Homo sapi
134	31	56.4	85543	9	AC010553	AC010553 Homo sapi	c 207	28	50.9	159691	9	AC025160	AC025160 Homo sapi
135	31	56.4	96678	9	AC108104	AC108104 Homo sapi	c 208	28	50.9	161449	9	AC005341	AC005341 Homo sapi
136	31	56.4	120510	9	AL356457	AL356457 Human DNA	209	28	50.9	162043	2	AC018803	AC018803 Homo sapi
137	31	56.4	127539	9	CNS01DSN	AL121821 Human chr	210	28	50.9	165458	2	AC090587	AC090587 Homo sapi
138	31	56.4	140233	2	AC009422	AC009422 Homo sapi	c 211	28	50.9	168230	2	AC010624	AC010624 Homo sapi

212	28	50.9	172893	2	AC024596	Homo sapi	AC024596	26	47.3	194372	9	AC019184	Homo sapi
213	28	50.9	174396	2	AC021645	Homo sapi	AC021645	26	47.3	197031	2	AC019121	Homo sapi
214	28	50.9	174535	2	AC106872	Homo sapi	AC106872	26	47.3	199384	2	AP003531	Homo sapi
215	28	50.9	175426	2	AC034296	Homo sapi	AC034296	26	47.3	216681	2	AC006534	Homo sapi
216	28	50.9	175999	2	AC021154	Homo sapi	AC021154	26	47.3	220450	2	HS53110	Homo sapi
217	28	50.9	177720	2	AC025680	Homo sapi	AC025680	26	47.3	234626	2	AC009095	Homo sapi
218	28	50.9	178256	2	AC009027	Homo sapi	AC009027	26	47.3	340000	9	HS21C103	Homo sapi
219	28	50.9	181188	2	AC067983	Homo sapi	AC067983	25	45.5	1090	9	AB03277S09	Homo sapi
220	28	50.9	183597	2	AL356285	Human DNA	AL356285	25	45.5	2996	9	AK091414	Homo sapi
221	28	50.9	183901	2	AL356425	Homo sapi	AL356425	25	45.5	3295	9	AK023237	Homo sapi
222	28	50.9	186199	2	AC093708	Pan trogl	AC093708	25	45.5	9712	9	AF272157	Homo sapi
223	28	50.9	189672	2	AL133480	Human DNA	AL133480	25	45.5	10708	6	AX398422	Sequence
224	28	50.9	191546	9	AC015982	Homo sapi	AC015982	297	45.5	11744	9	AF217485	Homo sapi
225	28	50.9	191584	9	AP002992	Homo sapi	AP002992	298	45.5	12096	9	AF217486	Homo sapi
226	28	50.9	194385	9	CNS00001	Human chr	AL049776	25	45.5	26128	9	HSJ885H15	Human DNA
227	28	50.9	205886	2	AC103204	Homo sapi	AC103204	300	45.5	28320	9	HS395F10	Human DNA
228	28	50.9	215645	2	AC109329	Homo sapi	AC109329	301	45.5	33666	2	AC027214	Homo sapi
229	28	50.9	219820	9	AC008738	Homo sapi	AC008738	302	45.5	33770	9	AC004400	Homo sapi
230	28	50.9	224292	2	AC026873	Homo sapi	AC026873	303	45.5	35138	9	AL353799	Human DNA
231	28	50.9	230956	9	AC090614	Homo sapi	AC090614	304	45.5	35749	9	AC007162	Homo sapi
232	28	50.9	240379	9	AC005077	Homo sapi	AC005077	305	45.5	39924	9	AC006274	Homo sapi
233	28	49.1	97653	9	AC091700	Homo sapi	AC091700	306	45.5	42176	2	AC008980	Homo sapi
234	27	49.1	123211	9	AC005208	Homo sapi	AC005208	307	45.5	43390	9	AC007191	Homo sapi
235	27	49.1	125378	9	AL391416	Human DNA	AL391416	308	45.5	50343	2	AC091190	Homo sapi
236	27	49.1	125429	9	AC084291	Homo sapi	AC084291	309	45.5	51381	2	AF322456	Homo sapi
237	27	49.1	128728	9	AL136179	Human DNA	AL136179	310	45.5	55256	9	HSJ735G18	Human DNA
238	27	49.1	146410	2	AC079002	Homo sapi	AC079002	311	45.5	58000	9	AP001273	Homo sapi
239	27	49.1	146810	9	AL159170	Human DNA	AL159170	312	45.5	58326	2	AC108383	Pan trogl
240	27	49.1	151094	2	AC011769	Homo sapi	AC011769	313	45.5	61404	9	AL360002	Human DNA
241	27	49.1	151123	9	AC005520	Homo sapi	AC005520	314	45.5	62421	9	HSJ784K2	Human DNA
242	27	49.1	156506	2	AC068038	Homo sapi	AC068038	315	45.5	62844	2	AC023982	Homo sapi
243	27	49.1	156895	9	AC013526	Homo sapi	AC013526	316	45.5	66000	2	AL391119	Human DNA
244	27	49.1	158288	2	AC092770	Homo sapi	AC092770	317	45.5	66745	2	AC090817	Homo sapi
245	27	49.1	160387	2	AC022159	Homo sapi	AC022159	318	45.5	67478	9	AL161432	Human DNA
246	27	49.1	168353	2	AL390024	Homo sapi	AL390024	319	45.5	72614	9	HS496N17	Human DNA
247	27	49.1	174639	9	AC009949	Homo sapi	AC009949	320	45.5	72788	2	AC016317	Homo sapi
248	27	49.1	179643	2	AC131159	Homo sapi	AC131159	321	45.5	78241	9	AL358392	Human DNA
249	27	49.1	180270	9	AC007923	Homo sapi	AC007923	322	45.5	79470	2	AL391000	Homo sapi
250	27	49.1	190690	9	HS3424I22	Human DNA	AL117336	323	45.5	79815	9	AC005212	Homo sapi
251	27	49.1	193411	2	AC087484	Homo sapi	AC087484	324	45.5	82806	9	AC007111	Homo sapi
252	27	49.1	194142	2	AC092634	Homo sapi	AC092634	325	45.5	83412	2	AC106778	Homo sapi
253	27	49.1	195554	9	AC092079	Homo sapi	AC092079	326	45.5	84388	9	AL589984	Human DNA
254	27	49.1	196247	2	HSJ651N20	Human DNA	AL117346	327	45.5	85836	2	AC108384	Pan trogl
255	27	49.1	201545	9	AC103967	Homo sapi	AC103967	328	45.5	87616	2	AL133540	Homo sapi
256	27	49.1	206467	2	AC067931	Homo sapi	AC067931	329	45.5	89448	9	AC005067	Homo sapi
257	27	49.1	212030	2	AC019148	Homo sapi	AC019148	330	45.5	91287	9	AC023906	Homo sapi
258	27	49.1	223879	9	AC008735	Homo sapi	AC008735	331	45.5	93634	2	AC127088	Homo sapi
259	27	49.1	281662	2	AC117374	Homo sapi	AC117374	332	45.5	94673	2	AC009018	Homo sapi
260	26	47.3	68589	9	HS237J2	Human DNA	AL021394	333	45.5	95597	2	AC012555	Homo sapi
261	26	47.3	110000	2	AC117465_2	Continuation (3 of	AC004702	334	45.5	97082	2	AC103888	Homo sapi
262	26	47.3	120821	9	AC004702	Continuation (3 of	AC004702	335	45.5	98069	9	AC011496	Homo sapi
263	26	47.3	129389	9	HS526114	Human DNA	282214	336	45.5	99411	9	AC005207	Homo sapi
264	26	47.3	132937	2	AC115097	Homo sapi	AC115097	337	45.5	100152	9	AC000085	Homo sapi
265	26	47.3	136943	9	AL359842	Human DNA	AL359842	338	45.5	101805	9	AC073508	Homo sapi
266	26	47.3	146811	2	AC084706	Homo sapi	AC084706	339	45.5	102479	9	AC115107	Homo sapi
267	26	47.3	148973	2	CNS01DUZ	Homo sapi	AL133374	340	45.5	103370	9	AL161656	Human DNA
268	26	47.3	158779	9	AL713851	Human DNA	AL713851	341	45.5	103421	9	AC004920	Homo sapi
269	26	47.3	162996	9	AC027682	Homo sapi	AC027682	342	45.5	104871	9	AC004584	Homo sapi
270	26	47.3	164519	9	AL138712	Human DNA	AL138712	343	45.5	107965	9	AC093678	Homo sapi
271	26	47.3	165159	9	CNS01DUV5	Human chr	AL133454	344	45.5	108048	9	AC115108	Homo sapi
272	26	47.3	168720	2	AC078781	Homo sapi	AC078781	345	45.5	108893	9	AC079169	Homo sapi
273	26	47.3	173456	9	AL158198	Human DNA	AL158198	346	45.5	108916	9	AC010450	Homo sapi
274	26	47.3	174713	2	AC079083	Homo sapi	AC079083	347	45.5	112685	2	AC016592	Homo sapi
275	26	47.3	178432	2	AC068873	Homo sapi	AC068873	348	45.5	114001	9	HSJ760G15	Human DNA
276	26	47.3	179017	2	AC012520	Homo sapi	AC012520	349	45.5	115828	9	AL356458	Human DNA
277	26	47.3	179460	9	AC012512	Homo sapi	AC012512	350	45.5	117051	9	AC115106	Homo sapi
278	26	47.3	183186	9	AC093817	Homo sapi	AC093817	351	45.5	121050	9	AC074135	Homo sapi
279	26	47.3	183807	9	AC091778	Papio cyn	AC091778	352	45.5	121394	2	AL137799	Homo sapi
280	26	47.3	191280	2	AC087389	Homo sapi	AC087389	353	45.5	124001	9	HS886K2	Human DNA
281	26	47.3	192961	9	AP002770	Homo sapi	AP002770	354	45.5	124034	9	HS416J7	Human DNA
282	26	47.3	193234	2	AC024293	Homo sapi	AC024293	355	45.5	124048	9	HUAC002045	Human Chr
283	26	47.3	193519	2	AC023123	Homo sapi	AC023123	356	45.5	124343	9	AC079188	Homo sapi
284	26	47.3	194334	2	AC046140	Homo sapi	AC046140	357	45.5	126613	2	HSJ603114	Human DNA

C 358	25	45.5	126643	9	AC092637	Homo sapi	AL354798	Human DNA
C 359	25	45.5	127761	9	AC006014	Homo sapi	AC023068	Homo sapi
C 360	25	45.5	129435	9	AL391314	Human DNA	AC018636	Homo sapi
C 361	25	45.5	129677	2	AC127035	Homo sapi	AC016032	Homo sapi
C 362	25	45.5	130146	9	AL590489	Human DNA	AC093520	Homo sapi
C 363	25	45.5	130467	9	HS798A17	Human DNA	AC021971	Homo sapi
C 364	25	45.5	130526	2	AF000715	Homo sapi	AL357672	Human DNA
C 365	25	45.5	134946	2	AC069568	Homo sapi	AC007371	Homo sapi
C 366	25	45.5	135837	9	AC004837	Homo sapi	AC026549	Homo sapi
C 367	25	45.5	135849	9	AF114156	Homo sapi	AL011816	Homo sapi
C 368	25	45.5	136371	9	AC025451	Homo sapi	AL592211	Homo sapi
C 369	25	45.5	137043	9	AC068794	Homo sapi	AC022078	Homo sapi
C 370	25	45.5	137830	9	AC003029	Homo sapi	AL355336	Human DNA
C 371	25	45.5	139376	9	HS095742	Human chrom	AC087257	Homo sapi
C 372	25	45.5	140053	2	AC007873	Homo sapi	AC026696	Homo sapi
C 373	25	45.5	140179	2	AC084688	Homo sapi	AL161728	Human DNA
C 374	25	45.5	141963	2	AC121253	Homo sapi	AC004127	Homo sapi
C 375	25	45.5	142723	9	HS1039K5	Human DNA	AC027537	Homo sapi
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C 379	25	45.5	145329	2	AC055850	Homo sapi	AC074200	Homo sapi
C 380	25	45.5	145495	2	AC093273	Homo sapi	AC007216	Homo sapi
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C 382	25	45.5	146327	9	AL162253	Human DNA	AC023818	Homo sapi
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C 384	25	45.5	147724	9	HS395P12	Human DNA	AP007041	Homo sapi
C 385	25	45.5	148312	2	AP001886	Homo sapi	AL359092	Human DNA
C 386	25	45.5	148697	9	AC010432	Homo sapi	AC004963	Homo sapi
C 387	25	45.5	149062	9	AC098805	Homo sapi	AC069293	Homo sapi
C 388	25	45.5	149132	9	AP000908	Homo sapi	AC023831	Homo sapi
C 389	25	45.5	149597	2	AC034271	Homo sapi	AL137139	Human DNA
C 390	25	45.5	149773	2	AC041029	Homo sapi	AL126766	Homo sapi
C 391	25	45.5	150110	2	AC097722	Homo sapi	AC009452	Homo sapi
C 392	25	45.5	150172	9	AC006285	Homo sapi	AL353745	Human DNA
C 393	25	45.5	150601	2	AC012272	Homo sapi	AF235104	Homo sapi
C 394	25	45.5	150728	2	AL158034	Homo sapi	AC018718	Homo sapi
C 395	25	45.5	151557	2	AC006078	Homo sapi	AC024357	Mus muscu
C 396	25	45.5	152224	2	AC007933	Homo sapi	AC016611	Homo sapi
C 397	25	45.5	152626	2	AL357252	Homo sapi	AF000501	Homo sapi
C 398	25	45.5	153444	2	AC040948	Homo sapi	AC068231	Homo sapi
C 399	25	45.5	154251	2	AC116974	Homo sapi	AL357752	Human DNA
C 400	25	45.5	154415	2	AF165139	Homo sapi	AC022732	Homo sapi
C 401	25	45.5	154592	9	AL591215	Human DNA	AC063948	Homo sapi
C 402	25	45.5	155362	2	AC022244	Homo sapi	AC023857	Homo sapi
C 403	25	45.5	155609	9	HS0813016	Human DNA	AC073022	Homo sapi
C 404	25	45.5	155735	9	AC007683	Homo sapi	AC091059	Homo sapi
C 405	25	45.5	156300	9	AC005919	Homo sapi	AC009161	Homo sapi
C 406	25	45.5	156399	9	AC002456	Homo sapi	AC016025	Homo sapi
C 407	25	45.5	156801	9	AC104740	Homo sapi	AC117181	Homo sapi
C 408	25	45.5	157324	9	AC013643	Homo sapi	AC027011	Homo sapi
C 409	25	45.5	158264	2	AC015497	Homo sapi	AC025194	Homo sapi
C 410	25	45.5	159169	9	AL133414	Human DNA	AC024348	Homo sapi
C 411	25	45.5	159229	9	AL359180	Human DNA	AC069331	Homo sapi
C 412	25	45.5	159593	9	AC004832	Homo sapi	AC090302	Homo sapi
C 413	25	45.5	159906	2	AL590706	Homo sapi	AC087455	Homo sapi
C 414	25	45.5	161284	2	AC015912	Homo sapi	AC021053	Homo sapi
C 415	25	45.5	161505	9	AP001888	Homo sapi	AC005488	Homo sapi
C 416	25	45.5	161549	9	AC044913	Homo sapi	AC006040	Homo sapi
C 417	25	45.5	161696	2	AC093250	Homo sapi	AC093207	Homo sapi
C 418	25	45.5	161911	2	AC021497	Homo sapi	AC026471	Homo sapi
C 419	25	45.5	162294	9	AC012321	Homo sapi	AC105389	Homo sapi
C 420	25	45.5	162445	9	AL158151	Human DNA	AC016688	Homo sapi
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C 422	25	45.5	163173	2	AC013244	Homo sapi	AL391845	Homo sapi
C 423	25	45.5	163389	9	AL589765	Human DNA	AC009727	Homo sapi
C 424	25	45.5	164049	2	AC126763	Homo sapi	AL360172	Human DNA
C 425	25	45.5	165509	2	AC009886	Homo sapi	AC018739	Homo sapi
C 426	25	45.5	165611	9	AP003181	Homo sapi	AC087791	Homo sapi
C 427	25	45.5	166173	2	AC023060	Homo sapi	AC100832	Homo sapi
C 428	25	45.5	166234	9	HS273P12	Human DNA	AL157894	Homo sapi
C 429	25	45.5	166500	9	AC007785	Homo sapi	AC126614	Homo sapi
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C 504	25	45.5	191943	2	AC024475	AC024475 Homo sapi	C 577	24	43.6	2272	9	HSU34054	U34054 Human Down
C 505	25	45.5	192573	9	AC073344	AC073344 Homo sapi	C 578	24	43.6	2342	9	AK097130	AK097130 Homo sapi
C 506	25	45.5	192954	2	AC012054	AC012054 Homo sapi	C 579	24	43.6	2357	9	HSM805079	AL833766 Homo sapi
C 507	25	45.5	192983	2	AC074122	AC074122 Homo sapi	C 580	24	43.6	2360	9	AK074353	AK074353 Homo sapi
C 508	25	45.5	193681	9	AC069382	AC069382 Homo sapi	C 581	24	43.6	2476	9	AK097927	AK097927 Homo sapi
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C 510	25	45.5	196544	9	AC015974	AC015974 Homo sapi	C 583	24	43.6	2646	9	AK095142	AK095142 Homo sapi
C 511	25	45.5	196806	9	AC104212	AC104212 Homo sapi	C 584	24	43.6	2941	9	BC005407	BC005407 Homo sapi
C 512	25	45.5	197067	2	AC079203	AC079203 Homo sapi	C 585	24	43.6	3019	9	AK056809	AK056809 Homo sapi
C 513	25	45.5	198084	2	AC019339	AC019339 Homo sapi	C 586	24	43.6	3069	9	HSTRAP	X67123 H. sapiens
C 514	25	45.5	198172	2	AC009065	AC009065 Homo sapi	C 587	24	43.6	3079	9	AB058709	AB058709 Homo sapi
C 515	25	45.5	198806	2	AC025580	AC025580 Homo sapi	C 588	24	43.6	3270	9	HSM803853	AL832544 Homo sapi
C 516	25	45.5	200274	2	AC115088	AC115088 Homo sapi	C 589	24	43.6	3429	9	S79267	S79267 CD4 recepto
C 517	25	45.5	200926	2	AC008121	AC008121 Homo sapi	C 590	24	43.6	3447	9	AL390014	AL390014 Human DNA
C 518	25	45.5	201155	9	AC009086	AC009086 Homo sapi	C 591	24	43.6	3492	9	HSAPDEVLP3	U72845 Homo sapien
C 519	25	45.5	201387	2	AC026565	AC026565 Homo sapi	C 592	24	43.6	3498	9	AC093072	AC093072 Homo sapi
C 520	25	45.5	202689	2	AC034281	AC034281 Homo sapi	C 593	24	43.6	3896	9	HSU50434	U50434 Human Down
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C 522	25	45.5	205640	9	AC022483	AC022483 Homo sapi	C 595	24	43.6	4178	9	BC036445	BC036445 Homo sapi
C 523	25	45.5	206231	9	AL592309	AL592309 Human DNA	C 596	24	43.6	4434	9	AK024494	AK024494 Homo sapi
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C 525	25	45.5	207256	9	AC010321	AC010321 Homo sapi	C 598	24	43.6	5152	9	AC007089	AC007089 Homo sapi
C 526	25	45.5	208157	2	AC124916	AC124916 Homo sapi	C 599	24	43.6	5170	9	HSN37D7	273421 Human DNA s
C 527	25	45.5	208600	9	AP002348	AP002348 Homo sapi	C 600	24	43.6	5445	9	HSM803455	AL833214 Homo sapi
C 528	25	45.5	208980	2	AC128673	AC128673 Homo sapi	C 601	24	43.6	5981	6	AX321910	AX321910 Sequence
C 529	25	45.5	209384	2	AC016618	AC016618 Homo sapi	C 602	24	43.6	6023	9	HSMTGRIE13	AF076461 Homo sapi
C 530	25	45.5	211937	9	AP003064	AP003064 Homo sapi	C 603	24	43.6	6135	9	AF060972S1	AF060972 Homo sapi
C 531	25	45.5	212444	2	AC010538	AC010538 Homo sapi	C 604	24	43.6	6233	9	HSM803453	AL833214 Homo sapi
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C 533	25	45.5	213442	9	CNS01DSK	AL121809 Human chr	C 606	24	43.6	7004	9	HSPDEEX13	X90589 H. sapiens D
C 534	25	45.5	213447	2	AC083833	AC083833 Homo sapi	C 607	24	43.6	7161	9	AB011168	AB011168 Homo sapi
C 535	25	45.5	220333	2	AC025886	AC025886 Homo sapi	C 608	24	43.6	7174	9	HSM804580	AL833267 Homo sapi
C 536	25	45.5	221220	9	AC027281	AC027281 Homo sapi	C 609	24	43.6	9432	9	AC110617	AC110617 Homo sapi
C 537	25	45.5	223399	2	AC104158	AC104158 Pan t/Ogl	C 610	24	43.6	10229	9	AF242862S2	AF242862 Homo sapi
C 538	25	45.5	224710	2	AC061712	AC061712 Homo sapi	C 611	24	43.6	10988	9	AL592286	AL592286 Human DNA
C 539	25	45.5	224959	2	AC113210	AC113210 Homo sapi	C 612	24	43.6	12053	9	AL590722	AL590722 Human DNA
C 540	25	45.5	225940	2	AC078799	AC078799 Homo sapi	C 613	24	43.6	12253	9	AL450285	AL450285 Human DNA
C 541	25	45.5	227245	9	AC008569	AC008569 Homo sapi	C 614	24	43.6	12610	9	HS30A23	AL022156 Human DNA
C 542	25	45.5	235338	2	AL357893	AL357893 Homo sapi	C 615	24	43.6	13133	9	HSCD4ALU	X87579 H. sapiens C
C 543	25	45.5	235553	2	AC020742	AC020742 Homo sapi	C 616	24	43.6	13135	9	AL589908	AL589908 Human DNA
C 544	25	45.5	236281	9	AC004673	AC004673 Homo sapi	C 617	24	43.6	13208	9	AB028893	AB028893 Homo sapi
C 545	25	45.5	239434	2	AC012171	AC012171 Homo sapi	C 618	24	43.6	13271	9	AL365231	AL365231 Human DNA
C 546	25	45.5	240579	2	AL360154	AL360154 Homo sapi	C 619	24	43.6	13472	9	AF020057	AF020057 Homo sapi
C 547	25	45.5	243558	2	AC010310	AC010310 Homo sapi	C 620	24	43.6	13996	9	AC112722	AC112722 Homo sapi
C 548	25	45.5	245202	2	AC092369	AC092369 Homo sapi	C 621	24	43.6	14140	9	HS24F8	269666 Human DNA s
C 549	25	45.5	245202	9	AE006639	AE006639 Homo sapi	C 622	24	43.6	17072	9	HMPDHAL	D90084 Human pyruv
C 550	25	45.5	270150	2	AL590728	AL590728 Homo sapi	C 623	24	43.6	17586	9	AL591507	AL591507 Human DNA
C 551	25	45.5	270269	2	AC091918	AC091918 Homo sapi	C 624	24	43.6	18285	9	HS437O22	AC035496 Human DNA
C 552	25	45.5	279308	2	AC093024	AC093024 Homo sapi	C 625	24	43.6	18922	9	AC108208	AC108208 Homo sapi
C 553	25	45.5	283396	2	AC022506	AC022506 Homo sapi	C 626	24	43.6	19654	9	D86566	D86566 Human DNA f
C 554	25	45.5	285493	2	AL442068	AL442068 Homo sapi	C 627	24	43.6	20267	9	AB000877	AB000877 Homo sapi
C 555	24	43.6	361	9	HS238WF10	Z17067 H. sapiens	C 628	24	43.6	22038	9	HSPMFG2	AF141309 Homo sapi
C 556	24	43.6	483	6	AX386453	AX386453 Sequence	C 629	24	43.6	23433	6	AX491283	AX491283 Sequence
C 557	24	43.6	529	11	G63631	G63631 SHGC-141659	C 630	24	43.6	24345	9	AL133256	AL133256 Human DNA
C 558	24	43.6	571	9	HUMQ02604	AF075066 Homo sapi	C 631	24	43.6	24420	9	AC073079	AC073079 Homo sapi
C 559	24	43.6	700	6	AX183424	AX183424 Sequence	C 632	24	43.6	25183	9	AC033585	AC033585 Human DNA
C 560	24	43.6	731	9	HS60T060	Z96665 H. sapiens t	C 633	24	43.6	26420	9	AC073079	AC073079 Homo sapi
C 561	24	43.6	897	9	AF278736	AF278736 Pygathrix	C 634	24	43.6	26078	9	AF376770	AF376770 Homo sapi
C 562	24	43.6	915	6	AX188339	AX188339 Sequence	C 635	24	43.6	27084	9	AL133297	AL133297 Human DNA
C 563	24	43.6	1572	9	HSR404852	AX140852 Homo sapi	C 636	24	43.6	27745	9	AC112915	AC112915 Homo sapi
C 564	24	43.6	1693	9	AK055893	AK055893 Homo sapi	C 637	24	43.6	27847	9	HSCGMP4	X62695 H. sapiens D
C 565	24	43.6	1728	9	AK021930	AK021930 Homo sapi	C 638	24	43.6	28945	9	AF048729	AF048729 Homo sapi
C 566	24	43.6	1813	9	AK024205	AK024205 Homo sapi	C 639	24	43.6	29145	9	AL138771	AL138771 Human DNA
C 567	24	43.6	1868	9	AK025326	AK025326 Homo sapi	C 640	24	43.6	29186	9	AL357560	AL357560 Human DNA
C 568	24	43.6	1880	9	AB072764	AB072764 Macaca fa	C 641	24	43.6	29359	2	AP001083	AP001083 Homo sapi
C 569	24	43.6	1889	9	HSJ474M20	AL110117 Human DNA	C 642	24	43.6	29507	9	AL391064	AL391064 Human DNA
C 570	24	43.6	1896	9	AK092411	AK092411 Homo sapi	C 643	24	43.6	29518	9	AL136361	AL136361 Human DNA
C 571	24	43.6	2086	9	AK091792	AK091792 Homo sapi	C 644	24	43.6	29862	9	AL662798	AL662798 Human DNA
C 572	24	43.6	2128	9	AK098787	AK098787 Homo sapi	C 645	24	43.6	30110	9	HSU124H12	Z49918 Human DNA s
C 573	24	43.6	2145	9	AK094096	AK094096 Homo sapi	C 646	24	43.6	30190	9	AC108010	AC108010 Homo sapi
C 574	24	43.6	2167	9	AK095488	AK095488 Homo sapi	C 647	24	43.6	30625	6	AX491281	AX491281 Sequence
C 575	24	43.6	2227	9	AK097443	AK097443 Homo sapi	C 648	24	43.6	30676	9	AX491284	AX491284 Sequence
C 576	24	43.6	2235	9	AK022396	AK022396 Homo sapi	C 649	24	43.6	30980	9	AC003102	AC003102 Homo sapi

c 650	24	43.6	31325	9	AP000274	Homo sapi	723	24	43.6	46460	2	AC113248	AC113248 Homo sapi
c 651	24	43.6	31679	9	AL772330	Human DNA	c 724	24	43.6	46894	9	AC114729	AC114729 Homo sapi
c 652	24	43.6	31720	9	HS196633	Human DNA s	c 725	24	43.6	47084	9	AC011515	AC011515 Homo sapi
c 653	24	43.6	31874	9	HSB444467	Human DNA	c 726	24	43.6	47152	9	AP001542	AP001542 Homo sapi
c 654	24	43.6	32360	9	AL607067	Human DNA	c 727	24	43.6	47159	9	AL160011	AL160011 Human DNA
c 655	24	43.6	32633	9	AC009402	Homo sapi	c 728	24	43.6	47972	9	AL391843	AL391843 Human DNA
c 656	24	43.6	33963	9	AB065669	Homo sapi	c 729	24	43.6	48036	9	HS633019	AL022302 Human DNA
c 657	24	43.6	34335	9	AC126776	Homo sapi	c 730	24	43.6	48606	2	AC025671	AC025671 Homo sapi
c 658	24	43.6	34336	9	AC000094	Homo sapi	c 731	24	43.6	48730	9	AL136301	AL136301 Human DNA
c 659	24	43.6	34680	9	AC023159	Homo sapi	c 732	24	43.6	49049	9	AC108023	AC108023 Homo sapi
c 660	24	43.6	34864	9	U73649	Human Chrom	c 733	24	43.6	49217	9	HS179D3	281363 Human DNA s
c 661	24	43.6	35116	9	AC004151	Homo sapi	c 734	24	43.6	49322	9	AC112788	AC112788 Homo sapi
c 662	24	43.6	36037	9	AC003966	Homo sapi	c 735	24	43.6	49996	9	HSJ816K9	AL117349 Human DNA
c 663	24	43.6	36787	9	AC108072	Homo sapi	c 736	24	43.6	50675	2	AC087448	AC087448 Homo sapi
c 664	24	43.6	36838	9	AC020947	Homo sapi	c 737	24	43.6	50675	2	AC087448	AC087448 Homo sapi
c 665	24	43.6	36892	9	AC099797	Homo sapi	c 738	24	43.6	51190	9	AC091637	AC091637 Pan trogl
c 666	24	43.6	37000	9	AL663061	Human DNA	c 739	24	43.6	51859	9	HSJ1193N1	AL121915 Human DNA
c 667	24	43.6	37001	9	AC005513	Homo sapi	c 740	24	43.6	51874	2	AC129511	AC129511 Homo sapi
c 668	24	43.6	37107	9	AC009000	Homo sapi	c 741	24	43.6	52193	9	AL139011	AL139011 Human DNA
c 669	24	43.6	37107	9	AC009000	Homo sapi	c 742	24	43.6	52884	2	AC068018	AC068018 Homo sapi
c 670	24	43.6	37392	9	AC005946	Homo sapi	c 743	24	43.6	53000	2	AC003656	Continuation (8 of
c 671	24	43.6	37425	9	AP000308	Homo sapi	c 744	24	43.6	53402	9	AL158844	AL158844 Human DNA
c 672	24	43.6	37535	9	AC113341	Homo sapi	c 745	24	43.6	53430	2	AC116166	AC116166 Homo sapi
c 673	24	43.6	37552	9	AL391993	Human DNA	c 746	24	43.6	53448	2	AC103682	AC103682 Homo sapi
c 674	24	43.6	38055	2	AC006190	Homo sapi	c 747	24	43.6	53773	9	AL355342	AL355342 Human DNA
c 675	24	43.6	38149	9	AC022154	Homo sapi	c 748	24	43.6	53805	9	AC109360	AC109360 Homo sapi
c 676	24	43.6	38411	9	AC005257	Homo sapi	c 749	24	43.6	54054	2	AC013600	AC013600 Homo sapi
c 677	24	43.6	38476	9	U73034	Homo sapien	c 750	24	43.6	54058	2	AL611965	Continuation (4 of
c 678	24	43.6	38649	9	AC004391	Homo sapi	c 751	24	43.6	54184	9	AL713889	AL713889 Human DNA
c 679	24	43.6	38888	9	AC092301	Homo sapi	c 752	24	43.6	55001	9	AL133507	AL133507 Human DNA
c 680	24	43.6	38939	9	AC004678	Homo sapi	c 753	24	43.6	55459	9	AL445490	AL445490 Human DNA
c 681	24	43.6	39196	9	AB023060	Homo sapi	c 754	24	43.6	55860	9	AC112505	AC112505 Homo sapi
c 682	24	43.6	39198	6	AX078379	Sequence	c 755	24	43.6	56295	9	AC004011	AC004011 Human BAC
c 683	24	43.6	39383	9	AC022149	Homo sapi	c 756	24	43.6	56570	9	AL353194	AL353194 Human DNA
c 684	24	43.6	39426	9	AC008983	Homo sapi	c 757	24	43.6	56611	2	AC111183	AC111183 Homo sapi
c 685	24	43.6	39443	9	AC010505	Homo sapi	c 758	24	43.6	56813	9	AL390955	AL390955 Human DNA
c 686	24	43.6	39594	9	AC005624	Homo sapi	c 759	24	43.6	56827	9	HSM9C3A5	U89335 Homo sapien
c 687	24	43.6	39744	9	AC068296	Homo sapi	c 760	24	43.6	57316	9	AL353796	AL353796 Human DNA
c 688	24	43.6	40111	9	AL603833	Human DNA	c 761	24	43.6	57408	9	AL670471	AL670471 Human DNA
c 689	24	43.6	40352	9	AF272142	Homo sapi	c 762	24	43.6	57688	9	AP000048	AP000048 Homo sapi
c 690	24	43.6	40583	9	AC005621	Homo sapi	c 763	24	43.6	57722	2	HSCB33B10	282175 Homo sapien
c 691	24	43.6	41459	9	AC004637	Homo sapi	c 764	24	43.6	57759	9	AL137162	AL137162 Human DNA
c 692	24	43.6	41503	9	AL137185	Human DNA	c 765	24	43.6	57966	2	AC027692	AC027692 Homo sapi
c 693	24	43.6	41618	9	AL355473	Human DNA	c 766	24	43.6	58274	2	AC084092	AC084092 Homo sapi
c 694	24	43.6	41907	9	AC009001	Homo sapi	c 767	24	43.6	58345	9	AC011999	AC011999 Homo sapi
c 695	24	43.6	41918	9	AC114765	Homo sapi	c 768	24	43.6	59105	9	AC004013	AC004013 Human BAC
c 696	24	43.6	42019	9	AC000082	Homo sapi	c 769	24	43.6	59505	2	AC130706	AC130706 Homo sapi
c 697	24	43.6	42213	9	AC010527	Homo sapi	c 770	24	43.6	59506	2	AC060787	AC060787 Homo sapi
c 698	24	43.6	42213	9	AC010527	Homo sapi	c 771	24	43.6	59510	2	AC126384	AC126384 Homo sapi
c 699	24	43.6	42265	9	AC010504	Homo sapi	c 772	24	43.6	59596	9	HS449017	298749 Human DNA s
c 700	24	43.6	42393	9	AC005400	Homo sapi	c 773	24	43.6	59634	9	AC062028	AC062028 Homo sapi
c 701	24	43.6	42949	9	AC104665	Homo sapi	c 774	24	43.6	59634	9	AC074013	AC074013 Homo sapi
c 702	24	43.6	42987	9	AC005576	Homo sapi	c 775	24	43.6	59731	9	AC068442	AC068442 Homo sapi
c 703	24	43.6	43018	9	AL356142	Human DNA	c 776	24	43.6	59776	9	AC098831	AC098831 Homo sapi
c 704	24	43.6	43034	9	HSN5H6	Human DNA s	c 777	24	43.6	60385	2	AC009511	AC009511 Homo sapi
c 705	24	43.6	43456	9	AL353113	Human DNA	c 778	24	43.6	60481	2	AC099844	AC099844 Homo sapi
c 706	24	43.6	43473	9	AF022141	Homo sapi	c 779	24	43.6	60857	2	AC103980	AC103980 Homo sapi
c 707	24	43.6	43632	9	AC108358	Homo sapi	c 780	24	43.6	61101	2	AC083975	AC083975 Homo sapi
c 708	24	43.6	44073	2	AC110293	Homo sapi	c 781	24	43.6	61169	2	AC129487	AC129487 Homo sapi
c 709	24	43.6	44185	9	AP000701	Homo sapi	c 782	24	43.6	61209	9	AP000220	AP000220 Homo sapi
c 710	24	43.6	44348	9	AC006046	Homo sapi	c 783	24	43.6	61541	9	AC005232	AC005232 Homo sapi
c 711	24	43.6	44379	9	AC006163	Homo sapi	c 784	24	43.6	61633	2	AC084075	AC084075 Homo sapi
c 712	24	43.6	44544	9	AC004262	Homo sapi	c 785	24	43.6	62138	2	AC100831	AC100831 Homo sapi
c 713	24	43.6	44767	9	AL669893	Human DNA	c 786	24	43.6	62147	2	AC026510	AC026510 Homo sapi
c 714	24	43.6	44830	9	HSJ738A13	Human DNA	c 787	24	43.6	62186	2	AC110604	AC110604 Homo sapi
c 715	24	43.6	44868	9	AL353892	Human DNA	c 788	24	43.6	62249	2	AC091592	AC091592 Homo sapi
c 716	24	43.6	45333	9	HS10618A	Human DNA	c 789	24	43.6	62825	2	AC090452	AC090452 Homo sapi
c 717	24	43.6	45381	2	AC018585	Homo sapi	c 790	24	43.6	62825	2	AC090452	AC090452 Homo sapi
c 718	24	43.6	45572	9	AC011530	Homo sapi	c 791	24	43.6	62906	9	AL391628	AL391628 Human DNA
c 719	24	43.6	45858	9	AC006123	Homo sapi	c 792	24	43.6	63367	2	AC090915	AC090915 Homo sapi
c 720	24	43.6	45980	6	AX473125	Sequence	c 793	24	43.6	63629	2	AC091187	AC091187 Homo sapi
c 721	24	43.6	46225	9	AC069305	Homo sapi	c 794	24	43.6	63650	2	AC084342	AC084342 Homo sapi
c 722	24	43.6	46239	9	AP003391	Homo sapi	c 795	24	43.6	63905	9	AC022515	AC022515 Homo sapi

C 796	24	43.6	63930	2	AC106017	Homo sapi	C 869	24	43.6	72568	9	AC106762	Homo sapi
C 797	24	43.6	64196	9	AC110804	Homo sapi	C 870	24	43.6	72826	9	AC1391539	Human DNA
C 798	24	43.6	64329	9	AL449188	Human DNA	C 871	24	43.6	73087	9	HS147M19	Homo sapi
C 799	24	43.6	64359	9	AC005233	Homo sapi	C 872	24	43.6	73141	2	AC025123	Homo sapi
C 800	24	43.6	64544	2	AC117551	Mus muscu	C 873	24	43.6	73149	9	AL590642	Human DNA
C 801	24	43.6	64693	9	AL662907	Human DNA	C 874	24	43.6	73246	2	AC089463	Homo sapi
C 802	24	43.6	64789	2	AC083839	Homo sapi	C 875	24	43.6	73246	2	AC066592	Homo sapi
C 803	24	43.6	65111	2	AC055857	Homo sapi	C 876	24	43.6	73899	9	AC005156	Homo sapi
C 804	24	43.6	65111	2	AC055857	Homo sapi	C 877	24	43.6	73947	9	AL445248	Human DNA
C 805	24	43.6	65138	9	AL590812	Human DNA	C 878	24	43.6	74037	9	HS1071N3	Human DNA
C 806	24	43.6	65694	2	AC091065	Homo sapi	C 879	24	43.6	74196	2	AC023875	Homo sapi
C 807	24	43.6	65777	2	AC124299	Homo sapi	C 880	24	43.6	75008	9	AP000471	Homo sapi
C 808	24	43.6	65961	2	AC090266	Homo sapi	C 881	24	43.6	75008	9	AP000471	Homo sapi
C 809	24	43.6	66058	2	AC090065	Homo sapi	C 882	24	43.6	75737	2	AC124655	Homo sapi
C 810	24	43.6	66353	2	AC095348	Homo sapi	C 883	24	43.6	75737	2	AC074059	Homo sapi
C 811	24	43.6	66403	9	AC074295	Homo sapi	C 884	24	43.6	75886	2	AP000583	Homo sapi
C 812	24	43.6	66477	9	AL591133	Human DNA	C 885	24	43.6	76165	2	AP000583	Homo sapi
C 813	24	43.6	66497	2	AC073026	Homo sapi	C 886	24	43.6	76211	9	HS03336M4	Human DNA
C 814	24	43.6	66660	9	AC013270	Homo sapi	C 887	24	43.6	76653	2	AC015506	Homo sapi
C 815	24	43.6	66761	2	AC044823	Homo sapi	C 888	24	43.6	76854	2	AC130321	Homo sapi
C 816	24	43.6	66768	2	AC126389	Homo sapi	C 889	24	43.6	76875	2	AC018419	Homo sapi
C 817	24	43.6	66788	9	AL353653	Human DNA	C 890	24	43.6	76988	9	AC006578	Homo sapi
C 818	24	43.6	66817	9	AC005201	Homo sapi	C 891	24	43.6	77313	9	AC110757	Homo sapi
C 819	24	43.6	66867	2	AC073170	Homo sapi	C 892	24	43.6	77702	9	AL138743	Human DNA
C 820	24	43.6	66933	6	AX277532	Sequence	C 893	24	43.6	77808	9	AL512634	Human DNA
C 821	24	43.6	66933	6	AX418096	Sequence	C 894	24	43.6	78204	2	AC021943	Homo sapi
C 822	24	43.6	67120	2	AC130331	Homo sapi	C 895	24	43.6	78438	2	AC126385	Homo sapi
C 823	24	43.6	67289	2	AC040994	Homo sapi	C 896	24	43.6	79319	9	AL512274	Human DNA
C 824	24	43.6	67434	2	AC090801	Homo sapi	C 897	24	43.6	79470	2	AL391000	Homo sapi
C 825	24	43.6	67529	2	AC069312	Homo sapi	C 898	24	43.6	79509	9	AL353769	Human DNA
C 826	24	43.6	67610	2	AC084344	Homo sapi	C 899	24	43.6	79516	9	AC004834	Homo sapi
C 827	24	43.6	68001	9	AP001442	Homo sapi	C 900	24	43.6	80010	9	AC005995	Homo sapi
C 828	24	43.6	68048	9	AC004764	Homo sapi	C 901	24	43.6	80119	9	AC111152	Homo sapi
C 829	24	43.6	68049	9	AL513322	Human DNA	C 902	24	43.6	80146	9	AL583963	Human DNA
C 830	24	43.6	68049	9	AL513322	Human DNA	C 903	24	43.6	80198	9	AP003040	Homo sapi
C 831	24	43.6	68065	2	AC110285	Homo sapi	C 904	24	43.6	80218	2	AC084700	Homo sapi
C 832	24	43.6	68273	9	AL138695	Human DNA	C 905	24	43.6	80547	9	AC007382	Homo sapi
C 833	24	43.6	68468	9	MB9651	Human DNA f	C 906	24	43.6	80858	9	AC007360	Homo sapi
C 834	24	43.6	68589	2	AC087682	Homo sapi	C 907	24	43.6	81149	9	AC093751	Homo sapi
C 835	24	43.6	68651	9	AC027343	Homo sapi	C 908	24	43.6	81171	2	AC016218	Homo sapi
C 836	24	43.6	68692	2	AP003163	Homo sapi	C 909	24	43.6	81207	9	HS12513	Human DNA
C 837	24	43.6	69012	2	AC023849	Homo sapi	C 910	24	43.6	81483	9	AL354699	Human DNA
C 838	24	43.6	69097	9	AL356235	Human DNA	C 911	24	43.6	81631	9	HS745114	Human DNA
C 839	24	43.6	69113	9	AL359960	Human DNA	C 912	24	43.6	81740	9	AP001614	Homo sapi
C 840	24	43.6	69291	2	AC107957	Homo sapi	C 913	24	43.6	81896	9	AP001614	Homo sapi
C 841	24	43.6	69373	9	AL513331	Human DNA	C 914	24	43.6	81914	9	HS0363M2	Human DNA
C 842	24	43.6	69397	2	AC036233	Homo sapi	C 915	24	43.6	82329	9	AL160162	Human DNA
C 843	24	43.6	69413	9	AL136172	Human DNA	C 916	24	43.6	82494	9	AL357146	Human DNA
C 844	24	43.6	69570	2	AC021246	Homo sapi	C 917	24	43.6	82771	2	AC011953	Homo sapi
C 845	24	43.6	69570	2	AC055831	Homo sapi	C 918	24	43.6	82998	9	AP000967	Homo sapi
C 846	24	43.6	69637	9	AL138745	Human DNA	C 919	24	43.6	83003	9	AC027547	Homo sapi
C 847	24	43.6	69656	9	AL390729	Human DNA	C 920	24	43.6	83187	9	AC009778	Homo sapi
C 848	24	43.6	69684	9	AC006475	Homo sapi	C 921	24	43.6	83306	9	AC062021	Homo sapi
C 849	24	43.6	69967	2	AC126337	Homo sapi	C 922	24	43.6	83557	9	AL138735	Human DNA
C 850	24	43.6	70128	9	AC007536	Homo sapi	C 923	24	43.6	83709	9	HS0403A15	Human DNA
C 851	24	43.6	70193	9	AL627303	Human DNA	C 924	24	43.6	83727	9	AL356120	Human DNA
C 852	24	43.6	70203	2	AC024012	Homo sapi	C 925	24	43.6	83731	2	AC079747	Homo sapi
C 853	24	43.6	70288	9	AL662867	Human DNA	C 926	24	43.6	83762	2	AC008707	Homo sapi
C 854	24	43.6	70299	9	AL161945	Human DNA	C 927	24	43.6	84193	9	AL163538	Human DNA
C 855	24	43.6	70638	9	AC079306	Homo sapi	C 928	24	43.6	84216	9	AL157718	Human DNA
C 856	24	43.6	70975	2	AP000579	Homo sapi	C 929	24	43.6	84364	9	HS522J7	Human DNA
C 857	24	43.6	71132	2	AC130383	Homo sapi	C 930	24	43.6	84759	9	AL100838	Homo sapi
C 858	24	43.6	71132	2	AC092184	Homo sapi	C 931	24	43.6	84841	9	AL391813	Human DNA
C 859	24	43.6	71206	2	AC027744	Homo sapi	C 932	24	43.6	84997	9	AL583832	Human DNA
C 860	24	43.6	71353	9	AF104455	Homo sapi	C 933	24	43.6	85086	9	AL589946	Human DNA
C 861	24	43.6	71418	9	AL732442	Human DNA	C 934	24	43.6	85275	9	AC092180	Homo sapi
C 862	24	43.6	71438	9	AC026754	Homo sapi	C 935	24	43.6	85322	9	AL138923	Human DNA
C 863	24	43.6	72049	6	AX277530	Sequence	C 936	24	43.6	85543	2	AC010553	Homo sapi
C 864	24	43.6	72049	6	AX418094	Sequence	C 937	24	43.6	85591	2	AC023409	Homo sapi
C 865	24	43.6	72302	2	AC090995	Homo sapi	C 938	24	43.6	85927	9	AC093244	Homo sapi
C 866	24	43.6	72356	9	AL583861	Human DNA	C 939	24	43.6	86000	9	AP005133	Homo sapi
C 867	24	43.6	72383	2	AC027746	Homo sapi	C 940	24	43.6	86136	9	AL359742	Human DNA
C 868	24	43.6	72417	2	AC087497	Homo sapi	C 941	24	43.6	86196	9	AL592046	Human DNA
										86640	9	HSU50871	Human famil

[illegible]



## AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeters, R., Meldrim, J., Meneus, J., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

## Direct Submission

Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 173264)

## REFERENCE

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, J., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Robert, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## Direct Submission

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jun 17, 2002 this sequence version replaced gi:21321864.  
All repeats were identified using RepeatMasker:  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Smit, A.F.A. & Green, P. (1996-1997)

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information

Center project name: L7454

Center clone name: 353\_K\_12

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 39461: contig of 39461 bp in length  
39462 39561: gap of 100 bp

## FEATURES

source  
\* 39562 108347: contig of 68786 bp in length  
\* 108348 108447: gap of 100 bp  
\* 108448 173264: contig of 64817 bp in length.

## Location/Qualifiers

1..173264  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="8"  
/map="8"  
/clones="RP11-353K12"  
/clone\_lib="RP11-11 Human Male BAC"  
BASE COUNT 47355 a 38864 c 39235 g 47493 t 317 others  
ORIGIN

Query Match 100.0%; Score 55; DB 2; Length 173264;  
Best Local Similarity 100.0%; Pred. No. 2.3e-21;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGCAGCGAGACCTTGAGGTGAGGATTCGAGATCAGCTGCCCAACATGAG 55

Db 26665 GAGCAGCGAGACCTTGAGGTGAGGATTCGAGATCAGCTGCCCAACATGAG 26719

## RESULT 3

AB037741/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..5321

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clones="fhl3757"

/tissue type="brain"

/clone\_lib="pBluescriptII SK plus"

1..5321

/gene="KIAA1320"

<2051..3754

/gene="KIAA1320"

/note="Start codon is not identified."

/codon\_start=1

/product="KIAA1320 protein"

/protein\_id="BAA92558.1"

/db\_xref="GI:7243021"

/translation="SCSLRMWFKHFCFSOPLELLHSLDEWLVLIAELMKNKRDST

ETISILLKOKGQDQDAASIPFPFGPGSVENLSTGTRESKPDALAGRASACQDV

ISMTANFLSAVIQAFYMCCSCOMPQMTSPRFIEFYCKHDEVLCKFVNRKPIIDFHE

HFLCEPCLMSRFMHIIKAQPFKDRCEHFLHLSGGQSDMHRPNNVDILVHRD

SIFRSCCVVSKANCAKLKOGIAVRFHGEEMGGQVVRWFDFILNSIENVDPYALFTQ

SADGTTFPQNSYVNPFDHLNIFRFAGIILGALNHLNLYIYTRFYKHILGIPVN

YQDVASIDPEYAKNLQWILDNDISDLGLELTFSVETDVFAGMEVPLKPGGSLVLTQ

NNKAEYVOLATELMTBAIQOINAFLOGFHMFRIPPSLIQOLFDEYELLLSGMPEID  
VSDWIKNTYTSVGEREDPVIOMFWUEVEDITQBERVLLLOFVTGSRVRPHGCFANIM  
GGSLQNTTIAAVPYTNLLSTSTCINMLKLPYPSKEIKDKORLLVALHCHGSGTYIM  
A"

BASE COUNT 1592 a 822 c 1004 g 1903 t

ORIGIN

Query Match 72.7%; Score 40; DB 9; Length 5321;

Best Local Similarity 100.0%; Pred. No. 1.5e-12;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 14 CACTTGAGTCCAGGAATTCGAGATCAGCTGCCCAACATG 53

Db 1303 CACTTGAGTCCAGGAATTCGAGATCAGCTGCCCAACATG 1264

RESULT 4

AX015917/c

LOCUS

DEFINITION

ACCESSION

VERSION

AX015917.1

GI:10041660

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 49999)

Aligner,T., Hess,J., Rosenthal,A., Rump,A. and Wirth,T.

Nucleic acid molecules which code proteins influencing bone

development

JOURNAL

Patent: WO 950284-A 20 OCT-1999;

AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP

ANDREAS (DE); WIRTH THOMAS (DE)

FEATURES

Location/Qualifiers

1..49999

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

BASE COUNT 10382 a 14932 c 14107 g 10578 t

ORIGIN

Query Match 72.7%; Score 40; DB 6; Length 49999;

Best Local Similarity 100.0%; Pred. No. 1.4e-12;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 14 CACTTGAGTCCAGGAATTCGAGATCAGCTGCCCAACATG 53

Db 24864 CACTTGAGTCCAGGAATTCGAGATCAGCTGCCCAACATG 24825

RESULT 5

AL513472

LOCUS

DEFINITION

Human DNA sequence from clone RP11-271J19 on chromosome 6, complete

sequence.

ACCESSION

AL513472

VERSION

AL513472.9

GI:14031111

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 70328)

Laird,G.

Direct Submission

Submitted (10-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On May 14, 2001 this sequence version replaced gi:13751550.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6

RP11-271J19 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-271J19 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-271J19 is at 1 in this sequence.

The true left end of clone RP11-809N15 is at 70229 in this sequence.

FEATURES

Location/Qualifiers

1..70328

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="6"

/clone="RP11-271J19"

/clone\_lib="RPCI-11.1"

16..830

/note="L1ME3A repeat: matches 5280. 6153 of consensus"

2379..2984

/note="L2 repeat: matches 1844. 2412 of consensus"

2979..3100

/note="L2 repeat: matches 2617. 2750 of consensus"

3272..3428

/note="L2 repeat: matches 2617. 2750 of consensus"

3714..3777

/note="FRAM repeat: matches 4. 157 of consensus"

/note="32 copies 2 mer aa 78% conserved"

5007..7916

/note="L1PA7 repeat: matches -567. 3339 of consensus"

7918..8213

/note="L1PA7 repeat: matches 2. 296 of consensus"

8363..14484

/note="L1PA7 repeat: matches 11. 6141 of consensus"

14495..14800

/note="AluX repeat: matches 1. 306 of consensus"

15089..15553

/note="AluX repeat: matches 1. 303 of consensus"

15554..15853

/note="AluX repeat: matches 1. 303 of consensus"

15854..15864

/note="AluX repeat: matches 1. 296 of consensus"

15865..16163

/note="AluX repeat: matches 1. 296 of consensus"

16164..18241

/note="Tigger4 (Zombi) repeat: matches 1. 2265 of consensus"

18608..18677

/note="Tigger4 (Zombi) repeat: matches 1. 71 of consensus"

18680..18839

/note="U6 repeat: matches 1. 71 of consensus"

19021..19555

/note="WIR repeat: matches 63. 251 of consensus"

20821..21093

/note="L2 repeat: matches 1850. 2371 of consensus"

repeat\_region /note="AluJo repeat: matches 28. .298 of consensus"  
21779. .21848 /note="LIPa6 repeat: matches 11. .6143 of consensus"  
repeat\_region 57966. .58253 /note="AluJo repeat: matches 1. .288 of consensus"  
2223. .22522 /note="AluX repeat: matches 1. .300 of consensus"  
repeat\_region 24173. .24214 /note="21 copies 2 mer ac 83% conserved"  
repeat\_region 24555. .24825 /note="LIPa4 repeat: matches 5909. .6184 of consensus"  
repeat\_region 24951. .25016 /note="L2 repeat: matches 2641. .2710 of consensus"  
repeat\_region 25752. .25837 /note="MIR repeat: matches 173. .262 of consensus"  
repeat\_region 25867. .26175 /note="AluY5 repeat: matches 1. .308 of consensus"  
repeat\_region 26180. .26465 /note="AluX repeat: matches 5. .289 of consensus"  
repeat\_region 26846. .27189 /note="AluB8 repeat: matches 1. .308 of consensus"  
repeat\_region 28316. .28454 /note="MIR repeat: matches 38. .188 of consensus"  
repeat\_region 29560. .29844 /note="AluX repeat: matches 1. .286 of consensus"  
repeat\_region 30299. .30607 /note="AluJo repeat: matches 1. .295 of consensus"  
repeat\_region 31460. .31626 /note="MIR repeat: matches 23. .196 of consensus"  
repeat\_region 31665. .31799 /note="MIR repeat: matches 124. .262 of consensus"  
repeat\_region 32065. .32098 /note="17 copies 2 mer ca 85% conserved"  
repeat\_region 32368. .32965 /note="LIMC4 repeat: matches 7167. .7837 of consensus"  
repeat\_region 32975. .33268 /note="LIMC4 repeat: matches 5335. .6939 of consensus"  
repeat\_region 33309. .33415 /note="LIMC4 repeat: matches 6445. .6574 of consensus"  
repeat\_region 33779. .33886 /note="MADE1 repeat: matches 2. .80 of consensus"  
repeat\_region 33956. .33993 /note="MIR repeat: matches 1. .36 of consensus"  
repeat\_region 33994. .34297 /note="AluB repeat: matches 3. .311 of consensus"  
repeat\_region 34298. .34438 /note="MIR repeat: matches 36. .189 of consensus"  
repeat\_region 35192. .35360 /note="MIR repeat: matches 64. .259 of consensus"  
repeat\_region 35678. .35727 /note="L2 repeat: matches 2656. .2705 of consensus"  
repeat\_region 37839. .38143 /note="AluX repeat: matches 1. .299 of consensus"  
repeat\_region 38242. .38418 /note="AluB repeat: matches 135. .311 of consensus"  
repeat\_region 42257. .42569 /note="AluB repeat: matches 1. .311 of consensus"  
repeat\_region 44398. .44773 /note="LTR3 repeat: matches 1. .369 of consensus"  
repeat\_region 44774. .45072 /note="AluY repeat: matches 2. .301 of consensus"  
repeat\_region 45896. .46024 /note="MIR repeat: matches 94. .239 of consensus"  
repeat\_region 46408. .46698 /note="AluX repeat: matches 1. .295 of consensus"  
repeat\_region 47883. .48195 /note="AluB repeat: matches 1. .307 of consensus"  
repeat\_region 49573. .49884 /note="AluS repeat: matches 1. .313 of consensus"  
repeat\_region 50973. .51063 /note="MER93 repeat: matches 1. .91 of consensus"  
repeat\_region 51111. .51331 /note="MER93 repeat: matches 179. .397 of consensus"  
repeat\_region 51333. .51451 /note="MIR repeat: matches 28. .151 of consensus"

repeat\_region 51549. .57643 /note="LIPa6 repeat: matches 11. .6143 of consensus"  
repeat\_region 57966. .58253 /note="AluJo repeat: matches 1. .288 of consensus"  
repeat\_region 58803. .59107 /note="AluS repeat: matches 1. .304 of consensus"  
repeat\_region 59691. .59991 /note="AluX repeat: matches 1. .300 of consensus"  
repeat\_region 60098. .60266 /note="MIR repeat: matches 79. .249 of consensus"  
repeat\_region 60903. .61893 /note="L2 repeat: matches 1685. .2710 of consensus"  
repeat\_region 62439. .62517 /note="L2 repeat: matches 2628. .2710 of consensus"  
repeat\_region 62995. .63070 /note="38 copies 2 mer ta 81% conserved"  
repeat\_region 63395. .63587 /note="MER3 repeat: matches 8. .199 of consensus"  
repeat\_region 63995. .64246 /note="AluJo repeat: matches 49. .296 of consensus"  
repeat\_region 64994. .65149 /note="AluJo repeat: matches 3. .157 of consensus"  
repeat\_region 65242. .65443 /note="MER20 repeat: matches 1. .214 of consensus"  
repeat\_region 65583. .65802 /note="110 copies 2 mer aa 57% conserved"  
repeat\_region 65831. .66432 /note="HAL1 repeat: matches 325. .988 of consensus"  
repeat\_region 66442. .66786 /note="MSTa repeat: matches 40. .426 of consensus"  
repeat\_region 66789. .67156 /note="MSTa-internal repeat: matches 3. .382 of consensus"  
repeat\_region 67157. .67446

Query Match 72.7%; Score 40; DB 9; Length 70328;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTCAGGTTCAGAAATTCAGATCAGCTGCGCCAAACATG 53  
|||||  
DB 37900 CACTTCAGGTTCAGAAATTCAGATCAGCTGCGCCAAACATG 37939  
|||||

RESULT 6  
AC092165/c 100020 bp DNA linear PRI 21-FEB-2002  
LOCUS Homo sapiens BAC clone RP11-753F4 from 2, complete sequence.  
DEFINITION AC092165  
ACCESSION AC092165.4 GI:18056750  
VERSION HTG.  
KEYWORDS SOURCE  
Homo sapiens.  
Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 100020)  
AUTHORS Sulston, J.E. and Waterston, R.  
TITLE Toward a complete human genome sequence  
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
MEDLINE 99063792  
PUBMED 9847074  
REFERENCE 2 (bases 1 to 100020)  
AUTHORS Abbott, S. and Haglund, K.  
TITLE The sequence of Homo sapiens BAC clone RP11-753F4  
JOURNAL Unpublished (2001)  
REFERENCE 3 (bases 1 to 100020)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission  
JOURNAL Submitted (22-JUN-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 4 (bases 1 to 100020)  
AUTHORS Waterston, R.H.  
TITLE Direct Submission

## JOURNAL

Submitted (04-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

## REFERENCE

5 (bases 1 to 100020)

## AUTHORS

Waterston,R.

## TITLE

Direct Submission

## JOURNAL

Submitted (21-FEB-2002) Department of Genetics, Washington University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA

## COMMENT

On Jan 4, 2002 this sequence version replaced gi:17981677.

----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
----- Summary Statistics  
Center project name: H\_NH0753F04  
-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tatenoe,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-762N20, 2000 bp overlap; the clone sequenced to the right is RP11-485D7. Actual start of this clone is at base position 98039 of RP11-762N20; actual end is at base position 100020 of RP11-753F4.

Data from AC09338 and AC074188 was used to finish this clone, AC092165. Polymorphisms have been identified between AC074188 and AC092165.

## FEATURES

## source

## Location/Qualifiers

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/map="2"  
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177..459  
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456..501  
/rpt\_family="(CA)n"  
501..3543  
/rpt\_family="L1"  
4004..4114

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

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8894..9319  
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894..9258  
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8896..9178  
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8897..9319  
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complete sequence.
ACCESSION AF002498 GI:14861115
VERSION AP002498.3
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:CTD-2547H18.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2000)
REFERENCE 2
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@psc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Jul 17, 2001 this sequence version replaced gi:11320563.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clones="CTD-2547H18"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 14 CACTTGAGTTCAGGAATTCGAGATCAGCTGCGCAACATG 53
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Db 8217 CACTTGAGTTCAGGAATTCGAGATCAGCTGCGCAACATG 8178

RESULT 9
AC104184
LOCUS AC104184 143034 bp DNA linear PRI 23-MAR-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-188P20, complete sequence.
ACCESSION AC104184 AC027581
VERSION AC104184.2 GI:19697457
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Mar 23, 2002 this sequence version replaced gi:17386316.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC

```

Web site: <http://www.genome.washington.edu>  
 Contact: [uwgchgs@u.washington.edu](mailto:uwgchgs@u.washington.edu)  
 Drafting Center: BCM

# ----- Project Information

Center project name: chr-3  
 Center clone name: RP11-188P20 (bc0291)  
 ----- Summary Statistics  
 Sequencing vector: unknown; 58% of reads  
 Sequencing vector: plasmid; L08752; 42% of reads  
 Chemistry: Dye-terminator ET; 67% of reads  
 Chemistry: Dye-terminator Big Dye; 33% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 142918 bases at least Q40  
 Consensus quality: 143028 bases at least Q30  
 Consensus quality: 143034 bases at least Q20  
 Insert size: 142838; sum-of-contigs  
 Quality coverage: 8.0x in Q20 bases; sum-of-contigs

## ----- Overlapping Sequences:

5': Mapping in progress  
 3': RP11-258N2 (UWGC:bc0637) AC024378

## ----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## ----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI			HindIII			BglII			
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8704	1129	1114	10270	10243				
6	<800	6382	6515	2067	2063				
2882	2945	512	<800	5480	5668				
2540	2530	449	<800	3606	3574				
3643	3781	2552	2517	928	930				
1514	1486	3416	3369	365	<800				
631	<800	7168	7307	7579	7709				
865	847	1854	1889	782	<800				

2055	2049	1696	1655	4596	4559
909	897	397	<800	2776	2784
3796	3781	2926	2977	184	<800
5481	5462	4712	4619	2132	2156
1935	1951	45	<800	856	867
507	<800	825	895	659	<800
120	<800	5281	5260	1899	1874
1153	1139	4614	4619	1261	1259
2641	2663	2273	2249	2817	2784
2145	2184	2075	2065	6712	6648
1526	1486	14383	14415	128	<800
1000	997	10039	9940	4209	4192
1126	1139	8620	8673	46	<800
1649	1651	501	<800	2157	2156
637	<800	11469	11355	6593	6648
788	<800	1883	1889	6080	6248
18870	19027	4982	4848	3363	3421
1312	1314	1943	1889	5134	5104
172	<800	886	895	5754	5668
3298	3303	881	895	4281	4192
1332	1314	85	<800	4197	4192
5959	5917	4281	4178	3177	3210
10560	10431	593	<800	9088	9070
7179	7208	66	<800	150	<800
3985	4046	3551	3581	2704	2784
9799	9561	488	<800	3282	3210
4653	4680	5651	5589	708	<800
1150	1139	2443	2517	8040	8083
7764	7701	1249	1229	3827	3766
5866	5917	4839	4848	228	<800
1182	1139	1244	1229	662	<800
1154	1139	185	<800	4221	4192
973	997	1386	1353	9761	9678
2345	2368	2602	2517	1167	1161
225	<800	1492	1453	7807	7709
326	<800	2460	2517	---	---
2508	2530	72	<800	---	---

## FEATURES

source

Location/Qualifiers

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 /db\_xref="taxon:9606"  
 /chromosome="3"  
 /clone="RP11-188P20"  
 /clone\_lib="RPCI human BAC library 11"

BASE COUNT 41310 a 29565 c 30285 g 41874 t  
 ORIGIN

Query Match 72.7%; Score 40; DB 9; Length 143034;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-12;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTGAGGTGAGAAATTCGAGATCAGCTGCGCCACATG 53

Db 132437 CACTTGAGGTGAGAAATTCGAGATCAGCTGCGCCACATG 132476

## RESULT 10

AC005883/c

LOCUS

DEFINITION

AC005883

AC005883

AC005883.14

HTG.

SOURCE

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 146224)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C.,

Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K.,

Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R.,

Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A.,

Herena, L., Horton, L., Howland, J. C., Jacotot, L., Jones, C., Kann, L.,

Karatas, A., Lehoczy, J., Macdonald, P., Marquis, N., McEwan, P.,

McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J.,

Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T.,

O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A.,

Severy, P., Stange-Thomann, N., Stillwell, J., Stojanovic, N., Stone, C.,

Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I.,

Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,

Ye, W. J., Zhao, J. and Zody, M.

Direct Submission

Submitted (28-OCT-1998) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 146224)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B., Brown, A.,

Camranta, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S.,

Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,



Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, P., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Sougniez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strausz, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (10-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Feb 10, 2001 this sequence version replaced gi:11991319.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence-submissions@genome.wi.mit.edu](mailto:sequence-submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L439  
 Center clone name: 958\_E\_11  
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Only 146.2 kilobases from the middle of this clone are being submitted. The remainder overlaps either accession number AC002090 (WICGR project L106) or accession number AC005823 (WICGR project L448).

# FEATURES

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/rpt_family="GA-rich"
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of missing sequence here"
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23892..23933
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/rpt_family=" (TTCA)n"
complement(24499..24642)

Query Match 72.7%; Score 40; DB 9; Length 146224;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCTGCCCAACATG 53
|||||
Db 102073 CACTTGAGGTCAGGAATTCGAGATCAGCTGCCCAACATG 102034

RESULT 11
AC068081/c 152591 bp DNA linear HTG 04-MAY-2001
LOCUS Homo sapiens chromosome 11 clone RP11-259H21 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 10 unordered pieces.
AC068081
VERSION AC068081.2 GI:8576212
HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152591)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Melidrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thumann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (28-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2000 this sequence version replaced gi:7658355.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

```

```

Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10094
Center clone name: 259_H_21
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145477 bases at least Q40
Consensus quality: 149315 bases at least Q30
Consensus quality: 150842 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 151691; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1378: contig of 1378 bp in length
* 1379 1478: gap of 100 bp
* 1479 3504: contig of 2026 bp in length
* 3505 3604: gap of 100 bp
* 3605 3778: contig of 174 bp in length
* 3779 3878: gap of 100 bp
* 3879 13991: contig of 10113 bp in length
* 13992 14091: gap of 100 bp
* 14092 22007: contig of 7916 bp in length
* 22008 22107: gap of 100 bp
* 22108 31212: contig of 9105 bp in length
* 31213 31312: gap of 100 bp
* 31313 44192: contig of 12880 bp in length
* 44193 44292: gap of 100 bp
* 44293 57334: contig of 13042 bp in length
* 57335 57434: gap of 100 bp
* 57435 86879: contig of 29445 bp in length
* 86880 86979: gap of 100 bp
* 86980 152591: contig of 65612 bp in length.
FEATURES
source
1..152591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-259H21"
/clone_lib="RPC1-11 Human Male BAC"
1..1378
/note="assembly_fragment"
1479..3504
/note="assembly_fragment"
3605..3778
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
3879..13991
/note="assembly_fragment"
14092..22007
/note="assembly_fragment"
22108..31212
/note="assembly_fragment"
31313..44192
/note="assembly_fragment"
clone_end:T7
vector_side:left"
44293..57334
/note="assembly_fragment"
57435..86879

```

```

/note="assembly_fragment"
86980..152591
/note="assembly_fragment"
BASE COUNT 43817 a 29008 c 29323 g 49535 t 908 others
ORIGIN
Query Match 72.7%; Score 40; DB 2; Length 152591;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
Db 43245 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 43206

RESULT 12
AC012033 158276 bp DNA linear HTG 04-SEP-2000
LOCUS
DEFINITION Homo sapiens clone RP11-91N19, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
AC012033
VERSION AC012033.20 GI:9966196
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158276)
Mozny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K.,
Budny,D.M., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
David,R., Delgado,O., Deshazo,D., Ding,Y., Donah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Forcuna-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
Lichter,O., Liu,J., Liu,W., Logan,O., Lozano,R.J., Lu,J.,
Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
Taber,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M.,
Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A.,
Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D., and
Gibbs,R.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 158276)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 4, 2000 this sequence version replaced gi:9929521.

COMMENT
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMOR
Center clone name: RP11-91N19
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 135987 bases at least Q40
Consensus quality: 145984 bases at least Q30
Consensus quality: 149762 bases at least Q20
Estimated insert size: 149946; sum-of-contigs estimation
Estimated insert size: 249006; agarose-ep estimation
Quality coverage: 2.8x in Q20 bases; agarose-ep estimation
Quality coverage: 4.6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 44367: contig of 44367 bp in length
* 44368: gap of unknown length
* 73078: contig of 28611 bp in length
* 73079: gap of unknown length
* 94206: contig of 21028 bp in length
* 94207: gap of unknown length
* 112789: contig of 18482 bp in length
* 112889: gap of unknown length
* 120323: contig of 7435 bp in length
* 120424: gap of unknown length
* 130441: contig of 10017 bp in length
* 130540: gap of unknown length
* 135819: contig of 5278 bp in length
* 135919: gap of unknown length
* 141234: contig of 5316 bp in length
* 141335: gap of unknown length
* 145232: contig of 3898 bp in length
* 145332: gap of unknown length
* 145333: contig of 4328 bp in length
* 149661: gap of unknown length
* 150931: contig of 1171 bp in length
* 150932: gap of unknown length
* 151032: contig of 1726 bp in length
* 152857: gap of unknown length
* 152858: contig of 2076 bp in length
* 154933: gap of unknown length
* 154934: contig of 1684 bp in length
* 156718: gap of unknown length
* 156818: contig of 1459 bp in length.

FEATURES
Location/Qualifiers
1..158276
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone="RP11-91N19"

BASE COUNT 36546 a 42190 c 43059 g 35064 t 1417 others
ORIGIN

Query Match 72.7%; Score 40; DB 2; Length 158276;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
Db 22780 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 22819

RESULT 13
CNS05TDJ/c
LOCUS CNS05TDJ 158608 bp DNA linear PRI 08-JUN-2001
DEFINITION Human chromosome 14 DNA sequence BAC R-45419 of library RPCL-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL356801
VERSION AL356801.5 GI:14347105
KEYWORDS HTG; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158608)
Heilig,R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., DeBerardinis,V., Cruaud,C.,

```

Gyapay,G., Saurin,W. and Weissenbach,J.  
 Sequencing of the human chromosome 14  
 Unpublished  
 2 (bases 1 to 158608)  
 Genoscope.  
 Direct Submission  
 Submitted (07-JUN-2001) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 On Jun 11, 2001 this sequence version replaced gi:12657330.

## COMMENT

----- Genome Center  
 Center: Genoscope / Centre National de Sequencage  
 Center code: GS  
 Web site: http://www.genoscope.cns.fr/  
 Contact: SeqRef@genoscope.cns.fr  
 -----  
 The following BAC sequence is oriented from the T7 to the SP6 end.  
 Upstream BAC (overlapping the T7 end) : R-132J14 (AC=AL138499)  
 Downstream BAC (overlapping the SP6 end) : R-665C16 -----  
 Summary Statistics  
 Assembly program: Phrap; version 2.0  
 Quality coverage: 8.46x in Q20 bases; sum-of-contigs

## Overall quality chart :

Range : bases

0 :

1 - 9 :

10 - 19 :

20 - 29 :

30 - 39 :

40 - 49 :

50 - 59 :

60 - 69 :

70 - 79 :

80 - 89 :

90 - 99 :

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES  
source

Location/Qualifiers

1..158608

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="14"

/clone="R-454L9"

/clone\_lib="RPCI-11"

16635..16756

/note="Matching EMBL:N62946

RHdb:RH69643

dbSTS:STS49521

Identified using the e-PCR software (G. Schuler)"

16717..16841

/note="Matching EMBL:N62939

RHdb:RH46155

dbSTS:STS39223

Identified using the e-PCR software (G. Schuler)"

127255..127385

/note="Matching EMBL:G33247

RHdb:RH100175

RHdb:RH42873

dbSTS:STS36291

Identified using the e-PCR software (G. Schuler)"

132342..132540

/note="Matching EMBL:T96658

RHdb:RH64855

dbSTS:STS44788

Identified using the e-PCR software (G. Schuler)"

132444..132591

/note="Matching EMBL:H73005

RHdb:RH68681

dbSTS:STS48588

Identified using the e-PCR software (G. Schuler)"

46768 a 32989 c 33903 g 44948 t

## BASE COUNT

## ORIGIN

Query Match 72.7%; Score 40; DB 9; Length 158608;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTGAGGTGAGAAATTCGAGATCAGCCTGGCCCAACATG 53  
 |||||  
 Db 130174 CACTTGAGGTGAGAAATTCGAGATCAGCCTGGCCCAACATG 130135

RESULT 14  
 AC020592/c

## LOCUS

DEFINITION

AC020592

Homo sapiens chromosome 6 clone RP11-159G14, WORKING DRAFT

SEQUENCE, 21 unordered pieces.

AC020592

AC020592.4 GI:8954237

HTG; HTGS\_PHASE1; HTGS\_DRAFT.

KEYWORDS

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 162190)

Waterston,R.H.

The sequence of Homo sapiens clone

Unpublished

2 (bases 1 to 162190)

Waterston,R.H.

Direct Submission

Submitted (05-JAN-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Jul 7, 2000 this sequence version replaced gi:8569833.

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

----- Project Information -----

Center project name: H\_NH0159G14

----- Summary Statistics -----

Sequencing vector: M13; 78%

Chemistry: Dye-primer ET; 78% of reads

Chemistry: Dye-terminator Big Dye; 22% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 152536 bases at least Q40

Consensus quality: 155427 bases at least Q30

Consensus quality: 157179 bases at least Q20

Insert size: 151000; agarose-fp

Insert size: 160190; sum-of-contigs

Quality coverage: 4.51 in Q20 bases; agarose-fp

Quality coverage: 4.09 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 21 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1

\* 1038: contig of 1038 bp in length

\* 1139

\* 1138: gap of unknown length

\* 2539

\* 2539: contig of 1401 bp in length

\* 2640

\* 2639: gap of unknown length

\* 4204

\* 4204: contig of 1565 bp in length

\* 4305

\* 4304: gap of unknown length

\* 4305

\* 4302: contig of 1598 bp in length

\* 5903

\* 6002: gap of unknown length

\* 6003

\* 9034: contig of 3032 bp in length

\* 9035

\* 9134: gap of unknown length

```

* 9135 12275: contig of 3141 bp in length
* 12276 12375: gap of unknown length
* 12376 16345: contig of 3970 bp in length
* 16346 19575: gap of unknown length
* 19576 24774: contig of 3130 bp in length
* 24775 24874: gap of unknown length
* 24875 29734: contig of 5099 bp in length
* 29734 29833: gap of unknown length
* 29834 35072: contig of 4859 bp in length
* 35072 35171: contig of 5238 bp in length
* 35171 42515: gap of unknown length
* 42515 42615: contig of 7344 bp in length
* 42615 51228: gap of unknown length
* 51228 51329: contig of 8613 bp in length
* 51329 60180: gap of unknown length
* 60180 60281: contig of 8852 bp in length
* 60281 68857: gap of unknown length
* 68857 79903: contig of 8576 bp in length
* 79903 80004: gap of unknown length
* 80004 93922: contig of 10947 bp in length
* 93922 94022: gap of unknown length
* 94022 109397: contig of 13919 bp in length
* 109397 109496: gap of unknown length
* 109496 127194: contig of 15374 bp in length
* 127194 127293: gap of unknown length
* 127293 145291: contig of 17697 bp in length
* 145291 145391: contig of 17998 bp in length
* 145391 162190: gap of unknown length
* 162190 162190: contig of 17999 bp in length.
FEATURES             .Location/Qualifiers
    1..162190
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="6"
    /clone="RP11-159G14"

```

```

BASE COUNT  48548 a 29894 c 30463 g 51262 t 2023 others
ORIGIN

```

```

Query Match      72.7% Score 40; DB 2; Length 162190;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 14 CACTTCAGTCAGGAATTCGAGATCAGCTGCCACATG 53
    |||||
Db 149897 CACTTCAGTCAGGAATTCGAGATCAGCTGCCACATG 149858
    |||||

```

```

RESULT 15
LOCUS AC097638 170330 bp DNA linear PRI 25-FEB-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-353H3, complete sequence.
ACCESSION AC097638
VERSION AC097638.2 GI:18874944
KEYWORDS HTG
SOURCE Homo sapiens.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170330)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 170330)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (20-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 170330)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.

```

```

TITLE Direct Submission
JOURNAL Unpublished
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 170330)
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.

```

# TITLE JOURNAL COMMENT

Direct Submission  
Submitted (25-FEB-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
On Feb 25, 2002 this sequence version replaced gi:15303437.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgctgs@u.washington.edu  
----- Project Information  
Center project name: chr-3  
Center clone name: RP11-353H3 (bc0380)  
----- Summary Statistics  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator ET; 92% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 170013 bases at least Q40  
Consensus quality: 170315 bases at least Q30  
Consensus quality: 170330 bases at least Q20  
Insert size: 170227; sum-of-contigs  
Quality coverage: 8.0x in Q20 bases; sum-of-contigs  
-----

Overlapping Sequences:  
5': RP11-316123 AC027592  
3': RP11-258N2 (UMGC:bc0637) AC024378  
-----  
Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
Genbank flat file format but are available as part  
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an  
alternate chemistry or covered by high quality data (i.e., Phred  
quality >= 30); an attempt was made to resolve all sequencing  
problems, such as compressions and repeats; all regions were  
covered by at least one plasmid subclone or more than one M13  
subclone; and the assembly was confirmed by restriction digest.  
-----  
Sequence Validation:  
This sequence has been validated by Multiple Complete Digest  
fingerprinting. Comparison of the experimentally derived digest  
fragments with sequence-predicted fragments is given below.  
The electronically-digested sequence consists of both insert and  
vector, in order to accurately represent the entire circular BAC.  
Small fragments below a variable cutoff (approximately 400-800 bp)  
are not resolved in the fingerprint and hence do not appear  
in the table. There are no significant remaining discrepancies  
between the experimental and predicted values. Uniquely ordered  
fragments are separated by dashed lines.  
-----  
BgIII EcoRI HindIII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
2325	2289	8696	8822	3039	3001
2067	2139	6	<800	6382	6486
5402	5514	18870	19040	512	<800
6080	6227	788	<800	449	<800
6593	6638	637	<800	6244	6256
2157	2139	1649	1609	14383	14433

46	<800	1126	1124	2075	2223	884	859	123	<800	776	806
4209	4178	1000	1062	2273	2223	4792	4710	2395	2485	3300	3264
128	<800	1526	1560	4614	4602	1108	1081	12934	12772	2236	2223
6712	6638	2145	2154	5281	5253	1765	1728	3843	3825	2223	2223
2817	2790	2641	2746	825	806	4110	4045	893	884	5130	5079
1261	1242	1153	1124	45	<800	728	<800	1605	1560	1835	1778
1899	2045	120	<800	4712	4602	9197	9115	4253	4220	1748	1778
659	<800	507	<800	2926	3001	14971	15022	2249	2234	280	<800
856	859	1935	1928	397	<800	1638	1593	10057	9933	217	<800
2132	2139	5481	5476	1696	1778	7966	7911	701	<800	711	<800
184	<800	3796	3825	1854	1930	3016	2950	2354	2358	1966	2040
2776	2950	909	956	7168	7232	2607	2552	2269	2234	412	<800
4596	4541	2055	2014	3416	3339	852	859	4013	3825	4296	4251
782	859	865	884	2984	3001	3016	2950	2354	2358	1966	2040
7579	7639	631	<800	5188	5079	2607	2552	2269	2234	412	<800
365	<800	1514	1462	1512	1482	852	859	4013	3825	4296	4251
928	859	3643	3606	8533	8484	7966	7911	701	<800	711	<800
3606	3555	2540	2642	2796	2816	3016	2950	2354	2358	1966	2040
2976	2950	2882	3085	3181	3264	3016	2950	2354	2358	1966	2040
865	859	3629	3606	1215	1166	2607	2552	2269	2234	412	<800
4748	4710	907	884	2989	3173	852	859	4013	3825	4296	4251
1729	1728	50	<800	3082	3001	3016	2950	2354	2358	1966	2040
1081	1081	1560	1560	1521	1482	2607	2552	2269	2234	412	<800
7175	7093	10518	10409	6228	6256	2607	2552	2269	2234	412	<800
1039	1081	824	813	616	<800	3016	2950	2354	2358	1966	2040
3147	3128	9	<800	5676	5551	2607	2552	2269	2234	412	<800
3249	3252	1076	1124	4665	4602	2607	2552	2269	2234	412	<800
814	859	1192	1124	338	<800	3016	2950	2354	2358	1966	2040
1897	1861	2257	2234	163	<800	2607	2552	2269	2234	412	<800
2556	2552	141	<800	1398	1368	2607	2552	2269	2234	412	<800
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Query Match 72.7%: Score 40: DB 9: Length 170330;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCCTGGCCCAACATG 53  
Db 122509 CACTTGAGGTCAGGAATTCGAGATCAGCCTGGCCCAACATG 122470

Search completed: June 17, 2003, 03:56:16  
Job time : 155.346 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 9.70963 Seconds  
(without alignments)

12756.396 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_4365\_4419

Perfect score: 55

Sequence: 1 gaggcaggcagacacttga.....atcagctgcgaacatgag 55

Scoring table: Oligo NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
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c 2	40	72.7	49999	20 AA223904 Human LOBO homolog
3	36	65.5	824	22 AAH03907 Human CDNA clone (
4	36	65.5	1524	22 AAH17143 Human CDNA sequenc
5	35	63.6	570	24 ABN65352 Human cancer relat
6	35	63.6	10740	22 AAK64788 Human immune/haema
7	25	45.5	218	24 ABL77817 Human ovarian canc
c 8	25	45.5	250	22 ABA16332 Human nervous syst
9	25	45.5	320	21 AAC05198 Human secreted pro

DNA encoding novel  
Human CDNA sequenc  
Human transporter  
Human nervous syst  
Human immune/haema  
Human immune/haema  
Human immune/haema  
Human genomic DNA  
Human immune/haema  
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Human immune/haema  
Human 3-hydroxy-3-  
Human HMGL gene,  
Human cDNA differe  
Genomic sequence #  
Genomic sequence #  
Human excretory re  
Human kidney relat  
Human immune/haema  
Human secreted pro  
Human immune/haema  
Human immune/haema  
Human polynucleoti  
Human prostate exp  
Human reproductive  
Human testicular a  
Human secreted pro  
Human nervous syst  
Human ovarian canc  
DNA encoding novel  
Human ovarian canc  
Human prostate exp  
Human cancer relat  
Human prostate exp  
Human nervous syst  
Human prostate exp  
Human nervous syst  
Human CDNA clone ( )  
Human CDNA clone ( )  
Human CDNA clone ( )  
Human prostate exp  
Human prostate exp  
Human prostate exp  
Human immune/haema  
Human inflammatory  
Human neuroblastom  
Human EST-derived  
Human gene express  
Human gene express  
Human prostate exp  
Human secreted pro  
Human cervical can  
Human immune/haema  
Human full-length  
Human reproductive  
Human testicular a  
Human CDNA encodin  
Human musculoskele  
Human immune/haema  
Human CDNA sequenc  
Human CDNA sequenc  
Human secreted pro  
Human CDNA sequenc  
Human AD4 gene gen  
Human genomic DNA  
Genomic sequence #  
Human immune/haema

C 83	24	43.6	2884	22	AAI60494	Human polynucleoti	156	24	43.6	121162	21	AA66548	Human kinesin-like
C 84	24	43.6	3089	22	AAK72379	Human immune/haema	157	24	43.6	122888	24	ABK83569	Human CDNA differe
C 85	24	43.6	3223	22	AAI36276	Human musculooskele	C 158	24	43.6	125439	24	ABQ88177	Human osteoblast d
C 86	24	43.6	3223	22	AAI36277	Human musculooskele	C 159	24	43.6	138183	21	AAK34791	Human adenosine re
C 87	24	43.6	3224	22	AAI36275	Human musculooskele	C 160	24	43.6	141589	21	AAK20913	Human ELAM-1 polyn
C 88	24	43.6	4015	22	AAK301490	Human secreted, pro	C 161	24	43.6	141589	21	AAK21127	Human low adenosin
C 89	24	43.6	5075	22	ABAI66701	Human nervous syst	C 162	24	43.6	141589	21	AAK21152	Human low adenosin
C 90	24	43.6	5076	22	ABAI66699	Human nervous syst	C 163	24	43.6	141589	21	AAK35005	Human adenosine re
C 91	24	43.6	5526	23	AAK76845	DNA encoding novel	C 164	24	43.6	141589	21	AAK35030	Human adenosine re
C 92	24	43.6	5734	22	AAK67406	Human immune/haema	C 165	24	43.6	145831	24	ABL62309	Colon adenocarcino
C 93	24	43.6	5778	22	AAK53086	Human polynucleoti	C 166	24	43.6	145831	24	ABL66806	Lung cancer relate
C 94	24	43.6	5804	22	AAK52102	Human polynucleoti	C 167	24	43.6	145831	24	ABL68588	Kidney cancer rela
C 95	24	43.6	5981	23	AAK23461	Human lung tumour-	C 168	24	43.6	145831	24	ABL69213	Prostate cancer re
C 96	24	43.6	6135	24	ABQ88237	Human osteoblast d	C 169	24	43.6	146981	21	AAK21442	Human ELAM-1 polyn
C 97	24	43.6	6598	22	AAI04660	Human reproductive	C 170	24	43.6	147708	24	ABK8154	Human CDNA differe
C 98	24	43.6	6598	23	ABL97567	Human testicular a	C 171	24	43.6	147724	24	ABK83566	Human CDNA differe
C 99	24	43.6	7686	22	ABAI4580	Human nervous syst	C 172	24	43.6	202973	21	AAK21437	Human factor-relat
C 100	24	43.6	8288	22	ABAI4581	Human nervous syst	C 173	24	43.6	222930	24	ABK84349	Human CDNA differe
C 101	24	43.6	9160	24	ABK69900	Human secreted pro	C 174	24	43.6	319608	21	AAH51601	Human chromosome 1
C 102	24	43.6	9266	24	ABK69899	Human secreted pro	C 175	24	43.6	319608	22	AAH509301	Human schizopreni
C 103	24	43.6	9268	24	ABK69898	Human secreted pro	C 176	24	43.6	325791	22	AAK43104	Human Oestrogen re
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C 110	24	43.6	14175	22	AAK27814	DNA encoding novel	C 183	23	41.8	420	22	AAI87441	Human polynucleoti
C 111	24	43.6	14175	22	AAK78859	Human immune/haema	C 184	23	41.8	443	22	AAK70738	Human immune/haema
C 112	24	43.6	14209	22	AAK89137	Human digestive sy	C 185	23	41.8	443	22	AAK70739	Human immune/haema
C 113	24	43.6	17357	22	AAK86680	Human immune/haema	C 186	23	41.8	443	22	AAK70741	Human immune/haema
C 114	24	43.6	17363	22	AAK86681	Human immune/haema	C 187	23	41.8	455	24	ABK83488	Human ovarian canc
C 115	24	43.6	17462	22	ABAI5655	Human nervous syst	C 188	23	41.8	488	24	ABK62650	Human cancer relat
C 116	24	43.6	17816	22	AAK33417	DNA encoding novel	C 189	23	41.8	492	23	ABV47522	Human prostate exp
C 117	24	43.6	19596	22	AAK73967	Human immune/haema	C 190	23	41.8	492	23	ABV47522	Human prostate exp
C 118	24	43.6	19596	22	AAK73968	Human immune/haema	C 191	23	41.8	500	23	ABV47522	Human prostate exp
C 119	24	43.6	21989	22	ABAI5942	Human nervous syst	C 192	23	41.8	509	24	ABK62664	Human cancer relat
C 120	24	43.6	22893	24	ABK12810	Human tumour suppr	C 193	23	41.8	519	23	ABV13595	Human prostate exp
C 121	24	43.6	22893	24	ABK12810	Human tumour suppr	C 194	23	41.8	519	23	ABV13595	Human prostate exp
C 122	24	43.6	25003	22	ABAI9679	Human immune/haema	C 195	23	41.8	566	22	AAH13293	Human CDNA clone (
C 123	24	43.6	25235	22	AAH45310	Human nervous syst	C 196	23	41.8	573	23	ABV23860	Human prostate exp
C 124	24	43.6	27333	22	ABAI9324	Human nervous syst	C 197	23	41.8	573	23	ABV23860	Human prostate exp
C 125	24	43.6	30625	24	ABK12808	Human tumour suppr	C 198	23	41.8	901	22	AAI97471	Human neuroblastom
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C 127	24	43.6	30826	22	ABAI07345	Human pancreatic c	C 200	23	41.8	2096	22	AAK07292	Human reproductive
C 128	24	43.6	30826	22	AAK32772	Human genomic DNA	C 201	23	41.8	2582	22	AAK94887	Human full-length
C 129	24	43.6	31584	22	AAK81054	Human immune/haema	C 202	23	41.8	2775	24	AAI43842	Human beta-glucuro
C 130	24	43.6	31749	22	AAK72959	Human immune/haema	C 203	23	41.8	2925	22	AAH79318	Human zinc finger
C 131	24	43.6	32199	22	AAK30296	Human digestive sy	C 204	23	41.8	3306	24	ABK41395	Human conjugated p
C 132	24	43.6	32199	22	AAI57673	Human colorectal c	C 205	23	41.8	3598	22	AAH18642	Human CDNA sequenc
C 133	24	43.6	32216	22	ABAI6118	Human nervous syst	C 206	23	41.8	4159	22	AAH16659	Human CDNA sequenc
C 134	24	43.6	33747	22	AAK69279	Human immune/haema	C 207	23	41.8	4167	22	AAK84449	Human immune/haema
C 135	24	43.6	33747	22	AAK73093	Human immune/haema	C 208	23	41.8	5814	22	AAK83448	Human immune/haema
C 136	24	43.6	34917	22	AAK70686	Human immune/haema	C 209	23	41.8	6088	22	AAK89200	Human digestive sy
C 137	24	43.6	38771	22	AAK81036	Human immune/haema	C 210	23	41.8	6096	22	AAK26766	Human genomic DNA
C 138	24	43.6	39198	22	AAK58067	Human polyamine-mo	C 211	23	41.8	6120	22	AAK86301	Human immune/haema
C 139	24	43.6	41684	21	AAK28150	Human purh gene ge	C 212	23	41.8	6801	22	AAK77606	Human immune/haema
C 140	24	43.6	44861	24	AAK20000	DNA encoding pyrid	C 213	23	41.8	6801	22	AAK77607	Human immune/haema
C 141	24	43.6	45993	24	AAK36070	Human liver glucok	C 214	23	41.8	6921	22	ABAI6675	Human nervous syst
C 142	24	43.6	46553	22	AAK67926	Human immune/haema	C 215	23	41.8	10038	22	AAK68407	Human immune/haema
C 143	24	43.6	46553	22	AAK81745	Human immune/haema	C 216	23	41.8	10113	22	AAK32838	Human immune/haema
C 144	24	43.6	47090	22	AAK68725	Human immune/haema	C 217	23	41.8	10139	22	AAK29226	Genomic sequence #
C 145	24	43.6	47090	22	AAK78219	Human immune/haema	C 218	23	41.8	10458	22	AAK77961	Human immune/haema
C 146	24	43.6	51474	22	AAK78219	Human neuroblastom	C 219	23	41.8	10855	22	AAK05277	Human reproductive
C 147	24	43.6	54108	24	ABK22782	Human high bone ma	C 220	23	41.8	10855	23	ABU98161	Human testicular a
C 148	24	43.6	57273	24	ABK22782	Human high bone ma	C 221	23	41.8	10985	22	AAK86420	Human immune/haema
C 149	24	43.6	58837	22	ABK52612	Human Claspin geno	C 222	23	41.8	10985	22	AAK86421	Human immune/haema
C 150	24	43.6	66937	22	ABA82625	Human HBM gene reg	C 223	23	41.8	10985	22	AAK86422	Human immune/haema
C 151	24	43.6	72049	22	ABA82623	Human HBM gene reg	C 224	23	41.8	11051	22	ABA08035	Human ovarian and
C 152	24	43.6	74037	22	ABK94412	DNA encoding endoc	C 225	23	41.8	11051	22	AAK06696	Human reproductive
C 153	24	43.6	78925	21	AAK69888	Human FN gene. Ho	C 226	23	41.8	11655	22	AAK32839	Human genomic DNA
C 154	24	43.6	109906	24	ABK94411	DNA encoding endoc	C 227	23	41.8	13927	22	AAK97853	Human neuroblastom
C 155	24	43.6	110096	24	ABN95044	Gene #1542 used to	C 228	23	41.8	15571	24	ABN95889	Gene #2387 used to

229	23	41.8	15571	24	ABL68256	Kidney cancer rela	c 302	22	40.0	16877	22	AAL36984	Human musculoskele
230	23	41.8	15571	24	ABL68528	Kidney cancer rela	c 303	22	40.0	18596	22	AAF31109	Thymidylate synth
c 231	23	41.8	16892	22	AAS39748	Genomic sequence #	c 304	22	40.0	18596	22	AAF31109	Thymidylate synth
c 232	23	41.8	16892	22	AAK80873	Human immune/haema	c 305	22	40.0	18596	22	ABN95092	Gene #1590 used to
c 233	23	41.8	16892	22	AAK89201	Human digestive sy	c 306	22	40.0	18596	24	ABK43334	Human Thymidylate
c 234	23	41.8	16892	22	AAK90086	Human digestive sy	c 307	22	40.0	18596	24	ABL62854	Breast cancer rela
c 235	23	41.8	17335	23	ABK423393	Genomic sequence #	c 308	22	40.0	18596	24	ABL63078	Breast cancer rela
c 236	23	41.8	17509	24	ABN95599	Gene #2097 used to	c 309	22	40.0	18596	24	ABL67927	Ovary cancer relat
c 237	23	41.8	18443	20	AAK83942	Bacterial artifici	310	22	40.0	19659	22	AAK64731	Human immune/haema
c 238	23	41.8	19882	23	ABK42394	Genomic sequence #	311	22	40.0	19659	22	AAK75600	Human immune/haema
c 239	23	41.8	22813	22	AAK65271	Human immune/haema	312	22	40.0	19659	22	AAK91504	Human digestive sy
c 240	23	41.8	22813	22	AAK82016	Human immune/haema	c 313	22	40.0	20210	22	AAK77417	Human immune/haema
c 241	23	41.8	22813	22	AAK86303	Human immune/haema	314	22	40.0	20210	22	AAK31519	Human DNA for a no
c 242	23	41.8	22813	22	AAK87333	Human immune/haema	315	22	40.0	20210	24	ABQ66843	Human polynucleoti
c 243	23	41.8	22900	22	AAK82210	Human immune/haema	c 316	22	40.0	22735	23	AAK87198	Human ion3 coding
c 244	23	41.8	25837	22	AAK85952	Human immune/haema	c 317	22	40.0	25950	22	AAK31518	Human DNA for a no
c 245	23	41.8	27571	22	ABK19222	Human nervous syst	c 318	22	40.0	25950	24	ABQ66842	Human polynucleoti
c 246	23	41.8	27572	22	ABK19222	Human nervous syst	c 319	22	40.0	29449	22	AAK16846	Human novel protei
c 247	23	41.8	30175	24	AAK32742	Human drug metabol	c 320	22	40.0	29449	22	AAK30343	DNA encoding rena
c 248	23	41.8	31132	22	AAK36697	Human musculoskele	321	22	40.0	31871	23	ABK42516	Genomic sequence #
c 249	23	41.8	31132	22	AAK36697	Human musculoskele	322	22	40.0	40742	22	AAK68089	Human immune/haema
c 250	23	41.8	32064	22	AAK29832	Human genomic DNA	323	22	40.0	40742	22	AAK79886	Human immune/haema
c 251	23	41.8	32169	22	ABK14358	Human cytoskeletal	c 324	22	40.0	51719	24	ABK31365	52Kb gene fragment
c 252	23	41.8	32176	22	AAK5628	Human nervous syst	c 325	22	40.0	81001	22	AAK30035	Human apolipoprote
c 253	23	41.8	32187	23	ABK42663	Human reproductive	c 326	22	40.0	92139	24	AAK31364	Human apolipoprote
c 254	23	41.8	32193	23	ABK42662	Genomic sequence #	c 327	22	40.0	119950	20	AAK90201	Human yes1 gene
c 255	23	41.8	32206	22	AAK89374	Genomic sequence #	c 328	22	40.0	149480	20	ABK61947	Colon adenocarcino
c 256	23	41.8	32250	22	AAK05627	Human digestive sy	c 329	22	40.0	149480	24	ABK61948	Colon adenocarcino
c 257	23	41.8	34680	22	AAK81232	Human reproductive	c 330	22	40.0	149480	24	ABK68365	Kidney cancer rela
c 258	23	41.8	34680	22	AAK85743	Human immune/haema	c 331	22	40.0	220895	24	ABK84798	Human cDNA differe
c 259	23	41.8	39353	22	AAK65396	Human immune/haema	c 332	22	40.0	465237	24	ABQ87681	Human oestrogen re
c 260	23	41.8	39353	22	AAK67232	Human immune/haema	c 333	22	40.0	465237	24	ABQ87681	Human oestrogen re
c 261	23	41.8	39358	22	AAK65397	Human immune/haema	c 334	21	38.2	51	21	AAI79826	Human Alu subfamil
c 262	23	41.8	39358	22	AAK67233	Human immune/haema	c 335	21	38.2	51	21	AAI79826	Human nonconservat
c 263	23	41.8	80240	20	AAK83940	NC-contig derived	c 336	21	38.2	98	22	AAK83970	Human immune/haema
c 264	23	41.8	80595	20	AAK83939	NC-contig derived	c 337	21	38.2	101	22	ABK19435	Human nervous syst
c 265	23	41.8	121162	21	AAK66548	Human kinesin-like	c 338	21	38.2	104	22	ABK19435	Human nervous syst
c 266	23	41.8	147708	24	ABQ88154	Human osteoblast d	c 339	21	38.2	104	22	ABK19435	Human nervous syst
c 267	23	41.8	148834	24	ABQ883570	Human cDNA differe	c 340	21	38.2	199	21	AAK16755	Human secreted pro
c 268	23	41.8	172570	24	ABQ88207	Human osteoblast d	c 341	21	38.2	272	22	AAH10435	Human cDNA clone (
c 269	22	40.0	81	21	AAK29919	Human secreted pro	c 342	21	38.2	295	23	ABK34122	Human prostate exp
c 270	22	40.0	90	22	AAK31036	Human digestive sy	c 343	21	38.2	295	23	ABK42984	Human prostate exp
c 271	22	40.0	90	22	AAS32071	Human liver associ	c 344	21	38.2	311	23	ABK34589	Human prostate exp
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c 274	22	40.0	313	22	AAK66501	Human immune/haema	c 347	21	38.2	335	14	AAO60863	Human brain expres
c 275	22	40.0	324	22	AAS40103	Human immune/haema	c 348	21	38.2	336	23	ABK15036	Human prostate exp
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c 278	22	40.0	389	22	AAS40374	DNA encoding human	c 351	21	38.2	355	23	ABK34589	Human prostate exp
c 279	22	40.0	389	22	AAK03972	DNA encoding human	c 352	21	38.2	355	23	ABK34589	Human prostate exp
c 280	22	40.0	389	22	AAK03974	Human reproductive	c 353	21	38.2	363	23	ABK36148	Human prostate exp
c 281	22	40.0	393	22	AAK192196	Human reproductive	c 354	21	38.2	364	23	ABK37603	Human prostate exp
c 282	22	40.0	400	22	AAK189040	Human polynucleoti	c 355	21	38.2	368	23	ABK10113	Human prostate exp
c 283	22	40.0	401	21	AAK98244	Human polynucleoti	c 356	21	38.2	368	23	ABK14736	Human prostate exp
c 284	22	40.0	457	23	ABK04426	Human colon cancer	c 357	21	38.2	369	23	ABK14736	Human prostate exp
c 285	22	40.0	459	24	ABN65237	Human prostate exp	c 358	21	38.2	370	23	ABK31584	Human prostate exp
c 286	22	40.0	503	24	ABK65847	Human cancer relat	c 359	21	38.2	374	23	ABK06008	Human prostate exp
c 287	22	40.0	503	24	ABK34891	Human cDNA encodin	c 360	21	38.2	374	23	ABK06008	Human prostate exp
c 288	22	40.0	594	22	AAK39398	cDNA encoding nove	c 361	21	38.2	374	23	ABK13851	Human prostate exp
c 289	22	40.0	768	22	AAK82462	Human digestive sy	c 362	21	38.2	375	23	ABK13851	Human prostate exp
c 290	22	40.0	768	22	AAK67842	Human immune/haema	c 363	21	38.2	376	23	ABK10046	Human prostate exp
c 291	22	40.0	768	22	AAK67845	Human immune/haema	c 364	21	38.2	378	23	ABK05867	Human prostate exp
c 292	22	40.0	786	22	AAK67847	Human immune/haema	c 365	21	38.2	378	23	ABK05867	Human prostate exp
c 293	22	40.0	786	22	ABQ89229	Human prostate exp	c 366	21	38.2	379	23	ABK10414	Human prostate exp
c 294	22	40.0	1123	22	ABK08720	Human secreted pro	c 367	21	38.2	379	23	ABK10414	Human prostate exp
c 295	22	40.0	1377	21	AAK69638	Human secreted pro	c 368	21	38.2	382	23	ABK13402	Human prostate exp
c 296	22	40.0	1434	24	ABK97051	Human 2-hydroxy ac	c 369	21	38.2	383	23	ABK10146	Human prostate exp
c 297	22	40.0	2482	22	AAH16305	Human cDNA sequenc	c 370	21	38.2	390	23	ABK13250	Human prostate exp
c 298	22	40.0	2512	22	AAH17890	Human cDNA sequenc	c 371	21	38.2	396	23	ABK13509	Human prostate exp
c 299	22	40.0	2816	22	ABA21323	Human nervous syst	c 372	21	38.2	399	23	ABK13592	Human prostate exp
c 300	22	40.0	9397	22	AAK78065	Human immune/haema	c 373	21	38.2	400	23	ABK34624	Human prostate exp
c 301	22	40.0	14991	22	AAS33441	DNA encoding human	c 374	21	38.2	403	23	ABK04340	Human prostate exp
	22	40.0	16877	22	ABA20494	Human nervous syst	c 375	21	38.2	403	23	ABK13433	Human prostate exp

c 375	21	38.2	403	23	ABV34058	Human prostate exp	c 448	21	38.2	559	23	ABV43378	Human prostate exp
c 376	21	38.2	406	22	AAI91420	Human polynucleoti	c 449	21	38.2	565	24	ABN63987	Human cancer relat
c 377	21	38.2	406	23	ABV34520	Human prostate exp	c 450	21	38.2	570	23	ABV40598	Human prostate exp
c 378	21	38.2	407	23	ABV31285	Human prostate exp	c 451	21	38.2	570	23	ABV43230	Human prostate exp
c 379	21	38.2	407	23	ABV34365	Human prostate exp	c 452	21	38.2	570	23	ABV43562	Human prostate exp
c 380	21	38.2	408	23	ABV34338	Human prostate exp	c 453	21	38.2	570	23	ABV43844	Human prostate exp
c 381	21	38.2	409	23	ABV35813	Human prostate exp	c 454	21	38.2	570	23	ABV43847	Human prostate exp
c 382	21	38.2	409	23	ABV31399	Human prostate exp	c 455	21	38.2	571	24	ABN62519	Human cancer relat
c 383	21	38.2	410	23	ABV00877	Human prostate exp	c 456	21	38.2	572	22	AAK69488	Human immune/haema
c 384	21	38.2	416	23	ABV34963	Human prostate exp	c 457	21	38.2	583	22	AAI92237	Human polynucleoti
c 385	21	38.2	417	22	AAK84004	Human immune/haema	c 458	21	38.2	583	24	ABN64637	Human cancer relat
c 386	21	38.2	419	23	ABV13473	Human prostate exp	c 459	21	38.2	589	23	ABV54592	Human prostate exp
c 387	21	38.2	419	23	ABV30889	Human prostate exp	c 460	21	38.2	609	22	AAH31418	Human secreted pro
c 388	21	38.2	419	23	ABV43408	Human prostate exp	c 461	21	38.2	613	23	ABV58362	Human prostate exp
c 389	21	38.2	420	23	ABV04077	Human prostate exp	c 462	21	38.2	619	24	ABN60465	Human cancer relat
c 390	21	38.2	420	23	ABV31317	Human prostate exp	c 463	21	38.2	627	23	ABV40286	Human prostate exp
c 391	21	38.2	421	23	ABV34935	Human prostate exp	c 464	21	38.2	627	23	ABV43800	Human prostate exp
c 392	21	38.2	421	23	ABV45205	Human prostate exp	c 465	21	38.2	655	23	ABV39857	Human prostate exp
c 393	21	38.2	422	23	ABV04050	Human prostate exp	c 466	21	38.2	667	22	AAI09720	Human breast cance
c 394	21	38.2	422	23	ABV05567	Human prostate exp	c 467	21	38.2	719	22	AAI96912	Human neuroblastom
c 395	21	38.2	422	23	ABV31218	Human prostate exp	c 468	21	38.2	732	22	AAI18392	Human breast cance
c 396	21	38.2	424	23	ABV04081	Human prostate exp	c 469	21	38.2	745	22	AAI04175	Human reproductive
c 397	21	38.2	425	23	ABV04233	Human prostate exp	c 470	21	38.2	812	24	ABQ89826	Human prostate exp
c 398	21	38.2	427	23	ABV34369	Human prostate exp	c 471	21	38.2	937	22	AAK73117	Human immune/haema
c 399	21	38.2	427	23	ABV43220	Human prostate exp	c 472	21	38.2	937	22	AAK87588	Human immune/haema
c 400	21	38.2	431	23	ABV10460	Human prostate exp	c 473	21	38.2	968	22	AAK52687	Human immune/haema
c 401	21	38.2	431	23	ABV55839	Human prostate exp	c 474	21	38.2	1002	22	AAK82253	Human immune/haema
c 402	21	38.2	432	22	AAI93171	Human polynucleoti	c 475	21	38.2	1061	22	ABA08722	Human secreted pro
c 403	21	38.2	432	23	ABV13887	Human prostate exp	c 476	21	38.2	1128	22	AAH72873	Human cervical can
c 404	21	38.2	435	23	ABV15355	Human prostate exp	c 477	21	38.2	1173	20	AAZ24883	Human secreted pro
c 405	21	38.2	437	23	ABV04654	Human prostate exp	c 478	21	38.2	1195	24	AAK62498	cDNA sequence #285
c 406	21	38.2	437	23	ABV37582	Human prostate exp	c 479	21	38.2	1361	23	ABK42147	Genomic sequence #
c 407	21	38.2	437	23	ABV43226	Human prostate exp	c 480	21	38.2	1391	22	AAK32591	Human genomic DNA
c 408	21	38.2	438	23	ABV13839	Human prostate exp	c 481	21	38.2	1808	23	ABK42148	Genomic sequence #
c 409	21	38.2	438	23	ABV34707	Human prostate exp	c 482	21	38.2	1808	23	ABK42149	Genomic sequence #
c 410	21	38.2	439	23	ABV13884	Human prostate exp	c 483	21	38.2	1906	21	AAZ26302	Human secreted pro
c 411	21	38.2	439	23	ABV42925	Human prostate exp	c 484	21	38.2	1954	22	AAK73112	Human immune/haema
c 412	21	38.2	440	23	ABV13246	Human prostate exp	c 485	21	38.2	1954	22	AAK73118	Human immune/haema
c 413	21	38.2	441	23	ABV04670	Human prostate exp	c 486	21	38.2	1954	22	AAK87581	Human immune/haema
c 414	21	38.2	441	23	ABV31630	Human prostate exp	c 487	21	38.2	1954	22	AAK87589	Human immune/haema
c 415	21	38.2	441	23	ABV3681	Human prostate exp	c 488	21	38.2	1963	22	AAK65736	Human immune/haema
c 416	21	38.2	441	23	ABV44907	Human prostate exp	c 489	21	38.2	1963	22	AAK65738	Human immune/haema
c 417	21	38.2	442	23	ABV04423	Human prostate exp	c 490	21	38.2	1963	22	AAK70033	Human immune/haema
c 418	21	38.2	442	23	ABV55150	Human prostate exp	c 491	21	38.2	1963	22	AAK70034	Human immune/haema
c 419	21	38.2	444	23	ABV35978	Human prostate exp	c 492	21	38.2	2349	22	AAI04170	Human reproductive
c 420	21	38.2	445	22	AAK32414	Human cDNA encodin	c 493	21	38.2	2349	22	AAI04171	Human reproductive
c 421	21	38.2	446	23	ABV07674	Human prostate exp	c 494	21	38.2	2361	22	AAH14258	Human cDNA sequenc
c 422	21	38.2	446	23	ABV43445	Human prostate exp	c 495	21	38.2	2455	22	AAK64162	Human cDNA P776P s
c 423	21	38.2	446	23	ABV43480	Human prostate exp	c 496	21	38.2	2455	22	AAK64163	Human cDNA P776P s
c 424	21	38.2	448	23	ABV36436	Human prostate exp	c 497	21	38.2	2455	22	AAH93926	P776P full length
c 425	21	38.2	450	23	ABV34996	Human prostate exp	c 498	21	38.2	2455	22	AAH93927	P776P full length
c 426	21	38.2	450	23	ABV40552	Human prostate exp	c 499	21	38.2	2455	24	ABL95533	Human P776P splice
c 427	21	38.2	450	23	ABV45041	Human prostate exp	c 500	21	38.2	2455	24	ABL95534	Human P776P splice
c 428	21	38.2	451	23	ABV36710	Human prostate exp	c 501	21	38.2	2470	22	AAH31369	Human secreted pro
c 429	21	38.2	451	23	ABV44902	Human prostate exp	c 502	21	38.2	2610	22	AAK69595	Human immune/haema
c 430	21	38.2	451	23	ABV44016	Human prostate exp	c 503	21	38.2	2956	22	AAH18381	Human cDNA sequenc
c 431	21	38.2	451	23	ABK41641	cDNA encoding nove	c 504	21	38.2	3022	22	AAH47883	Human Polyisopreny
c 432	21	38.2	452	23	ABV04718	Human prostate exp	c 505	21	38.2	3022	22	AAK92140	Prostate cancer-as
c 433	21	38.2	470	22	AAI91794	Human polynucleoti	c 506	21	38.2	3350	21	AAZ40700	Human EGFR poly
c 434	21	38.2	471	23	ABV40188	Human prostate exp	c 507	21	38.2	3350	22	AAK83868	Human immune/haema
c 435	21	38.2	471	23	ABV40254	Human prostate exp	c 508	21	38.2	3422	22	AAK67565	Human immune/haema
c 436	21	38.2	471	23	ABV43460	Human prostate exp	c 509	21	38.2	3422	22	AAK68610	Human immune/haema
c 437	21	38.2	471	23	ABV43812	Human prostate exp	c 510	21	38.2	3422	22	AAK68610	Human immune/haema
c 438	21	38.2	471	23	ABV44613	Human prostate exp	c 511	21	38.2	3422	22	AAK68610	Human immune/haema
c 439	21	38.2	479	23	ABV34999	Human prostate exp	c 512	21	38.2	3422	22	AAK68610	Human immune/haema
c 440	21	38.2	487	23	ABV13001	Human prostate exp	c 513	21	38.2	3422	22	AAK68610	Human immune/haema
c 441	21	38.2	498	23	ABV12933	Human prostate exp	c 514	21	38.2	3422	22	AAK68610	Human immune/haema
c 442	21	38.2	505	23	ABV13823	Human prostate exp	c 515	21	38.2	3422	22	AAK68610	Human immune/haema
c 443	21	38.2	505	24	ABN65626	Human cancer relat	c 516	21	38.2	3422	22	AAK68610	Human immune/haema
c 444	21	38.2	522	24	ABN64650	Human cancer relat	c 517	21	38.2	3422	22	AAK68610	Human immune/haema
c 445	21	38.2	524	23	ABV03832	Human prostate exp	c 518	21	38.2	3422	22	AAK68610	Human immune/haema
c 446	21	38.2	541	24	ABN60569	Human cancer relat	c 519	21	38.2	3422	22	AAK68610	Human immune/haema
c 447	21	38.2	558	24	ABQ56499	Human colon cancer	c 520	21	38.2	3422	22	AAK68610	Human immune/haema

C 521	21	38.2	9236	22	AAS03689	Rhesus gene locus:	594	21	38.2	34658	22	AAK69489	Human immune/haema
C 522	21	38.2	9236	22	AAS03690	Rhesus gene locus:	C 595	21	38.2	34831	22	ABK82518	Human immune/haema
C 523	21	38.2	9241	22	AAS03688	Rhesus gene locus:	C 596	21	38.2	35973	22	ABK13076	Human amyloid beta
C 524	21	38.2	10221	22	AAF58417	Human oligonucleot	C 597	21	38.2	37736	22	AAK86139	Human immune/haema
C 525	21	38.2	10545	22	AAK59132	Human ABC1 gene ex	C 598	21	38.2	39068	22	AAK71820	Human immune/haema
C 526	21	38.2	11244	22	AAK74606	Human immune/haema	C 599	21	38.2	39068	22	AAK73078	Human immune/haema
C 527	21	38.2	11655	22	AAK71335	Human immune/haema	C 600	21	38.2	39068	22	AAK85294	Human immune/haema
C 528	21	38.2	11860	22	ABA21528	Human nervous syst	C 601	21	38.2	39068	22	AAK87544	Human immune/haema
C 529	21	38.2	12221	22	AAK71585	Human immune/haema	C 602	21	38.2	39110	22	AAK71825	Human immune/haema
C 530	21	38.2	12542	22	AAS26800	Human genomic DNA	C 603	21	38.2	39110	22	AAK73087	Human immune/haema
C 531	21	38.2	12718	24	ABK52229	CDNA encoding huma	C 604	21	38.2	39110	22	AAK87555	Human immune/haema
C 532	21	38.2	13216	22	AAK73092	Human immune/haema	C 605	21	38.2	39887	22	AAK79153	Human immune/haema
C 533	21	38.2	13216	22	AAK87561	Human immune/haema	C 606	21	38.2	39887	22	AAK91263	Human immune/haema
C 534	21	38.2	13333	22	AAK79541	Human immune/haema	C 607	21	38.2	40308	22	AAK68184	Human immune/haema
C 535	21	38.2	14282	22	AAK68418	Human immune/haema	C 608	21	38.2	40308	22	ABO88150	Human osteoblast d
C 536	21	38.2	15090	22	AAK72319	Human immune/haema	C 609	21	38.2	44100	21	ABN97975	Human retroviral s
C 537	21	38.2	15090	24	ABK69842	Human secreted pro	C 610	21	38.2	44100	22	AAK77833	Human immune/haema
C 538	21	38.2	15090	24	ABK69842	Human secreted pro	C 611	21	38.2	44354	22	AAK77836	Human immune/haema
C 539	21	38.2	15296	22	AAK74605	Human immune/haema	C 612	21	38.2	44354	22	AAK77837	Human immune/haema
C 540	21	38.2	15783	22	AAS39803	Genomic sequence #	C 613	21	38.2	45300	22	AAK73079	Human immune/haema
C 541	21	38.2	15783	22	AAK90159	Human digestive sy	C 614	21	38.2	45300	22	AAK87547	Human immune/haema
C 542	21	38.2	16281	22	AAK70314	Human immune/haema	C 615	21	38.2	56093	24	ABL61744	Colon adenocarcino
C 543	21	38.2	16281	23	ABK42480	Genomic sequence #	C 616	21	38.2	68804	24	ABK67050	Human transporter
C 544	21	38.2	16285	22	AAK70315	Human immune/haema	C 617	21	38.2	81001	22	AAF30035	Human apolipoprote
C 545	21	38.2	16285	22	AAK70316	Human immune/haema	C 618	21	38.2	84495	24	AAS20588	Human methionine a
C 546	21	38.2	16285	23	ABK42481	Genomic sequence #	C 619	21	38.2	106746	21	AAA10225	Human PCTA-1 genom
C 547	21	38.2	16285	23	ABK42482	Genomic sequence #	C 620	21	38.2	109201	24	ABO88125	Human osteoblast d
C 548	21	38.2	16579	22	ABA20363	Human nervous syst	C 621	21	38.2	110096	24	ABN95044	Gene #1542 used to
C 549	21	38.2	16579	22	AAK05755	Human reproductive	C 622	21	38.2	126512	24	ABN83429	Human transporter
C 550	21	38.2	16817	22	AAK87099	Human immune/haema	C 623	21	38.2	128978	24	ABK83459	Human cDNA differe
C 551	21	38.2	17154	22	AAK64803	Human immune/haema	C 624	21	38.2	138169	21	AAA34791	Human adenosine re
C 552	21	38.2	17687	22	AAS42069	Genomic sequence #	C 625	21	38.2	139904	24	ABK83562	Human cDNA differe
C 553	21	38.2	18636	22	AAS12088	Human tumour necro	C 626	21	38.2	139904	24	ABK83562	Human cDNA differe
C 554	21	38.2	19815	22	AAS42064	Genomic sequence #	C 627	21	38.2	141589	21	AAK20913	Human ELAM-1 polyn
C 555	21	38.2	20991	22	AAK87545	Human immune/haema	C 628	21	38.2	141589	21	AAK21127	Human low adenosin
C 556	21	38.2	21596	22	AAK71582	Human immune/haema	C 629	21	38.2	141589	21	AAK21152	Human low adenosin
C 557	21	38.2	21747	22	AAK76413	Human immune/haema	C 630	21	38.2	141589	21	AAA35005	Human adenosine re
C 558	21	38.2	23934	22	ABA19145	Human nervous syst	C 631	21	38.2	141589	21	AAA35030	Human ELAM-1 polyn
C 559	21	38.2	23934	22	AAK36171	Human musculoskele	C 632	21	38.2	146981	21	AAK21442	Human ELAM-1 polyn
C 560	21	38.2	23934	22	AAK36179	Human musculoskele	C 633	21	38.2	165199	24	ABK83460	Human cDNA differe
C 561	21	38.2	23934	22	AAK04522	Human reproductive	C 634	21	38.2	169739	24	ABO88186	Human osteoblast d
C 562	21	38.2	23934	22	AAS28343	Genomic sequence #	C 635	21	38.2	178896	24	ABO88186	Human osteoblast d
C 563	21	38.2	23934	22	AAK71442	Human immune/haema	C 636	21	38.2	183999	22	AAK92831	Human ABC1 genomic
C 564	21	38.2	23934	23	ABL97446	Human testicular a	C 637	21	38.2	201143	24	ABK83568	Human DNA differe
C 565	21	38.2	25231	22	AAK03112	Human reproductive	C 638	21	38.2	209273	21	AAK21437	Human factor-relat
C 566	21	38.2	26225	22	AAS35776	Human cardiovascular	C 639	21	38.2	227968	24	ABK83497	Human cDNA differe
C 567	21	38.2	26277	22	AAK70428	Human immune/haema	C 640	21	38.2	240825	22	AAK24497	Human PS-3 gene.
C 568	21	38.2	26372	22	AAK77103	Human immune/haema	C 641	21	38.2	302250	24	ABL67703	Oesophagus cancer
C 569	21	38.2	26928	24	ABN95780	Human prothrombin	C 642	21	38.2	302250	24	ABL67703	Oesophagus cancer
C 570	21	38.2	26928	24	ABN95780	Gene #2278 used to	C 643	21	38.2	302250	24	ABL67703	Human neurogulin-1
C 571	21	38.2	27118	22	ABA08223	Human ovarian and	C 644	21	38.2	1503900	22	AAK95240	Human neurogulin-1
C 572	21	38.2	27118	22	AAK07542	Human reproductive	C 645	21	38.2	1503900	22	AAK95240	Human nonconservat
C 573	21	38.2	27681	22	AAS36497	Human cardiovascular	C 646	21	38.2	1503900	22	AAK95240	Human digestive sy
C 574	21	38.2	27681	22	AAS36498	Human cardiovascular	C 647	21	38.2	1503900	22	AAK95240	Human liver associ
C 575	21	38.2	27681	22	AAK85843	Human immune/haema	C 648	21	38.2	1503900	22	AAK95240	Human liver antige
C 576	21	38.2	27960	22	AAK69779	Human immune/haema	C 649	21	38.2	1503900	22	AAK95240	Human immune/haema
C 577	21	38.2	27960	22	AAK73320	Human immune/haema	C 650	21	38.2	1503900	22	AAK95240	Human immune/haema
C 578	21	38.2	32169	22	ABA14358	Human nervous syst	C 651	21	38.2	1503900	22	AAK95240	Human immune/haema
C 579	21	38.2	32169	22	ABA19573	Human nervous syst	C 652	21	38.2	1503900	22	AAK95240	Human immune/haema
C 580	21	38.2	32169	22	AAK05917	Human reproductive	C 653	21	38.2	1503900	22	AAK95240	Human gene signatu
C 581	21	38.2	32169	23	ABL98481	Human testicular a	C 654	21	38.2	1503900	22	AAK95240	Human immune/haema
C 582	21	38.2	32169	23	ABK43076	Genomic sequence #	C 655	21	38.2	1503900	22	AAK95240	Human secreted pro
C 583	21	38.2	32189	22	ABA16341	Human nervous syst	C 656	21	38.2	1503900	22	AAK95240	Human secreted pro
C 584	21	38.2	32189	22	ABA17492	Human nervous syst	C 657	21	38.2	1503900	22	AAK95240	Human excretory re
C 585	21	38.2	32189	22	ABA17790	Human nervous syst	C 658	21	38.2	1503900	22	AAK95240	Human kidney relat
C 586	21	38.2	32189	22	ABA19572	Human nervous syst	C 659	21	38.2	1503900	22	AAK95240	Human ovarian cunc
C 587	21	38.2	32189	22	AAK36926	Human musculoskele	C 660	21	38.2	1503900	22	AAK95240	Human immune/haema
C 588	21	38.2	32189	22	AAK05916	Human reproductive	C 661	21	38.2	1503900	22	AAK95240	Human secreted pro
C 589	21	38.2	32189	23	ABL98480	Human testicular a	C 662	21	38.2	1503900	22	AAK95240	Human secreted pro
C 590	21	38.2	32190	22	AAK62927	Human genomic DNA	C 663	21	38.2	1503900	22	AAK95240	Gene #129 used to
C 591	21	38.2	32191	22	AAS32492	Human genomic DNA	C 664	21	38.2	1503900	22	AAK95240	Oesophagus cancer
C 592	21	38.2	32249	22	AAK62932	Human genomic DNA	C 665	21	38.2	1503900	22	AAK95240	Human ovarian cunc
C 593	21	38.2	33971	22	AAK69257	Human immune/haema	C 666	21	38.2	1503900	22	AAK95240	Human ovarian cunc

667	20	36.4	379	22	AAI87138	Human polynucleoti
668	20	36.4	392	22	AAI86178	Human polynucleoti
669	20	36.4	394	22	AAK67893	Human immune/haema
670	20	36.4	394	22	AAK67894	Human immune/haema
671	20	36.4	395	22	AAK67895	Human immune/haema
672	20	36.4	395	22	ABV16854	Human prostate exp
673	20	36.4	401	22	AAK64793	Novel human polynu
674	20	36.4	404	22	ABV10116	Human prostate exp
675	20	36.4	405	22	AAI83828	Human polynucleoti
676	20	36.4	406	22	AAI20753	Human breast cance
677	20	36.4	408	22	AAI11863	Human breast cance
678	20	36.4	410	22	ABV16846	Human prostate exp
679	20	36.4	415	22	AAI17159	Human breast cance
680	20	36.4	419	22	AAI17164	Human breast cance
681	20	36.4	421	22	AAK78678	Human immune/haema
682	20	36.4	421	22	ABV00947	Human prostate exp
683	20	36.4	423	24	ABL83796	Human ovarian can
684	20	36.4	424	21	AAC26715	Human secreted pro
685	20	36.4	425	24	ABL87604	Human ovarian can
686	20	36.4	432	22	AAI09270	Human breast cance
687	20	36.4	433	23	ABL16862	Human prostate exp
688	20	36.4	437	22	ABAI6769	Human nervous syst
689	20	36.4	439	22	ABAI6768	Human nervous syst
690	20	36.4	439	22	ABAI6770	Human nervous syst
691	20	36.4	445	22	AAK04524	Human reproductive
692	20	36.4	445	23	ABL97448	Human testicular a
693	20	36.4	450	24	ABN62921	Human cancer relat
694	20	36.4	455	23	ABV31288	Human prostate exp
695	20	36.4	455	23	ABV40257	Human prostate exp
696	20	36.4	464	22	AAI09275	Human breast cance
697	20	36.4	466	22	AAK63934	Human immune/haema
698	20	36.4	468	23	ABV46659	Human prostate exp
699	20	36.4	475	23	ABV46651	Human prostate exp
700	20	36.4	477	22	AAI188593	Human polynucleoti
701	20	36.4	481	23	ABV46643	Human prostate exp
702	20	36.4	491	22	AAI05281	Human reproductive
703	20	36.4	491	23	ABL98165	Human testicular a
704	20	36.4	493	22	AAI44750	Human breast cance
705	20	36.4	509	22	AAH09751	Human cDNA clone (
706	20	36.4	517	23	ABV51695	Human prostate exp
707	20	36.4	519	24	ABN62837	Human cancer relat
708	20	36.4	533	22	AAH13155	Human cDNA clone (
709	20	36.4	535	22	AAI12785	Human breast cance
710	20	36.4	556	22	ABN65570	Human cancer relat
711	20	36.4	562	22	AAH10364	Human cDNA clone (
712	20	36.4	565	24	ABN64610	Human cancer relat
713	20	36.4	570	22	AAH09368	Human cDNA clone (
714	20	36.4	572	23	ABV58617	Human prostate exp
715	20	36.4	581	22	AAK64519	Human immune/haema
716	20	36.4	583	24	ABN61233	Human cancer relat
717	20	36.4	599	22	AAI21656	Human breast cance
718	20	36.4	599	22	AAI23612	Human breast cance
719	20	36.4	614	24	ABN65960	Human cancer relat
720	20	36.4	615	23	ABV52452	Human prostate exp
721	20	36.4	623	22	AAI12256	Human breast cance
722	20	36.4	742	22	AAI196647	Human neuroblastom
723	20	36.4	758	23	ABV20606	Human prostate exp
724	20	36.4	758	23	ABV20624	Human prostate exp
725	20	36.4	758	23	ABV20706	Human prostate exp
726	20	36.4	758	23	ABV26446	Human prostate exp
727	20	36.4	758	23	ABV26465	Human prostate exp
728	20	36.4	758	23	ABV26548	Human prostate exp
729	20	36.4	777	22	AAK93642	Human immune/haema
730	20	36.4	826	22	AAK78909	Human immune/haema
731	20	36.4	839	22	AAI197451	Human neuroblastom
732	20	36.4	846	24	ABT04077	Human ovary specif
733	20	36.4	898	22	AAK71188	Human immune/haema
734	20	36.4	908	22	AAK78673	Human immune/haema
735	20	36.4	911	22	AAI21135	Human breast cance
736	20	36.4	927	23	AAK69262	DNA encoding novel
737	20	36.4	1005	22	AAK79470	Human immune/haema
738	20	36.4	1005	22	AAK79471	Human immune/haema
739	20	36.4	1129	22	ABAI19926	Human nervous syst
740	20	36.4	1159	22	AAH13849	Human cDNA sequenc
741	20	36.4	1237	21	AAC59111	Human secreted pro
742	20	36.4	1397	22	ABAI4291	Human nervous syst
743	20	36.4	1535	21	AAC60999	Human vesicle asso
744	20	36.4	1628	22	ABAI13358	Human nervous syst
745	20	36.4	1639	22	AAK33044	Human secreted pro
746	20	36.4	1826	22	AAH16610	Human cDNA sequenc
747	20	36.4	1904	21	AAC81106	Human secreted pro
748	20	36.4	2135	24	ABU55770	Human TNFR/NGFR pr
749	20	36.4	2233	22	AAK72556	Human immune/haema
750	20	36.4	2240	22	AAH43612	Human uroplakin II
751	20	36.4	2240	22	AAH70144	Human uroplakin II
752	20	36.4	2240	23	AAF87241	Uroplakin II-TRE f
753	20	36.4	2304	22	AAK89139	Human digestive sy
754	20	36.4	2304	22	AAS31887	Human liver associ
755	20	36.4	2304	24	ABN90242	Human liver antige
756	20	36.4	2405	22	AAH17253	Human cDNA sequenc
757	20	36.4	2581	24	AAS62492	cDNA sequence #279
758	20	36.4	2696	22	AAI07233	Human reproductive
759	20	36.4	2696	22	AAI07235	Human reproductive
760	20	36.4	2696	23	ABU98781	Human testicular a
761	20	36.4	2696	23	ABU98783	Human testicular a
762	20	36.4	3419	22	ABAI15562	Human nervous syst
763	20	36.4	3420	22	ABAI15563	Human nervous syst
764	20	36.4	3441	24	ABU53963	Leukaemia-associat
765	20	36.4	4593	22	AAK94929	Human full-length
766	20	36.4	4608	22	AAK74675	Human immune/haema
767	20	36.4	4610	22	AAK74677	Human immune/haema
768	20	36.4	4747	22	ABAI07815	Human ovarian and
769	20	36.4	4747	22	AAI03617	Human reproductive
770	20	36.4	5564	22	AAK81104	Human immune/haema
771	20	36.4	6073	22	AAK82558	Human immune/haema
772	20	36.4	6074	22	AAK82559	Human immune/haema
773	20	36.4	6159	22	AAK75604	Human immune/haema
774	20	36.4	6164	22	AAK75613	Human immune/haema
775	20	36.4	6165	22	AAK75603	Human immune/haema
776	20	36.4	6167	22	AAK75609	Human immune/haema
777	20	36.4	6248	22	AAI98941	Human excretory re
778	20	36.4	6248	22	AAI63291	Human kidney relat
779	20	36.4	6252	22	AAI98940	Human excretory re
780	20	36.4	6252	22	AAI63290	Human kidney relat
781	20	36.4	6259	22	AAK83975	Human immune/haema
782	20	36.4	6426	22	ABA20567	Human nervous syst
783	20	36.4	6618	22	ABAI18101	Human nervous syst
784	20	36.4	6960	22	AAK85579	Human immune/haema
785	20	36.4	7703	22	AAK90904	Human digestive sy
786	20	36.4	7703	22	AAK90945	Human digestive sy
787	20	36.4	7703	22	AAS31939	Human liver associ
788	20	36.4	7703	22	AAS31980	Human liver associ
789	20	36.4	7703	24	ABN90294	Human liver antige
790	20	36.4	7703	24	ABN90335	Human immune/haema
791	20	36.4	7760	22	AAK74676	Human immune/haema
792	20	36.4	7849	16	AAQ94109	HML encoding novel
793	20	36.4	7890	22	AAS27697	DNA encoding novel
794	20	36.4	8308	22	AAK68091	Human immune/haema
795	20	36.4	8308	22	AAK79820	Human immune/haema
796	20	36.4	8514	22	AAK81530	Human immune/haema
797	20	36.4	9324	22	AAK75610	Human immune/haema
798	20	36.4	9339	22	AAI02697	Human reproductive
799	20	36.4	10093	22	ABAI07820	Human ovarian and
800	20	36.4	10093	22	AAI03622	Human reproductive
801	20	36.4	10093	22	AAK68011	Human immune/haema
802	20	36.4	10515	24	ABK10772	Human small induci
803	20	36.4	10515	24	ABK10772	Human small induci
804	20	36.4	10612	22	AAI36946	Human musculoskele
805	20	36.4	10614	22	AAI36948	Human musculoskele
806	20	36.4	10842	21	AAI51381	Chromosome 16q tum
807	20	36.4	10901	22	AAI03236	Human reproductive
808	20	36.4	12026	22	AAK67211	Human immune/haema
809	20	36.4	12169	22	AAK61443	Human immune/haema
810	20	36.4	12309	22	AAK89483	Human digestive sy
811	20	36.4	12309	22	AAK90834	Human digestive sy
812	20	36.4	13204	20	AAZ32189	Human platelet gly





c 959 19 34.5 612 22 AAK38255 Human digestive sy  
c 960 19 34.5 614 22 ABA12806 Human nervous syst  
c 961 19 34.5 653 22 ABQ57345 Human colon cancer  
c 962 19 34.5 705 22 AAK68041 Human immune/haema  
c 963 19 34.5 725 20 AAZ15035 Human gene express  
c 964 19 34.5 783 22 ABA18325 Human nervous syst  
c 965 19 34.5 811 20 AAX20485 Human secreted pro  
c 966 19 34.5 814 22 AAH03306 Human cDNA clone (  
c 967 19 34.5 817 24 ABQ92220 Human prostate exp  
c 968 19 34.5 823 22 AAH06772 Human cDNA clone (  
c 969 19 34.5 839 22 AAK62054 Human immune/haema  
c 970 19 34.5 858 22 AAI97921 Human neuroblastom  
c 971 19 34.5 867 23 ABV28810 Human prostate exp  
c 972 19 34.5 904 24 ABL53184 Nucleotide sequenc  
c 973 19 34.5 954 22 AAK73641 Human immune/haema  
c 974 19 34.5 954 22 AAK73641 Human immune/haema  
c 975 19 34.5 1027 22 AAS39719 Genomic sequence #  
c 976 19 34.5 1027 22 AAS39720 Genomic sequence #  
c 977 19 34.5 1027 22 AAK90061 Human digestive sy  
c 978 19 34.5 1027 22 AAK90062 Human digestive sy  
c 979 19 34.5 1071 22 AAK78073 Human immune/haema  
c 980 19 34.5 1071 22 AAK78075 Human immune/haema  
c 981 19 34.5 1071 22 AAK78077 Human immune/haema  
c 982 19 34.5 1121 22 AAK75957 Human immune/haema  
c 983 19 34.5 1121 22 AAK6278 Human immune/haema  
c 984 19 34.5 1179 22 AAH16951 Human cDNA sequenc  
c 985 19 34.5 1209 22 AAK82755 Human immune/haema  
c 986 19 34.5 1225 22 AAH99064 Human EST-derived  
c 987 19 34.5 1313 24 ABK12347 Human nonerythroid  
c 988 19 34.5 1325 22 AAK63203 Human immune/haema  
c 989 19 34.5 1349 24 AAS15585 DNA encoding human  
c 990 19 34.5 1383 22 AAL05637 Human reproductive  
c 991 19 34.5 1420 18 AAT72167 Alzheimer's diseas  
c 992 19 34.5 1482 22 AAS33428 DNA encoding human  
c 993 19 34.5 1492 21 AAA51403 Chromosome 16q tum  
c 994 19 34.5 1505 22 AAH99119 Human EST-derived  
c 995 19 34.5 1590 22 AAH13675 Human cDNA sequenc  
c 996 19 34.5 1727 22 AAH18282 Human cDNA sequenc  
c 997 19 34.5 1734 22 AAH16375 Human cDNA sequenc  
c 998 19 34.5 1740 22 ABA18100 Human nervous syst  
c 999 19 34.5 1776 22 AAH31393 Human secreted pro  
c1000 19 34.5 2120 22 AAS21280 Human cDNA sequenc

## ALIGNMENTS

RESULT 1  
AAA64507  
ID AAA64507 standard; DNA; 9048 BP.

XX AAK64507;

AC AAK64507;

XX 02-JAN-2001 (first entry)

XX Nucleotide sequence comprising the human FEZ1 gene.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
XX tumour proliferation; tubulin; microtubule; protein Efr-gamma;  
XX tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
XX cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
XX tumorigenesis; tumour survival; metastasis; ss.

OS Homo sapiens.

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human  
XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
XX cancer -

XX Claim 2; Fig 5A; 255bp; English.

XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour  
XX suppressor gene, located at chromosome location 8p22. Decreased or no  
XX expression of FEZ1 is detected in a variety of cancer cells. Expression  
XX of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts  
XX with tubulin, with microtubules, and with protein Efr-gamma.XX Post-translational phosphorylation and dephosphorylation modulates the  
XX effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are  
XX useful for inducing cells to proliferate. Compounds which modulate FEZ1  
XX association with tubulin are useful for alleviating tubulin hyper- or  
XX hypo- polymerisation disorders, such as those associated with aberrant  
XX initiation of mitosis, modulation of the initiation and rate of cell  
XX proliferation and cell growth, modulation of cell shape, cell rigidity,  
XX cell motility, rate and stage of cellular DNA replication, intracellular  
XX distribution of organelles, metastatic potential of cell and cellular  
XX transformation from a non-cancerous to cancerous phenotype. Compounds  
XX which modulate FEZ1 binding and phosphorylation are also useful for  
XX alleviating a disorder, such as tumorigenesis, tumour survival, growth  
XX and metastasis.

XX Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;

XX Query Match 100.0%; Score 55; DB 21; Length 9048;

XX Best Local Similarity 100.0%; Pred. No. 3.1e-19;

XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGGACGACCTTGGAGTCAGGAATTCGAGATCAGCCTGGCCACATGAG 55

Db 4365 GAGCAGGACGACCTTGGAGTCAGGAATTCGAGATCAGCCTGGCCACATGAG 4419

## RESULT 2

AAZ23904/C

ID AAZ23904 standard; DNA; 49999 BP.

XX AAZ23904;

XX 25-JAN-2000 (first entry)

XX Human LOBO homologue genomic DNA fragment 6.

XX LOBO; long bones; bone development; bone extension; skull; osteopathic;  
XX diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;  
XX spondyloepiphyseal dysplasia; achondroplasia; human; ds.

XX Homo sapiens.

XX WO9950284-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-EF02055.

XX 27-MAR-1998; 98DE-1013799.

XX (ROSE/) ROSENTHAL A.

XX Rosenthal A, Rump A, Hess J, Aigner T, Wirth T;

XX WPI; 1999-601320/51.

XX Nucleic acids encoding proteins which influence bone development,  
XX PT



PT useful for treating and studying bone disorders -

PS Example 3; Page 356-384; 391pp; German.

XX This invention describes novel nucleic acids (I; designated LOBO (long  
XX bones)) encoding proteins influencing bone development in mammals. The  
XX proteins of the invention reduce and/or inactivate bone extension (i.e.  
XX development), with exception of the skull and have osteopathic activity.  
XX The nucleic acid molecules, proteins and antibodies can be used in  
XX diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods  
XX and nucleic acid molecules, etc. are useful for production of transgenic  
XX animals, especially a transgenic mouse for the study of diseases  
XX associated with bone development, e.g. spondyloepiphyseal dysplasia and  
XX achondroplasia. This sequence encodes a human LOBO protein described  
XX in the method of the invention.

SQ Sequence 49999 BP; 10382 A; 14932 C; 14107 G; 10578 T; 0 other;

Query Match 72.7%; Score 40; DB 20; Length 49999;

Best Local Similarity 100.0%; Pred. No. 1.7e-11;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53

Db 24864 CACTTGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 24825

RESULT 3

AAH03907

ID AAH03907 standard; cDNA; 824 BP.

AC AAH03907;

XX 26-JUN-2001 (first entry)

XX Human cDNA clone (5'-primer) SEQ ID NO:742.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602

XX full-length cDNAs defined in the specification, and for the detection

XX and/or diagnosis of the abnormality of the proteins encoded by the

XX full-length cDNAs -

XX Claim 1; SEQ ID 742; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602

XX full-length cDNAs defined in the specification. Where a primer set

XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary

XX to the complementary strand of a polynucleotide which comprises one of

XX the 5602 nucleotide sequences defined in the specification, where the

XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides, and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesising polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

SQ Sequence 824 BP; 227 A; 185 C; 226 G; 183 T; 3 other;

Query Match 65.5%; Score 36; DB 22; Length 824;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53

Db 583 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 618

RESULT 4

AAH17143

ID AAH17143 standard; cDNA; 1524 BP.

XX AAH17143;

XX 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:16486.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602

XX full-length cDNAs defined in the specification, and for the detection

XX and/or diagnosis of the abnormality of the proteins encoded by the

XX full-length cDNAs -

XX Claim 8; SEQ ID 16486; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602

XX full-length cDNAs defined in the specification. Where a primer set

XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary

XX to the complementary strand of a polynucleotide which comprises one of

XX the 5602 nucleotide sequences defined in the specification, where the

XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesising polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX SQ Sequence 1524 BP; 451 A; 339 C; 409 G; 325 T; 0 other;

Query Match 65.5%; Score 36; DB 22; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGAGGTCAGGAATTCGAGATCAGCCTGGCCCAACATG 53  
|||||  
DB 583 TGAGGTCAGGAATTCGAGATCAGCCTGGCCCAACATG 618  
|||||

RESULT 5  
ABN65352  
ID ABN65352 standard; cDNA; 570 BP.  
XX AC ABN65352;  
XX DT 28-JUN-2002 (first entry)  
XX DE Human cancer related polynucleotide SEQ ID NO 5319.  
XX KW Human; cytostatic; gene expression; gene mapping; tissue profiling;  
XX KW gene therapy; cancer; tumour; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200214500-A2.  
XX PD 21-FEB-2002.  
XX PF 16-AUG-2001; 2001WO-US25840.  
XX PR 16-AUG-2000; 2000US-226326P.  
XX PA (CHIR ) CHIRON CORP.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;  
XX PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I; .  
XX DR WPI; 2002-241905/29.  
XX PT New nucleic acid for producing a polypeptide, detecting differentially  
XX PT expressed genes correlated with a cancerous state of a mammalian cell,  
XX PT and inhibiting tumor growth -  
XX PS Claim 1; SEQ ID NO 5319; 883pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (ABN27253-ABN33262)  
XX with cytostatic activity. The polynucleotide is used to produce a  
XX polypeptide, to detect differentially expressed genes correlated with a  
XX cancerous state of a mammalian cell and to inhibit tumour growth. The  
XX polynucleotide is used as a probe in mapping and tissue profiling. The  
XX encoded polypeptide and antibodies to the polypeptide can also be used  
XX for therapeutic and diagnostic purposes. The polynucleotide is useful for

CC gene therapy.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 570 BP; 158 A; 116 C; 156 G; 140 T; 0 other;

Query Match 63.6%; Score 35; DB 24; Length 570;  
Best Local Similarity 100.0%; Pred. No. 8.3e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACTTCAGGTCAGGAATTCGAGATCAGCCTGGCCA 48  
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DB 348 CACTTCAGGTCAGGAATTCGAGATCAGCCTGGCCA 382  
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RESULT 6  
AAK64788  
ID AAK64788 standard; DNA; 10740 BP.  
XX AC AAK64788;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19600.  
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX OS Homo sapiens.  
XX PN WO200157182-A2.  
XX PD 09-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US01354.  
XX PR 31-JAN-2000; 2000US-0179065.  
XX PR 04-FEB-2000; 2000US-0180628.  
XX PR 24-FEB-2000; 2000US-0184664.  
XX PR 02-MAR-2000; 2000US-0186350.  
XX PR 16-MAR-2000; 2000US-0189874.  
XX PR 17-MAR-2000; 2000US-0190076.  
XX PR 18-APR-2000; 2000US-0198123.  
XX PR 19-MAY-2000; 2000US-0205515.  
XX PR 07-JUN-2000; 2000US-0209467.  
XX PR 28-JUN-2000; 2000US-0214886.  
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XX PR 07-JUL-2000; 2000US-0216647.  
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XX PR 11-JUL-2000; 2000US-0217487.  
XX PR 14-JUL-2000; 2000US-0218290.  
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XX PR 14-AUG-2000; 2000US-0224518.  
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XX PR 14-AUG-2000; 2000US-0225213.  
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XX PR 22-AUG-2000; 2000US-0226681.  
XX PR 22-AUG-2000; 2000US-0226686.  
XX PR 22-AUG-2000; 2000US-0227182.  
XX PR 23-AUG-2000; 2000US-0227009.  
XX PR 30-AUG-2000; 2000US-0228924.

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PR 01-SEP-2000; 2000US-0229344.  
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PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
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PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
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PR 01-DEC-2000; 2000US-0250160.  
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PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
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PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-483426/52.  
XX  
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and  
PT metastasis -  
XX  
XX Disclosure; SEQ ID NO 19600; 3071pp + Sequence Listing; English.  
PS  
XX  
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)  
CC the nucleic acids may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 10740 BP; 3239 A; 1965 C; 2229 G; 3307 T; 0 other;  
Query Match 63.6%; Score 35; DB 22; Length 10740;  
Best Local Similarity 100.0%; Pred. No. 7.3e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 CACTTGAGGTGAGGAATTCGAGATCAGCTGCGCCA 48  
Db 1580 CACTTGAGGTGAGGAATTCGAGATCAGCTGCGCCA 1614  
RESULT 7  
ABL77817  
ID ABL77817 standard; cDNA; 218 BP.  
XX
```

AC ABL7781.7;  
 XX 17-MAY-2002 (first entry)  
 DT Human ovarian cancer related cDNA clone SEQ ID NO:795.  
 XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200192581-A2.  
 XX 06-DEC-2001.  
 PD  
 XX 29-MAY-2001; 2001WO-US17756.  
 PF  
 XX 26-MAY-2000; 2000US-207484P.  
 PR (CORI-) CORIXA CORP.  
 PA  
 XX Algate PA, Harlocker SL, Jones R;  
 FI WPI; 2002-122075/16.  
 XX  
 XX Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide -  
 XX  
 XX Claim 1; SEQ ID 795; 489pp; English.  
 PS  
 XX The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.  
 XX  
 XX Sequence 218 BP; 64 A; 42 C; 55 G; 51 T; 6 other;  
 SQ  
 Query Match 45.5%; Score 25; DB 24; Length 218;  
 Best Local Similarity 100.0%; Pred. No. 0.0013;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 30 TTCGAGATCAGCCTGGCCACATGA 54  
 Db 53 TTCGAGATCAGCCTGGCCACATGA 77  
 RESULT 8  
 ID ABA16332/c  
 ID ABA16332 standard; DNA; 250 BP.  
 XX  
 XX ABA16332;  
 AC  
 XX 23-JAN-2002 (first entry)  
 DT Human nervous system related polynucleotide SEQ ID NO 8663.  
 XX

XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
 KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;  
 KW antihemagic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;  
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
 XX  
 OS Homo sapiens.  
 XX WO200159063-A2.  
 XX 16-AUG-2001.  
 PD  
 XX 17-JAN-2001; 2001WO-US01334.  
 PF  
 XX 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
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 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.

PR 14-SEP-2000; 2000US-0232401.  
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PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251160.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 03-JAN-2001; 2001US-0259678.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Baraah SC, Ruben SM;  
XX WPI; 2001-541565/60.  
DR  
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating nervous system  
PT cancers and metastases  
XX  
XX Disclosure; SEQ ID NO 8663; 1701pp + Sequence Listing; English.  
XX  
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins  
CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease; multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 250 BP; 48 A; 71 C; 52 G; 79 T; 0 other;  
Query Match 45.5%; Score 25; DB 22; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 30 TTCGAGATCAGCTGGCCACATGA 54  
Db 229 TTCGAGATCAGCTGGCCACATGA 205  
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RESULT 9  
AAC05198  
ID AAC05198 standard; cDNA; 320 BP.  
XX AAC05198;  
XX  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 9273.  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; es.  
XX Homo sapiens.  
OS  
XX EP1033401-A2.  
XX  
XX 06-SEP-2000.  
PD  
XX 21-FEB-2000; 2000EP-0200610.  
PF  
XX 26-FEB-1999; 99US-0122487.  
XX

PA (GSET ) GENSET.  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX WPI; 2000-500381/45.  
 XX  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 XX Claim 1; SEQ ID 9273; 71pp + CD-ROM; English.  
 XX  
 XX The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.  
 XX  
 XX Sequence 320 BP; 86 A; 70 C; 71 G; 92 T; 1 other;  
 SQ  
 Query Match 45.5%; Score 25; DB 21; Length 320;  
 Best Local Similarity 100.0%; Pred. No. 0.0013;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 30 TTCGAGATCAGCTGGCCAAACATGA 54  
 Db 212 TTCGAGATCAGCTGGCCAAACATGA 236  
 RESULT 10  
 AAS91264/c  
 ID AAS91264 standard; cDNA; 1566 BP.  
 XX  
 XX AAS91264;  
 XX  
 XX 13-FEB-2002 (first entry)  
 DE DNA encoding novel human diagnostic protein #27068.  
 XX  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200175067-A2.  
 FN  
 XX 11-OCT-2001.  
 PD  
 XX 30-MAR-2001; 2001WO-US08631.  
 PF  
 XX 31-MAR-2000; 2000US-0540217.  
 PR  
 XX 23-AUG-2000; 2000US-0649167.  
 PR  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Drmanac RT, Liu C, Tang YT;  
 PI  
 XX WPI; 2001-639362/73.  
 DR  
 XX P-PSDB; ABG27077.  
 DR  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensic, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

Claim 1; SEQ ID No 27068; 103pp; English.  
 The invention relates to isolated polynucleotide (I) and  
 polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 polypeptide chain reaction (PCR) primers, oligomers, and for chromosome  
 and gene mapping, and in recombinant production of (II). The  
 polynucleotides are also used in diagnostics as expressed sequence tags  
 for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensic, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 1566 BP; 377 A; 390 C; 452 G; 347 T; 0 other;  
 SQ  
 Query Match 45.5%; Score 25; DB 23; Length 1566;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 30 TTCGAGATCAGCTGGCCAAACATGA 54  
 Db 36 TTCGAGATCAGCTGGCCAAACATGA 12  
 RESULT 11  
 AAH17905  
 ID AAH17905 standard; cDNA; 3295 BP.  
 XX  
 XX AAH17905;  
 XX  
 XX 26-JUN-2001 (first entry)  
 DT  
 XX Human cDNA sequence SEQ ID NO:17649.  
 DE  
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX EPI074617-A2.  
 PN  
 XX 07-FEB-2001.  
 PD  
 XX 28-JUL-2000; 2000EP-0116126.  
 PF  
 XX 29-JUL-1999; 99JP-0248036.  
 PR  
 XX 27-AUG-1999; 99JP-0300253.  
 PR  
 XX 11-JAN-2000; 2000JP-0118776.  
 PR  
 XX 02-MAY-2000; 2000JP-0183767.  
 PR  
 XX 09-JUN-2000; 2000JP-0241899.  
 PR  
 XX (HELI-) HELIX RES INST.  
 PA  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI  
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 DR  
 XX WPI; 2001-318749/34.  
 DR  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -

XX Claim 8; SEQ ID 17649; 2537pp + CD ROM; English.  
 XX The present invention describes primer sets for synthesising 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesising polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 3295 BP; 1013 A; 683 C; 768 G; 831 T; 0 other;  
 Query Match 45.5%; Score 25; DB 22; Length 3295;  
 Best Local Similarity 100.0%; Pred. NO. 0.0012;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 30 TTCGAGATCAGCTGGCCACATCA 54  
 Db 1656 TTCGAGATCAGCTGGCCACATCA 1680  
 RESULT 12  
 ABL55755  
 ID ABL55755 standard; DNA; 10708 BP.  
 XX  
 AC ABL55755;  
 XX  
 XX 08-OCT-2002 (first entry)  
 XX Human transporter protein related to permease subfamily gene.  
 XX Human; permease; transporter; gene therapy; gene; ds.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT variation replace(366,T)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT variation replace(812,G)  
 FT /\*tag= b  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT variation replace(825,G)  
 FT /\*tag= c  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT CDS 1225..8132  
 FT /\*tag= f  
 FT /product= "Transport protein"  
 FT /note= "Contains 11 introns"  
 FT 1225..1386  
 FT exon /\*tag= g  
 FT /number= 1  
 FT 1387..1530  
 FT intron /\*tag= h  
 FT /number= 1  
 FT 1531..1688  
 FT exon /\*tag= g

FT intron /number= 2  
 FT 1689..1802  
 FT /\*tag= h  
 FT /number= 2  
 FT 1803..1900  
 FT /\*tag= g  
 FT /number= 3  
 FT 1901..2106  
 FT /\*tag= h  
 FT /number= 3  
 FT replace(1975,G)  
 FT /tag= d  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT variation replace(2101,C)  
 FT /\*tag= e  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT exon 2107..2180  
 FT /\*tag= g  
 FT /number= 4  
 FT 2181..2375  
 FT /\*tag= h  
 FT /number= 4  
 FT 2376..2557  
 FT /\*tag= g  
 FT /number= 5  
 FT 2558..2890  
 FT /\*tag= h  
 FT /number= 5  
 FT 2891..3014  
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 FT /\*tag= h  
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 FT /number= 8  
 FT 4873..5702  
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 FT /number= 8  
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 FT /\*tag= g  
 FT /number= 10  
 FT 6654..7646  
 FT /\*tag= h  
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 FT 7647..7742  
 FT /\*tag= g  
 FT /number= 11  
 FT 7743..7836  
 FT /\*tag= h  
 FT /number= 11  
 FT 7837..8132  
 FT /\*tag= g  
 FT /number= 12  
 XX US2002028915-A1.  
 XX PN  
 XX 07-MAR-2002.  
 XX PD  
 XX 27-DEC-2000; 2000US-0748107.  
 XX PF

```

XX 07-SEP-2000; 2000US-230721P.
PR (WEIM/) WEI M.
XX (YEJ/) YE J.
PA (MOOR/) MOORE H M.
PA (MERK/) MERKULOV G V.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
XX
XX Wei M, Ye J, Moore HM, Merkulo GV, Di Francesco V, Beasley EM,
PI WPI: 2002-315053/35.
XX P-PSDB; ABB77086.
DR
DR Novel human transporter protein that is related to permease subfamily,
PT useful as models for development of human therapeutic targets and
PT serves as targets for developing human therapeutic agents -
XX
XX Claim 2; Fig 3; 36pp; English.
XX
XX The sequence encodes the novel human transporter protein related to the
CC permease subfamily of the invention. The sequence is found on chromosome
CC 2. The protein of the invention is useful for identifying a modulator of
CC a human permease. A pharmaceutical composition comprising an agent that
CC binds to the transporter protein is useful for treating a disease or
CC condition mediated by human transporter protein. A nucleic acid molecule
CC encoding the transporter protein of the invention provides vectors for
CC gene therapy in patients with aberrant transporter gene expression.
XX
XX Sequence 10708 BP; 2486 A; 2541 C; 2892 G; 2739 T; 50 other;
SQ
Query Match 45.5%; Score 25; DB 24; Length 10708;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 30 TTCGAGATCAGCCTGGCCACATGA 54
Db 6117 TTCGAGATCAGCCTGGCCACATGA 6141
RESULT 13
ID ABA20815/c
XX ABA20815 standard; DNA; 12842 BP.
XX
XX ABA20815;
AC
AC
DT 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 13146.
XX
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
XX WO200159063-A2.
FN
XX
XX 16-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0175065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.

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PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
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PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
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PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
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PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
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PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
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PR 14-SEP-2000; 2000US-0233064.  
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PR 21-SEP-2000; 2000US-0234223.  
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PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
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PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
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PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
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PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
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PR 08-NOV-2000; 2000US-0246526.  
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PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
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PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249246.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 08-DEC-2000; 2000US-0251030.  
PR 08-DEC-2000; 2000US-0251988.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI; 2001-483426/52.  
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
useful for preventing, diagnosing and/or treating cancers and  
metastasis -  
Disclosure; SEQ ID NO 26628; 3071pp + Sequence Listing; English.  
AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
activity, and can be used in gene therapy and vaccine production. (I)  
proteins and polynucleotides may be used in the prevention, diagnosis and  
treatment of diseases associated with inappropriate (I) expression. For  
example, they may be used to treat disorders associated with decreased  
expression by rectifying mutations or deletions in a patient's genome  
that affect the activity of (I) by expressing inactive proteins or to  
supplement the patients own production of (I). Additionally, (I)  
polynucleotides may be used to produce the secreted (I), by inserting  
the nucleic acids into a host cell and culturing the cell to express the  
protein. (I) proteins and polynucleotides may be used to prevent,  
diagnose and treat immune/hematopoietic-related diseases, especially  
cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
to AAK87694 represent human immune/hematopoietic antigen genomic  
sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
represent sequences used in the exemplification of the present invention.

XX Sequence 14417 BP; 3611 A; 3356 C; 3462 G; 3988 T; 0 other;  
Query Match 45.5%; Score 25; DB 22; Length 14417;  
Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATGA 54  
|||||  
Db 10166 TTCGAGATCAGCTGGCCACATGA 10142

## RESULT 15

AAK73113

ID AAK73113 standard; DNA; 14417 BP.

XX AC AAK73113;

XX DT 06-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27925.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX KW cytostatic; gene therapy; vaccine; metastasis; db.

XX OS Homo sapiens.

XX PN WC200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 13-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229613.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.

PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249267.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251988.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and  
PT metastasis -  
XX  
XX Disclosure; SEQ ID NO 27925; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
XX SQ Sequence 14417 BP; 3988 A; 3462 C; 3356 G; 3611 T; 0 other;

Query Match 45.5%; Score 25; DB 22; Length 14417;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 TTCGAGATCAGCTGGCCACATGA 54  
|||||  
Db 4252 TTCGAGATCAGCTGGCCACATGA 4276

Search completed: June 16, 2003, 20:02:46  
Job time : 34.7096 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 2.15297 Seconds  
(without alignments)  
7834.381 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_4365\_4419

Perfect score: 55

Sequence: 1 gaggcaggcagcacttg.....atcagctggccaacatgag 55

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA:\*

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6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	43.6	2387	4	US-09-375-318-38
C 2	23	41.8	18443	4	US-09-078-294-6
C 3	23	41.8	80246	4	US-09-078-294-4
C 4	23	41.8	80595	4	US-09-078-294-3
C 5	23	41.8	99500	4	US-09-798-096-10
C 6	23	41.8	112132	4	US-09-741-150-3
C 7	22	40.0	18596	4	US-09-318-448-11
C 8	22	40.0	81001	4	US-09-750-580-1
C 9	21	38.2	3350	3	US-09-110-116-2
C 10	21	38.2	8396	4	US-09-328-174A-1
C 11	21	38.2	8409	4	US-09-167-681-37
C 12	21	38.2	70000	4	US-09-851-896-3
C 13	21	38.2	81001	4	US-09-750-580-1
C 14	21	38.2	84495	4	US-09-797-506-3
C 15	21	38.2	99500	4	US-09-798-096-10
C 16	20	36.4	3441	4	US-09-026-033-17
C 17	20	36.4	17327	1	US-07-906-871-15
C 18	20	36.4	162450	4	US-09-345-882-1
C 19	20	36.4	246240	2	US-08-724-394A-20
C 20	20	36.4	246240	2	US-08-724-394A-21
C 21	20	36.4	246240	2	US-08-724-394A-22
C 22	19	34.5	240	1	US-08-222-177A-9
C 23	19	34.5	1420	2	US-08-909-965C-3
C 24	19	34.5	3336	4	US-09-026-033-1
C 25	19	34.5	3336	4	US-09-026-033-2
C 26	19	34.5	6987	4	US-09-026-033-3
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C 64	17	30.9	3507	1	US-08-832-883-67
C 65	17	30.9	3507	2	US-08-832-877-67
C 66	17	30.9	4084	3	US-08-866-340-1
C 67	17	30.9	4084	3	US-09-103-875-4
C 68	17	30.9	4450	4	US-09-140-804-9
C 69	17	30.9	4517	4	US-08-520-3730-5
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c 104	16	29.1	288	1	US-08-259-514-22	Sequence 22, Appl	177	16	29.1	1001	4	US-09-641-638-406	Sequence 406, App
c 105	16	29.1	288	2	US-08-858-311-22	Sequence 22, Appl	178	16	29.1	1001	4	US-09-641-638-464	Sequence 464, App
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C 411	16	29.1	10825	4	US-09-503-444A-7	Sequence 7, Appli	C 484	16	29.1	53526	3	US-08-658-136-2	Sequence 2, Appli
C 412	16	29.1	11298	1	US-07-869-933-31	Sequence 31, Appli	485	16	29.1	53526	3	US-08-658-136-2	Sequence 2, Appli
C 413	16	29.1	11298	1	US-08-201-879A-2	Sequence 2, Appli	C 486	16	29.1	53577	3	US-08-658-136-1	Sequence 1, Appli
C 414	16	29.1	11298	4	US-09-103-663-31	Sequence 31, Appli	487	16	29.1	53577	3	US-08-658-136-1	Sequence 1, Appli
C 415	16	29.1	11464	3	US-08-884-324-13	Sequence 13, Appli	C 488	16	29.1	55827	4	US-09-813-133A-3	Sequence 3, Appli
C 416	16	29.1	11531	1	US-08-068-945A-1	Sequence 1, Appli	489	16	29.1	56516	2	US-08-996-306-1	Sequence 1, Appli
C 417	16	29.1	11531	1	US-08-442-806-1	Sequence 1, Appli	C 490	16	29.1	56516	4	US-09-338-907-1	Sequence 1, Appli
C 418	16	29.1	11811	4	US-09-078-294-7	Sequence 7, Appli	491	16	29.1	56516	4	US-09-218-207-1	Sequence 1, Appli
C 419	16	29.1	11811	4	US-09-078-294-7	Sequence 7, Appli	C 492	16	29.1	56520	4	US-09-338-907-179	Sequence 179, App
C 420	16	29.1	12047	2	US-09-022-461-1	Sequence 1, Appli	493	16	29.1	56520	4	US-09-218-207-179	Sequence 179, App
C 421	16	29.1	12047	4	US-09-033-556-3	Sequence 3, Appli	C 494	16	29.1	59065	4	US-09-813-817-3	Sequence 3, Appli
C 422	16	29.1	12146	4	US-09-277-457-27	Sequence 27, Appli	495	16	29.1	59065	4	US-09-978-197-3	Sequence 3, Appli
C 423	16	29.1	12394	4	US-09-488-856A-10	Sequence 10, Appli	C 496	16	29.1	62804	4	US-09-800-960-3	Sequence 3, Appli
C 424	16	29.1	12597	4	US-09-705-299-12	Sequence 12, Appli	497	16	29.1	62804	4	US-09-784-316-3	Sequence 3, Appli
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C 427	16	29.1	13104	4	US-08-256-799-4	Sequence 4, Appli	C 500	16	29.1	72604	4	US-09-268-992-7	Sequence 7, Appli
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C 432	16	29.1	13865	3	US-09-009-217-11	Sequence 11, Appli	505	16	29.1	84495	4	US-09-797-906-3	Sequence 3, Appli
C 433	16	29.1	13865	3	US-09-009-656-11	Sequence 11, Appli	C 506	16	29.1	98844	4	US-09-791-211-10	Sequence 10, Appli
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C 437	16	29.1	14636	4	US-09-173-914-6	Sequence 6, Appli	510	16	29.1	152331	3	US-09-128-155-16	Sequence 16, Appli
C 438	16	29.1	14747	4	US-09-608-285A-42	Sequence 42, Appli	511	16	29.1	162450	4	US-09-345-882-1	Sequence 1, Appli
C 439	16	29.1	14753	4	US-09-821-736-3	Sequence 3, Appli	512	16	29.1	168575	4	US-09-426-290-1	Sequence 1, Appli
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C 442	16	29.1	15977	4	US-09-608-285A-59	Sequence 59, Appli	515	16	29.1	176373	3	US-09-128-155-17	Sequence 17, Appli
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C 444	16	29.1	16389	4	US-09-741-154-3	Sequence 3, Appli	C 517	15	27.3	15	4	US-09-081-646-11	Sequence 11, Appli
C 445	16	29.1	16595	4	US-09-146-053-7	Sequence 7, Appli	518	15	27.3	22	1	US-08-068-945A-58	Sequence 58, App
C 446	16	29.1	17425	4	US-09-511-625B-5	Sequence 5, Appli	C 519	15	27.3	22	1	US-08-442-806-58	Sequence 58, App
C 447	16	29.1	17606	4	US-08-943-731-4	Sequence 4, Appli	520	15	27.3	30	2	US-08-859-998-318	Sequence 318, App
C 448	16	29.1	17649	4	US-09-087-465-3	Sequence 3, Appli	C 521	15	27.3	30	2	US-09-225-928-318	Sequence 318, App
C 449	16	29.1	17949	4	US-09-087-465-3	Sequence 3, Appli	522	15	27.3	75	4	US-09-357-740-14	Sequence 14, Appli
C 450	16	29.1	18073	4	US-09-078-294-12	Sequence 12, Appli	C 523	15	27.3	75	4	US-09-357-740-14	Sequence 14, Appli
C 451	16	29.1	18596	4	US-09-318-448-11	Sequence 11, Appli	524	15	27.3	281	4	US-09-103-875-15	Sequence 15, Appli
C 452	16	29.1	19336	1	US-09-740-035-3	Sequence 3, Appli	C 525	15	27.3	283	4	US-08-118-200-11	Sequence 11, Appli
C 453	16	29.1	20303	1	US-08-370-975B-6	Sequence 6, Appli	526	15	27.3	283	4	US-08-458-745-11	Sequence 11, Appli
C 454	16	29.1	20674	4	US-09-641-638-651	Sequence 651, App	527	15	27.3	327	1	US-08-741-406-6	Sequence 6, Appli
C 455	16	29.1	26664	4	US-09-564-805-28	Sequence 28, Appli	528	15	27.3	327	2	US-09-024-472-6	Sequence 6, Appli
C 456	16	29.1	26764	1	US-08-370-975B-1	Sequence 1, Appli	C 529	15	27.3	347	2	US-08-367-101-44	Sequence 44, Appli
C 457	16	29.1	28720	4	US-09-341-587-7	Sequence 7, Appli	530	15	27.3	347	2	US-08-592-541-44	Sequence 44, Appli
C 458	16	29.1	28994	3	US-08-884-324-14	Sequence 14, Appli	C 531	15	27.3	347	3	US-09-124-698-44	Sequence 44, Appli
C 459	16	29.1	29629	4	US-09-729-995-3	Sequence 3, Appli	532	15	27.3	347	4	US-09-127-480-44	Sequence 44, Appli
C 460	16	29.1	29629	4	US-09-729-995-3	Sequence 3, Appli	C 533	15	27.3	347	4	US-08-496-841C-44	Sequence 44, Appli
C 461	16	29.1	31571	1	US-08-323-443B-1	Sequence 1, Appli	534	15	27.3	347	4	US-09-124-523-44	Sequence 44, Appli
C 462	16	29.1	32042	4	US-09-245-281-44	Sequence 44, Appli	C 535	15	27.3	388	2	US-08-367-101-68	Sequence 68, Appli
C 463	16	29.1	32042	4	US-09-245-281-44	Sequence 44, Appli	536	15	27.3	388	2	US-08-592-541-68	Sequence 68, Appli
C 464	16	29.1	35060	3	US-08-814-095-7	Sequence 7, Appli	C 537	15	27.3	388	3	US-09-124-698-68	Sequence 68, Appli
C 465	16	29.1	35100	1	US-08-306-691B-19	Sequence 19, Appli	C 538	15	27.3	388	4	US-09-127-480-68	Sequence 68, Appli



C 539	15	27.3	388	4	US-08-496-841C-68	Sequence 68, Appl	612	15	27.3	3715	4	US-09-085-199B-44	Sequence 44, Appl
C 540	15	27.3	388	4	US-09-124-523-68	Sequence 68, Appl	613	15	27.3	3885	1	US-08-688-145-1	Sequence 1, Appl
C 541	15	27.3	451	4	US-09-404-879A-101	Sequence 101, Appl	C 614	15	27.3	3993	4	US-09-167-109-5	Sequence 5, Appl
C 542	15	27.3	548	4	US-08-991-789A-15	Sequence 15, Appl	C 615	15	27.3	4066	4	US-09-367-750-1	Sequence 1, Appl
C 543	15	27.3	548	4	US-09-062-451-15	Sequence 15, Appl	C 616	15	27.3	4136	4	US-09-103-875-2	Sequence 2, Appl
C 544	15	27.3	548	4	US-09-598-226-15	Sequence 15, Appl	C 617	15	27.3	4326	2	US-08-852-807-12	Sequence 12, Appl
C 545	15	27.3	554	4	US-09-227-357-111	Sequence 111, Appl	C 618	15	27.3	4335	3	US-09-058-489-19	Sequence 19, Appl
C 546	15	27.3	567	1	US-08-480-784-30	Sequence 30, Appl	C 619	15	27.3	4630	3	US-09-442-143A-1	Sequence 1, Appl
C 547	15	27.3	567	1	US-08-483-553-30	Sequence 30, Appl	C 620	15	27.3	5375	3	US-08-757-223-7	Sequence 7, Appl
C 548	15	27.3	567	1	US-08-487-002-30	Sequence 30, Appl	C 621	15	27.3	5375	3	US-08-757-223-7	Sequence 7, Appl
C 549	15	27.3	567	1	US-08-483-554B-30	Sequence 30, Appl	C 622	15	27.3	5581	4	US-08-973-544-1	Sequence 1, Appl
C 550	15	27.3	567	1	US-08-488-011B-30	Sequence 30, Appl	C 623	15	27.3	5775	1	US-08-306-691B-15	Sequence 15, Appl
C 551	15	27.3	567	4	US-08-850-727-30	Sequence 30, Appl	C 624	15	27.3	5775	5	PCT-US93-06251-29	Sequence 29, Appl
C 552	15	27.3	567	5	PCT-US95-10202-30	Sequence 30, Appl	C 625	15	27.3	6232	4	US-08-456-200B-11	Sequence 11, Appl
C 553	15	27.3	567	5	PCT-US95-10203-30	Sequence 30, Appl	C 626	15	27.3	6330	4	US-09-880-427-2	Sequence 2, Appl
C 554	15	27.3	567	5	PCT-US95-10220-30	Sequence 30, Appl	C 627	15	27.3	6330	4	US-09-306-538B-2	Sequence 2, Appl
C 555	15	27.3	590	4	US-09-328-111-411	Sequence 411, Appl	C 628	15	27.3	6669	3	US-09-212-971-5	Sequence 5, Appl
C 556	15	27.3	603	4	US-08-949-155-3	Sequence 3, Appl	C 629	15	27.3	6669	3	US-08-800-929A-5	Sequence 5, Appl
C 557	15	27.3	603	4	US-09-819-964-3	Sequence 3, Appl	C 630	15	27.3	6669	4	US-09-617-053A-5	Sequence 5, Appl
C 558	15	27.3	621	4	US-09-328-111-7	Sequence 7, Appl	C 631	15	27.3	6709	4	US-09-285-601-3	Sequence 3, Appl
C 559	15	27.3	646	4	US-09-385-982-314	Sequence 314, Appl	C 632	15	27.3	6792	4	US-09-374-454-20	Sequence 20, Appl
C 560	15	27.3	661	2	US-08-529-878B-37	Sequence 37, Appl	C 633	15	27.3	6792	4	US-08-257-963B-10	Sequence 10, Appl
C 561	15	27.3	702	4	US-08-949-155-8	Sequence 8, Appl	C 634	15	27.3	7210	4	US-08-367-841A-10	Sequence 10, Appl
C 562	15	27.3	702	4	US-09-819-964-8	Sequence 8, Appl	C 635	15	27.3	7210	4	PCT-US95-07201-10	Sequence 10, Appl
C 563	15	27.3	755	4	US-09-288-143-29	Sequence 29, Appl	C 636	15	27.3	7605	4	US-09-417-455-8	Sequence 8, Appl
C 564	15	27.3	782	4	US-09-288-143-19	Sequence 19, Appl	C 637	15	27.3	7605	4	US-09-348-942-8	Sequence 8, Appl
C 565	15	27.3	900	2	US-08-518-862C-5	Sequence 5, Appl	C 638	15	27.3	7605	4	US-09-457-626-8	Sequence 8, Appl
C 566	15	27.3	901	1	US-08-832-883-65	Sequence 65, Appl	C 639	15	27.3	8133	4	US-09-659-791A-10	Sequence 10, Appl
C 567	15	27.3	901	2	US-08-832-877-65	Sequence 65, Appl	C 640	15	27.3	9278	1	US-08-243-542-9	Sequence 9, Appl
C 568	15	27.3	1000	4	US-09-018-584A-32	Sequence 32, Appl	C 641	15	27.3	9278	1	US-08-477-407-9	Sequence 9, Appl
C 569	15	27.3	1000	4	US-09-018-584A-34	Sequence 34, Appl	C 642	15	27.3	9278	1	US-08-484-355-9	Sequence 9, Appl
C 570	15	27.3	1000	4	US-09-641-638-460	Sequence 460, Appl	C 643	15	27.3	9301	4	US-09-449-218D-18	Sequence 18, Appl
C 571	15	27.3	1001	4	US-09-641-638-70	Sequence 70, Appl	C 644	15	27.3	9365	4	US-09-608-285A-8	Sequence 8, Appl
C 572	15	27.3	1001	4	US-09-641-638-293	Sequence 293, Appl	C 645	15	27.3	9365	4	US-09-350-836B-8	Sequence 8, Appl
C 573	15	27.3	1001	4	US-09-641-638-459	Sequence 459, Appl	C 646	15	27.3	9365	4	US-09-370-265-8	Sequence 8, Appl
C 574	15	27.3	1043	4	US-09-165-868-4	Sequence 4, Appl	C 647	15	27.3	9639	4	US-09-147-208-26	Sequence 26, Appl
C 575	15	27.3	1052	4	US-09-442-143A-9	Sequence 9, Appl	C 648	15	27.3	9690	4	US-09-182-145-55	Sequence 55, Appl
C 576	15	27.3	1145	3	US-08-755-587-36	Sequence 36, Appl	C 649	15	27.3	9704	4	US-09-814-951A-3	Sequence 3, Appl
C 577	15	27.3	1155	3	US-08-755-587-35	Sequence 35, Appl	C 650	15	27.3	10379	4	US-09-182-145-54	Sequence 54, Appl
C 578	15	27.3	1260	4	US-08-943-731-169	Sequence 169, Appl	C 651	15	27.3	11284	3	US-08-978-741-5	Sequence 5, Appl
C 579	15	27.3	1542	4	US-09-008-271A-13	Sequence 13, Appl	C 652	15	27.3	12565	4	US-09-345-217-3	Sequence 3, Appl
C 580	15	27.3	1804	1	US-08-306-691B-40	Sequence 40, Appl	C 653	15	27.3	12847	1	US-08-550-715-1	Sequence 1, Appl
C 581	15	27.3	1804	4	US-09-167-322-14	Sequence 14, Appl	C 654	15	27.3	13187	4	US-09-422-936-61	Sequence 61, Appl
C 582	15	27.3	1804	5	PCT-US93-06251-82	Sequence 82, Appl	C 655	15	27.3	13674	2	US-08-852-807-1	Sequence 1, Appl
C 583	15	27.3	1875	2	US-08-683-743-3	Sequence 3, Appl	C 656	15	27.3	13865	3	US-09-009-217-11	Sequence 11, Appl
C 584	15	27.3	1901	4	US-09-338-907-181	Sequence 181, Appl	C 657	15	27.3	13865	3	US-09-009-656-11	Sequence 11, Appl
C 585	15	27.3	1901	4	US-09-218-207-181	Sequence 181, Appl	C 658	15	27.3	13875	2	US-08-734-344-1	Sequence 1, Appl
C 586	15	27.3	1926	4	US-09-117-250-4	Sequence 4, Appl	C 659	15	27.3	14581	4	US-08-520-373D-4	Sequence 4, Appl
C 587	15	27.3	2048	1	US-07-602-608-11	Sequence 11, Appl	C 660	15	27.3	14796	4	US-08-975-080-35	Sequence 35, Appl
C 588	15	27.3	2048	1	US-08-261-578-11	Sequence 11, Appl	C 661	15	27.3	14796	4	US-09-630-706-10	Sequence 10, Appl
C 589	15	27.3	2061	2	US-08-960-022-11	Sequence 11, Appl	C 662	15	27.3	14796	4	US-09-496-694B-3	Sequence 3, Appl
C 590	15	27.3	2115	1	US-08-395-800A-7	Sequence 7, Appl	C 663	15	27.3	15297	4	US-09-817-180-3	Sequence 3, Appl
C 591	15	27.3	2141	1	US-08-463-931-1	Sequence 1, Appl	C 664	15	27.3	16063	4	US-09-801-052-3	Sequence 3, Appl
C 592	15	27.3	2141	4	US-09-224-048A-3	Sequence 3, Appl	C 665	15	27.3	17327	1	US-07-906-871-15	Sequence 15, Appl
C 593	15	27.3	2298	3	US-08-772-440-1	Sequence 1, Appl	C 666	15	27.3	19736	4	US-09-740-035-3	Sequence 3, Appl
C 594	15	27.3	2298	4	US-09-153-599A-1	Sequence 1, Appl	C 667	15	27.3	20303	1	US-08-370-975B-6	Sequence 6, Appl
C 595	15	27.3	2329	4	US-08-927-219-80	Sequence 80, Appl	C 668	15	27.3	21234	3	US-09-810-671-3	Sequence 3, Appl
C 596	15	27.3	2334	4	US-09-493-565-1	Sequence 1, Appl	C 669	15	27.3	22481	4	US-08-367-841A-43	Sequence 43, Appl
C 597	15	27.3	2409	1	US-07-911-531-18	Sequence 18, Appl	C 670	15	27.3	22481	5	PCT-US95-07201-43	Sequence 43, Appl
C 598	15	27.3	2409	1	US-07-693-686A-18	Sequence 18, Appl	C 671	15	27.3	22484	4	US-09-875-223-2	Sequence 2, Appl
C 599	15	27.3	2415	3	US-09-019-639A-1	Sequence 1, Appl	C 672	15	27.3	24979	2	US-08-147-777-3	Sequence 3, Appl
C 600	15	27.3	2477	1	US-08-429-742-1	Sequence 1, Appl	C 673	15	27.3	24979	3	US-08-452-872-3	Sequence 3, Appl
C 601	15	27.3	2680	4	US-08-949-155-50	Sequence 50, Appl	C 674	15	27.3	24979	5	PCT-US93-03985-3	Sequence 3, Appl
C 602	15	27.3	2680	4	US-08-819-964-50	Sequence 50, Appl	C 675	15	27.3	26764	1	US-08-370-975B-1	Sequence 1, Appl
C 603	15	27.3	2721	3	US-08-921-195-1	Sequence 1, Appl	C 676	15	27.3	40352	3	US-08-846-111D-15	Sequence 15, Appl
C 604	15	27.3	2741	1	US-08-832-883-59	Sequence 59, Appl	C 677	15	27.3	40352	4	US-09-443-077-15	Sequence 15, Appl
C 605	15	27.3	2741	2	US-08-832-877-59	Sequence 59, Appl	C 678	15	27.3	42571	4	US-09-810-347-3	Sequence 3, Appl
C 606	15	27.3	2822	4	US-08-819-872A-1	Sequence 1, Appl	C 679	15	27.3	50000	4	US-09-146-053-4	Sequence 4, Appl
C 607	15	27.3	2822	4	US-08-819-872A-10	Sequence 10, Appl	C 680	15	27.3	50000	4	US-09-146-053-4	Sequence 4, Appl
C 608	15	27.3	2822	4	US-08-819-872A-11	Sequence 11, Appl	C 681	15	27.3	55827	2	US-08-996-306-1	Sequence 1, Appl
C 609	15	27.3	3186	1	US-08-761-258-8	Sequence 8, Appl	C 682	15	27.3	56516	2	US-08-996-306-1	Sequence 1, Appl
C 610	15	27.3	3186	2	US-08-977-306-8	Sequence 8, Appl	C 683	15	27.3	56516	4	US-09-338-907-1	Sequence 1, Appl
C 611	15	27.3	3535	2	US-08-618-408B-1	Sequence 1, Appl	C 684	15	27.3	56516	4	US-09-218-207-1	Sequence 1, Appl

685	15	27.3	56520	4	US-09-338-907-179	Sequence 179, App	758	14	25.5	3611	3	US-08-447-314-1	Sequence 1, Appl
686	15	27.3	56520	4	US-09-218-207-179	Sequence 179, App	759	14	25.5	3611	3	US-08-445-461-1	Sequence 1, Appl
c 687	15	27.3	16998	4	US-09-676-6108-24	Sequence 2, Appl	c 760	14	25.5	4534	2	US-08-935-450-1	Sequence 1, Appl
c 688	15	27.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 761	14	25.5	4534	4	US-09-166-350-25	Sequence 25, Appl
c 689	15	27.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl	c 762	14	25.5	4853	2	US-08-881-450A-22	Sequence 22, Appl
c 690	15	27.3	35	4	US-09-605-785-829	Sequence 829, App	c 763	14	25.5	5543	2	US-08-687-080-101	Sequence 101, App
c 691	14	25.5	249	2	US-08-687-080-100	Sequence 100, App	764	14	25.5	6078	4	US-09-173-914-1	Sequence 1, Appl
c 692	14	25.5	411	4	US-09-385-982-5	Sequence 5, Appl	765	14	25.5	6246	4	US-08-943-731-640	Sequence 640, App
c 693	14	25.5	451	4	US-09-404-879A-43	Sequence 43, Appl	c 766	14	25.5	6709	4	US-09-285-601-3	Sequence 3, Appl
c 694	14	25.5	454	4	US-08-991-789A-49	Sequence 49, Appl	767	14	25.5	6719	4	US-09-740-235-36	Sequence 36, Appl
c 695	14	25.5	454	4	US-09-062-451-49	Sequence 49, Appl	768	14	25.5	7676	1	US-08-451-777A-7	Sequence 7, Appl
c 696	14	25.5	454	4	US-09-598-326-49	Sequence 49, Appl	769	14	25.5	7676	2	US-08-451-778A-7	Sequence 7, Appl
c 697	14	25.5	481	5	PCT-US95-08295-15	Sequence 15, Appl	770	14	25.5	7676	2	US-08-998-208-7	Sequence 7, Appl
c 698	14	25.5	568	4	US-09-221-017B-491	Sequence 491, App	771	14	25.5	7676	5	PCT-US95-06743-7	Sequence 7, Appl
c 699	14	25.5	598	4	US-09-641-638-60	Sequence 60, Appl	c 772	14	25.5	7705	2	US-08-687-080-115	Sequence 115, App
c 700	14	25.5	598	4	US-09-641-638-574	Sequence 574, App	773	14	25.5	8021	4	US-09-740-235-2	Sequence 2, Appl
c 701	14	25.5	600	3	US-09-078-317-1	Sequence 1, Appl	774	14	25.5	9704	4	US-09-814-951A-3	Sequence 3, Appl
c 702	14	25.5	600	4	US-09-454-818-1	Sequence 1, Appl	775	14	25.5	10614	1	US-08-135-511-35	Sequence 35, Appl
c 703	14	25.5	601	4	US-08-814-951A-5	Sequence 5, Appl	776	14	25.5	10614	1	US-08-187-453-35	Sequence 35, Appl
c 704	14	25.5	656	3	US-08-921-195-2	Sequence 2, Appl	777	14	25.5	10684	4	US-09-221-017B-401	Sequence 401, App
c 705	14	25.5	683	4	US-09-740-235-19	Sequence 19, Appl	778	14	25.5	11288	4	US-08-646-301A-1	Sequence 1, Appl
c 706	14	25.5	687	3	US-09-048-052-5	Sequence 5, Appl	779	14	25.5	11288	4	US-08-481-968A-4	Sequence 4, Appl
c 707	14	25.5	687	4	US-09-160-246-5	Sequence 5, Appl	780	14	25.5	11288	4	US-08-154-712B-4	Sequence 4, Appl
c 708	14	25.5	738	4	US-09-662-250A-23	Sequence 23, Appl	c 781	14	25.5	12141	4	US-09-488-671-10	Sequence 10, Appl
c 709	14	25.5	764	4	US-09-288-143-57	Sequence 57, Appl	782	14	25.5	15664	1	US-08-402-282-3	Sequence 3, Appl
c 710	14	25.5	789	2	US-08-394-152A-42	Sequence 42, Appl	783	14	25.5	15664	1	US-08-508-004-3	Sequence 3, Appl
c 711	14	25.5	799	4	US-09-166-350-11	Sequence 11, Appl	784	14	25.5	15664	1	US-08-402-066-3	Sequence 3, Appl
c 712	14	25.5	971	1	US-08-451-947-11	Sequence 11, Appl	785	14	25.5	15664	1	US-08-402-068-3	Sequence 3, Appl
c 713	14	25.5	971	3	US-08-928-694-11	Sequence 11, Appl	c 786	14	25.5	17041	1	US-08-076-011-1	Sequence 1, Appl
c 714	14	25.5	971	5	PCT-US91-06950-11	Sequence 11, Appl	c 787	14	25.5	19604	1	US-08-781-891-207	Sequence 207, App
c 715	14	25.5	985	4	US-09-160-246-9	Sequence 9, Appl	c 788	14	25.5	40352	3	US-08-846-111B-15	Sequence 15, Appl
c 716	14	25.5	985	4	US-09-160-246-13	Sequence 13, Appl	c 789	14	25.5	40352	4	US-09-443-077-15	Sequence 15, Appl
c 717	14	25.5	1000	2	US-08-747-121-20	Sequence 20, Appl	c 790	14	25.5	49136	4	US-09-422-869-1	Sequence 1, Appl
c 718	14	25.5	1001	4	US-09-641-638-291	Sequence 291, App	791	14	25.5	50000	4	US-09-146-053-3	Sequence 3, Appl
c 719	14	25.5	1001	4	US-09-641-638-304	Sequence 304, App	792	14	25.5	72928	3	US-09-009-913-1	Sequence 1, Appl
c 720	14	25.5	1001	4	US-09-641-638-458	Sequence 458, App	c 793	13	23.6	21	3	US-08-701-582D-22	Sequence 22, Appl
c 721	14	25.5	1045	1	US-08-599-252-92	Sequence 92, Appl	c 794	13	23.6	26	3	US-08-441-935-3	Sequence 3, Appl
c 722	14	25.5	1045	5	PCT-US96-06352-92	Sequence 92, Appl	c 795	13	23.6	26	3	US-08-441-943-3	Sequence 3, Appl
c 723	14	25.5	1045	5	PCT-US96-06583-92	Sequence 92, Appl	796	13	23.6	30	2	US-08-880-557-6	Sequence 6, Appl
c 724	14	25.5	1079	1	US-08-832-883-62	Sequence 62, Appl	797	13	23.6	30	3	US-08-441-935-4	Sequence 4, Appl
c 725	14	25.5	1079	2	US-08-832-877-62	Sequence 62, Appl	798	13	23.6	30	3	US-09-189-583-6	Sequence 6, Appl
c 726	14	25.5	1190	1	US-08-451-947-9	Sequence 9, Appl	c 800	13	23.6	36	3	US-08-441-943-5	Sequence 5, Appl
c 727	14	25.5	1190	2	US-08-424-826A-9	Sequence 9, Appl	c 801	13	23.6	36	3	US-08-441-943-5	Sequence 5, Appl
c 728	14	25.5	1190	3	US-08-928-694-9	Sequence 9, Appl	c 802	13	23.6	37	2	US-08-902-516-49	Sequence 49, Appl
c 729	14	25.5	1190	5	PCT-US91-06950-9	Sequence 9, Appl	803	13	23.6	53	2	US-08-282-030-21	Sequence 21, Appl
c 730	14	25.5	1300	2	US-08-474-020A-13	Sequence 13, Appl	804	13	23.6	53	5	PCT-US95-10219-21	Sequence 21, Appl
c 731	14	25.5	1404	1	US-07-796-106-22	Sequence 22, Appl	c 805	13	23.6	56	6	5439679-9	Patent No. 5439679
c 732	14	25.5	1589	1	US-07-971-092-1	Sequence 1, Appl	c 806	13	23.6	58	3	US-08-836-561-7	Sequence 7, Appl
c 733	14	25.5	1611	6	5198342-1	Sequence 1, Appl	c 807	13	23.6	64	3	US-08-836-561-8	Sequence 8, Appl
c 734	14	25.5	1620	2	US-08-977-847-2	Sequence 2, Appl	c 808	13	23.6	71	6	5439679-10	Patent No. 5439679
c 735	14	25.5	1620	2	US-09-195-021-2	Sequence 2, Appl	c 809	13	23.6	74	1	US-08-282-030-22	Sequence 22, Appl
c 736	14	25.5	1773	4	US-08-943-731-215	Sequence 215, App	c 810	13	23.6	74	5	PCT-US95-10219-22	Sequence 22, Appl
c 737	14	25.5	1827	2	US-08-737-371A-3	Sequence 3, Appl	c 811	13	23.6	77	4	US-09-320-424-18	Sequence 18, Appl
c 738	14	25.5	1827	5	PCT-US95-05853-3	Sequence 3, Appl	c 812	13	23.6	78	3	US-08-928-881-22	Sequence 22, Appl
c 739	14	25.5	1987	4	US-09-227-357-44	Sequence 44, Appl	c 813	13	23.6	78	4	US-09-543-921-22	Sequence 22, Appl
c 740	14	25.5	2002	2	US-08-747-121-1	Sequence 1, Appl	c 814	13	23.6	122	1	US-08-282-030-54	Sequence 54, Appl
c 741	14	25.5	2173	6	5168051-10	Sequence 10, Appl	815	13	23.6	122	5	PCT-US95-10219-54	Sequence 54, Appl
c 742	14	25.5	2309	3	US-09-078-317-3	Sequence 3, Appl	c 816	13	23.6	126	4	US-09-450-072-39	Sequence 39, Appl
c 743	14	25.5	2309	4	US-09-454-818-3	Sequence 3, Appl	c 817	13	23.6	126	4	US-09-351-348-39	Sequence 39, Appl
c 744	14	25.5	2742	1	US-08-286-305A-2	Sequence 2, Appl	c 818	13	23.6	130	1	US-08-282-030-24	Sequence 24, Appl
c 745	14	25.5	2742	2	US-08-441-104A-2	Sequence 2, Appl	c 819	13	23.6	130	5	PCT-US95-10219-24	Sequence 24, Appl
c 746	14	25.5	2742	2	US-08-440-816A-2	Sequence 2, Appl	c 820	13	23.6	145	4	US-09-450-072-6	Sequence 6, Appl
c 747	14	25.5	2742	4	US-09-417-381A-2	Sequence 2, Appl	c 821	13	23.6	146	4	US-09-351-348-6	Sequence 6, Appl
c 748	14	25.5	2743	1	US-08-317-707-1	Sequence 1, Appl	c 822	13	23.6	146	4	US-09-450-072-5	Sequence 5, Appl
c 749	14	25.5	2813	4	US-09-689-255C-3	Sequence 3, Appl	c 823	13	23.6	147	4	US-09-351-348-5	Sequence 5, Appl
c 750	14	25.5	2839	4	US-08-595-553A-1	Sequence 1, Appl	c 824	13	23.6	147	4	US-09-450-072-7	Sequence 7, Appl
c 751	14	25.5	2896	2	US-08-709-923-1	Sequence 1, Appl	c 825	13	23.6	147	4	US-09-351-348-7	Sequence 7, Appl
c 752	14	25.5	3176	2	US-08-910-733-17	Sequence 17, Appl	c 826	13	23.6	255	4	US-09-134-001C-2194	Sequence 2194, App
c 753	14	25.5	3176	2	US-08-910-884-17	Sequence 17, Appl	c 827	13	23.6	282	2	US-08-440-725A-4	Sequence 4, Appl
c 754	14	25.5	3303	1	US-08-081-610-3	Sequence 3, Appl	c 828	13	23.6	282	5	PCT-US95-15991-4	Sequence 4, Appl
c 755	14	25.5	3487	4	US-09-303-069-24	Sequence 24, Appl	c 829	13	23.6	289	2	US-08-481-658B-63	Sequence 63, Appl
c 756	14	25.5	3611	1	US-08-445-640-1	Sequence 1, Appl	830	13	23.6	289	2	US-08-477-504A-63	Sequence 63, Appl
757	14	25.5	3611	3	US-08-170-558-1	Sequence 1, Appl							

C 831	13	23.6	289	2	US-08-486-756A-63	Sequence 63, Appl	904	13	23.6	946	4	US-09-410-464-2	Sequence 2, Appl
C 832	13	23.6	289	2	US-08-485-862B-63	Sequence 63, Appl	905	13	23.6	955	4	US-09-641-638-19	Sequence 19, Appl
C 833	13	23.6	289	3	US-08-787-739-63	Sequence 63, Appl	906	13	23.6	998	4	US-09-237-357-62	Sequence 62, Appl
C 834	13	23.6	289	3	US-08-487-077A-63	Sequence 63, Appl	C 907	13	23.6	1000	4	US-09-018-584A-33	Sequence 33, Appl
C 835	13	23.6	289	3	US-08-485-863A-63	Sequence 63, Appl	C 908	13	23.6	1001	4	US-09-641-638-131	Sequence 131, App
C 836	13	23.6	289	4	US-08-485-049D-63	Sequence 63, Appl	C 909	13	23.6	1001	4	US-09-641-638-396	Sequence 396, App
C 837	13	23.6	289	4	US-08-178-115D-63	Sequence 63, Appl	C 910	13	23.6	1049	4	US-08-804-166-1	Sequence 1, Appl
C 838	13	23.6	289	4	US-08-177-776-63	Sequence 63, Appl	C 911	13	23.6	1049	4	US-08-804-166-1	Sequence 1, Appl
C 839	13	23.6	301	4	US-09-605-785-299	Sequence 299, App	C 912	13	23.6	1081	2	US-09-090-567-1	Sequence 1, Appl
C 840	13	23.6	301	4	US-09-439-313-299	Sequence 299, App	C 913	13	23.6	1147	4	US-08-804-166-5	Sequence 5, Appl
C 841	13	23.6	301	4	US-09-352-616A-299	Sequence 299, App	C 914	13	23.6	1147	4	US-08-910-991-5	Sequence 5, Appl
C 842	13	23.6	301	4	US-09-232-149A-299	Sequence 299, App	C 915	13	23.6	1164	3	US-08-755-587-32	Sequence 32, Appl
C 843	13	23.6	321	1	US-07-920-519-23	Sequence 23, Appl	C 916	13	23.6	1176	2	US-08-923-856-2	Sequence 2, Appl
C 844	13	23.6	321	1	US-08-314-586-23	Sequence 23, Appl	C 917	13	23.6	1176	3	US-09-216-294-2	Sequence 2, Appl
C 845	13	23.6	321	1	US-08-115-753-25	Sequence 25, Appl	C 918	13	23.6	1202	4	US-08-804-166-3	Sequence 3, Appl
C 846	13	23.6	334	2	US-08-440-725A-7	Sequence 7, Appl	C 919	13	23.6	1202	4	US-08-910-991-3	Sequence 3, Appl
C 847	13	23.6	334	5	PCT-US95-15991-7	Sequence 7, Appl	C 920	13	23.6	1227	2	US-08-080-386-1	Sequence 1, Appl
C 848	13	23.6	338	3	US-08-928-881-27	Sequence 27, Appl	C 921	13	23.6	1227	2	US-08-390-000A-1	Sequence 1, Appl
C 849	13	23.6	338	4	US-09-543-921-27	Sequence 27, Appl	C 922	13	23.6	1267	4	US-09-422-869-15	Sequence 15, Appl
C 850	13	23.6	341	4	US-09-404-879A-136	Sequence 136, App	C 923	13	23.6	1279	3	US-08-985-950-5	Sequence 5, Appl
C 851	13	23.6	440	2	US-08-967-101-105	Sequence 105, App	C 924	13	23.6	1298	3	US-08-948-705-3	Sequence 3, Appl
C 852	13	23.6	440	2	US-08-592-541-105	Sequence 105, App	C 925	13	23.6	1301	4	US-08-804-166-7	Sequence 7, Appl
C 853	13	23.6	440	3	US-09-124-698-105	Sequence 105, App	C 926	13	23.6	1301	4	US-08-910-991-7	Sequence 7, Appl
C 854	13	23.6	440	4	US-09-127-480-105	Sequence 105, App	C 927	13	23.6	1313	3	US-09-035-648-22	Sequence 22, Appl
C 855	13	23.6	440	4	US-08-496-841C-105	Sequence 105, App	C 928	13	23.6	1313	4	US-09-001-951-22	Sequence 22, Appl
C 856	13	23.6	440	4	US-09-124-523-105	Sequence 105, App	C 929	13	23.6	1313	4	US-08-818-829-22	Sequence 22, Appl
C 857	13	23.6	461	4	US-09-404-879A-1	Sequence 1, Appl	C 930	13	23.6	1320	4	US-09-370-838-22	Sequence 22, Appl
C 858	13	23.6	461	4	US-09-404-879A-3	Sequence 3, Appl	C 931	13	23.6	1328	4	US-09-370-838-24	Sequence 24, Appl
C 859	13	23.6	461	4	US-09-404-879A-47	Sequence 47, Appl	C 932	13	23.6	1331	4	US-09-370-838-27	Sequence 27, Appl
C 860	13	23.6	488	4	US-09-385-982-471	Sequence 471, App	C 933	13	23.6	1333	4	US-09-370-838-28	Sequence 28, Appl
C 861	13	23.6	503	4	US-08-936-165A-155	Sequence 155, App	C 934	13	23.6	1334	2	US-08-481-658B-44	Sequence 44, Appl
C 862	13	23.6	515	4	US-09-404-879A-143	Sequence 143, App	C 935	13	23.6	1334	4	US-08-477-504A-44	Sequence 44, Appl
C 863	13	23.6	526	1	US-08-686-878A-35	Sequence 35, Appl	C 936	13	23.6	1334	2	US-08-486-756A-44	Sequence 44, Appl
C 864	13	23.6	526	4	US-09-175-928-35	Sequence 35, Appl	C 937	13	23.6	1334	2	US-08-485-862B-44	Sequence 44, Appl
C 865	13	23.6	547	4	US-09-221-017B-1084	Sequence 1084, App	C 938	13	23.6	1334	3	US-08-787-739-44	Sequence 44, Appl
C 866	13	23.6	547	4	US-08-991-789A-158	Sequence 158, App	C 939	13	23.6	1334	3	US-08-487-077A-44	Sequence 44, Appl
C 867	13	23.6	547	4	US-09-062-451-158	Sequence 158, App	C 940	13	23.6	1334	3	US-08-485-863A-44	Sequence 44, Appl
C 868	13	23.6	547	4	US-09-598-326-158	Sequence 158, App	C 941	13	23.6	1334	4	US-08-485-049D-44	Sequence 44, Appl
C 869	13	23.6	552	4	US-09-370-838-266	Sequence 370, Appl	C 942	13	23.6	1334	4	US-09-178-115-44	Sequence 44, Appl
C 870	13	23.6	568	3	US-08-985-950-9	Sequence 9, Appl	C 943	13	23.6	1334	4	US-09-177-776-44	Sequence 44, Appl
C 871	13	23.6	573	4	US-09-328-111-89	Sequence 89, Appl	C 944	13	23.6	1336	4	US-09-257-179-13	Sequence 13, Appl
C 872	13	23.6	575	4	US-09-385-982-123	Sequence 123, App	C 945	13	23.6	1345	4	US-09-372-339-1	Sequence 1, Appl
C 873	13	23.6	579	1	US-07-749-446-1	Sequence 1, Appl	C 946	13	23.6	1345	4	US-09-372-339-2	Sequence 2, Appl
C 874	13	23.6	582	4	US-09-385-982-98	Sequence 98, Appl	C 947	13	23.6	1345	4	US-09-144-367-3	Sequence 3, Appl
C 875	13	23.6	602	4	US-09-385-982-369	Sequence 369, App	C 948	13	23.6	1355	4	US-09-370-838-31	Sequence 31, Appl
C 876	13	23.6	603	4	US-08-149-101A-5	Sequence 5, Appl	C 949	13	23.6	1461	1	US-08-403-634-1	Sequence 1, Appl
C 877	13	23.6	603	5	PCT-US94-12873-5	Sequence 5, Appl	C 950	13	23.6	1461	4	US-08-913-441B-1	Sequence 1, Appl
C 878	13	23.6	607	4	US-09-385-982-235	Sequence 235, App	C 951	13	23.6	1554	1	US-08-370-975B-10	Sequence 10, Appl
C 879	13	23.6	609	4	US-09-385-982-291	Sequence 291, App	C 952	13	23.6	1583	4	US-09-370-838-224	Sequence 224, App
C 880	13	23.6	633	1	US-08-388-267C-1	Sequence 1, Appl	C 953	13	23.6	1600	2	US-08-487-113D-117	Sequence 117, App
C 881	13	23.6	633	4	US-09-277-720-1	Sequence 1, Appl	C 954	13	23.6	1600	2	US-08-720-420A-117	Sequence 117, App
C 882	13	23.6	663	4	US-09-284-878-2	Sequence 2, Appl	C 955	13	23.6	1621	1	US-07-937-609-22	Sequence 22, Appl
C 883	13	23.6	681	4	US-09-410-464-3	Sequence 3, Appl	C 956	13	23.6	1621	4	US-08-029-170-22	Sequence 22, Appl
C 884	13	23.6	710	4	US-09-535-008-47	Sequence 47, Appl	C 957	13	23.6	1639	3	US-09-082-039A-1	Sequence 1, Appl
C 885	13	23.6	713	4	US-08-943-607-23	Sequence 23, Appl	C 958	13	23.6	1639	4	US-09-552-138-1	Sequence 1, Appl
C 886	13	23.6	713	4	US-08-943-607-24	Sequence 24, Appl	C 959	13	23.6	1651	3	US-08-155-005A-3	Sequence 3, Appl
C 887	13	23.6	713	4	US-08-943-607-26	Sequence 26, Appl	C 960	13	23.6	1651	4	US-09-363-783-3	Sequence 3, Appl
C 888	13	23.6	731	6	5304637-3	Patent No. 5304637	C 961	13	23.6	1662	4	US-09-370-398-1	Sequence 1, Appl
C 889	13	23.6	732	4	US-08-239-052-1	Sequence 1, Appl	C 962	13	23.6	1701	4	US-09-411-628-5	Sequence 5, Appl
C 890	13	23.6	737	2	US-08-257-863B-41	Sequence 41, Appl	C 963	13	23.6	1710	3	US-09-255-912-1	Sequence 1, Appl
C 891	13	23.6	737	4	US-08-367-841A-41	Sequence 41, Appl	C 964	13	23.6	1710	3	US-09-082-039A-14	Sequence 14, Appl
C 892	13	23.6	737	5	PCT-US95-07201-41	Sequence 41, Appl	C 965	13	23.6	1710	4	US-09-552-138-14	Sequence 14, Appl
C 893	13	23.6	757	1	US-08-126-587C-6	Sequence 6, Appl	C 966	13	23.6	1721	3	US-08-701-582D-3	Sequence 3, Appl
C 894	13	23.6	759	4	US-09-320-424-10	Sequence 10, Appl	C 967	13	23.6	1728	3	US-08-985-950-7	Sequence 7, Appl
C 895	13	23.6	782	1	US-07-865-878A-1	Sequence 1, Appl	C 968	13	23.6	1749	4	US-09-450-072-56	Sequence 56, Appl
C 896	13	23.6	782	2	US-08-308-736A-20	Sequence 20, Appl	C 969	13	23.6	1749	4	US-09-450-072-57	Sequence 57, Appl
C 897	13	23.6	782	2	US-08-603-010-1	Sequence 1, Appl	C 970	13	23.6	1749	4	US-09-450-072-58	Sequence 58, Appl
C 898	13	23.6	782	4	US-08-645-107A-20	Sequence 20, Appl	C 971	13	23.6	1749	4	US-09-149-476-54	Sequence 54, Appl
C 899	13	23.6	782	4	US-09-197-349-20	Sequence 20, Appl	C 972	13	23.6	1749	4	US-09-351-348-56	Sequence 56, Appl
C 900	13	23.6	828	4	US-09-693-147-1	Sequence 1, Appl	C 973	13	23.6	1749	4	US-09-351-348-57	Sequence 57, Appl
C 901	13	23.6	831	4	US-09-280-116-259	Sequence 259, App	C 974	13	23.6	1749	4	US-09-351-348-58	Sequence 58, Appl
C 902	13	23.6	851	4	US-08-470-369-3	Sequence 3, Appl	C 975	13	23.6	1758	4	US-09-370-838-25	Sequence 25, Appl
C 903	13	23.6	891	4	US-09-247-155-141	Sequence 141, App	C 976	13	23.6	1829	2	US-08-687-080-57	Sequence 57, Appl

c 977 13 23.6 1884 3 US-08-784-582-70 Sequence 70, Appl  
c 978 13 23.6 1921 4 US-08-840-767-51 Sequence 51, Appl  
c 979 13 23.6 1944 4 US-08-149-476-144 Sequence 144, App  
c 980 13 23.6 1992 4 US-08-840-767-1 Sequence 1, Appl  
c 981 13 23.6 2086 3 US-08-589-028-9 Sequence 9, Appl  
c 982 13 23.6 2086 3 US-08-784-582-9 Sequence 9, Appl  
c 983 13 23.6 2086 4 US-08-785-271-9 Sequence 9, Appl  
c 984 13 23.6 2119 4 US-08-227-357-48 Sequence 48, Appl  
c 985 13 23.6 2144 4 US-08-221-017B-731 Sequence 731, App  
c 986 13 23.6 2248 1 US-08-369-780-1 Sequence 1, Appl  
c 987 13 23.6 2248 1 US-08-475-682-1 Sequence 1, Appl  
c 988 13 23.6 2248 1 US-08-780-833-1 Sequence 1, Appl  
c 989 13 23.6 2248 1 US-08-636-036-1 Sequence 1, Appl  
c 990 13 23.6 2248 3 US-08-918-509-1 Sequence 1, Appl  
c 991 13 23.6 2248 3 US-08-108-262-1 Sequence 1, Appl  
c 992 13 23.6 2356 3 US-08-784-582-72 Sequence 72, Appl  
c 993 13 23.6 2392 1 US-08-171-382-5 Sequence 5, Appl  
c 994 13 23.6 2392 1 US-08-309-420-5 Sequence 5, Appl  
c 995 13 23.6 2392 1 US-08-309-419-5 Sequence 5, Appl  
c 996 13 23.6 2392 5 PCT-US95-11856-5 Sequence 5, Appl  
c 997 13 23.6 2392 5 PCT-US95-11878-5 Sequence 5, Appl  
c 998 13 23.6 2394 4 US-08-414-010-3 Sequence 3, Appl  
c 999 13 23.6 2419 2 US-08-765-662-13 Sequence 13, Appl  
c1000 13 23.6 2419 5 PCT-US95-08745-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-09-375-318-38/c  
; Sequence 38, Application US/09375318  
; Patent No. 6468791  
; GENERAL INFORMATION:  
; APPLICANT: Tanzi, Rudolph E.  
; Schellenberg, Gerard D.  
; Wasco, Wilma  
; Levy-Lahad, Ephrat  
; Bird, Thomas D.  
; Galas, David J.  
; TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO  
; ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BEERY LLP  
; STREET: 701 Fifth Ave, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/375,318  
; FILING DATE: 16-Aug-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verna, James M.  
; REGISTRATION NUMBER: 33,287  
; REFERENCE/DOCKET NUMBER: 920010.571C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2387 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-375-318-38  
Query Match 43.6%; Score 24; DB 4; Length 2387;  
Best Local Similarity 100.0%; Pred. No. 0.00032;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 30 TTCGAGATCAGCCTGGCCCAACATG 53  
Db 2207 TTCGAGATCAGCCTGGCCCAACATG 2184  
RESULT 2  
US-09-078-294-6/c  
; Sequence 6, Application US/09078294  
; Patent No. 6265211  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Kong-Hong Andy  
; APPLICANT: Du Sart, Desiree  
; APPLICANT: Cancilla, Michael R.  
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE  
; FILE REFERENCE: Davies Col  
; CURRENT APPLICATION NUMBER: US/09/078,294  
; CURRENT FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 18443  
; TYPE: DNA  
; ORGANISM: BAC-F2 contig 2  
US-09-078-294-6

Query Match 41.8%; Score 23; DB 4; Length 18443;  
Best Local Similarity 100.0%; Pred. No. 0.00098;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 30 TTCGAGATCAGCCTGGCCCAACAT 52  
Db 10385 TTCGAGATCAGCCTGGCCCAACAT 10363

RESULT 3  
US-09-078-294-4  
; Sequence 4, Application US/09078294  
; Patent No. 6265211  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Kong-Hong Andy  
; APPLICANT: Du Sart, Desiree  
; APPLICANT: Cancilla, Michael R.  
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE  
; FILE REFERENCE: Davies Col  
; CURRENT APPLICATION NUMBER: US/09/078,294  
; CURRENT FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 80246  
; TYPE: DNA  
; ORGANISM: Nucleotide sequence of NC-contig  
US-09-078-294-4

Query Match 41.8%; Score 23; DB 4; Length 80246;  
Best Local Similarity 100.0%; Pred. No. 0.00091;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 CACTTGAGGTCAGGAATTCGAGA 36  
Db 3415 CACTTGAGGTCAGGAATTCGAGA 3437  
RESULT 4  
US-09-078-294-3  
; Sequence 3, Application US/09078294  
; Patent No. 6265211

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; LOCATION: (1)...(112132)
; ; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3

Query Match 41.8%; Score 23; DB 4; Length 112132;
Best Local Similarity 100.0%; Pred.No. 0.0009;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTGAGGTCAGGAATTCGAGA 36
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Db 54719 CACTTGAGGTCAGGAATTCGAGA 54741

RESULT 7
US-09-318-448-11/c
; Sequence 11, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-11

Query Match 40.0%; Score 22; DB 4; Length 18596;
Best Local Similarity 100.0%; Pred.No. 0.0033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GAGATCAGCCTGGCCCAACATGA 54
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Db 14751 GAGATCAGCCTGGCCCAACATGA 14730

RESULT 8
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL
; FILE REFERENCE: 89.US2.CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10945..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; NAME/KEY: primer_bind
; LOCATION: 12029..12050
; OTHER INFORMATION: 17-42.pu
; NAME/KEY: primer_bind
; LOCATION: 12581..12603
; OTHER INFORMATION: 17-42.rp complement
; NAME/KEY: primer_bind
; LOCATION: 14992..15012
; OTHER INFORMATION: 17-41.pu
; NAME/KEY: primer_bind
; LOCATION: 15460..15482
; OTHER INFORMATION: 17-41.rp complement
; NAME/KEY: primer_bind
; LOCATION: 42070..42090
; OTHER INFORMATION: 20-841.pu
; NAME/KEY: primer_bind
; LOCATION: 42572..42591
; OTHER INFORMATION: 20-841.rp complement
; NAME/KEY: primer_bind
; LOCATION: 45328..45347
; OTHER INFORMATION: 20-842.pu
; NAME/KEY: primer_bind
; LOCATION: 45863..45883
; OTHER INFORMATION: 20-842.rp complement
; NAME/KEY: primer_bind
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; LOCATION: 76644..76664
; OTHER INFORMATION: 20-853.pu
; NAME/KEY: primer_bind
; LOCATION: 77166..77185
; OTHER INFORMATION: 20-853.rp complement
; NAME/KEY: primer_bind
; LOCATION: 1220..1238
; OTHER INFORMATION: 20-828-311.mis
; NAME/KEY: primer_bind
; LOCATION: 1240..1258
; OTHER INFORMATION: 20-828-311.mis complement
; NAME/KEY: primer_bind
; LOCATION: 12328..12346
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 12348..12366
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15222..15240
; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 15242..15260
; OTHER INFORMATION: 17-41-250.mis complement
; NAME/KEY: primer_bind
; LOCATION: 42199..42217
; OTHER INFORMATION: 20-841-149.mis
; NAME/KEY: primer_bind
; LOCATION: 42219..42237
; OTHER INFORMATION: 20-841-149.mis complement
; NAME/KEY: primer_bind
; LOCATION: 45423..45441
; OTHER INFORMATION: 20-842-115.mis
; NAME/KEY: primer_bind
; LOCATION: 45443..45461
; OTHER INFORMATION: 20-842-115.mis complement
; NAME/KEY: primer_bind
; LOCATION: 77039..77057
; OTHER INFORMATION: 20-853-415.mis
; NAME/KEY: primer_bind
; LOCATION: 77059..77077
; OTHER INFORMATION: 20-853-415.mis complement
; NAME/KEY: misc_binding
; LOCATION: 1227..1251
; OTHER INFORMATION: 20-828-311.probe
; NAME/KEY: misc_binding
; LOCATION: 12335..12359
; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc_binding
; LOCATION: 15229..15253
; OTHER INFORMATION: 17-41-250.probe
; NAME/KEY: misc_binding
; LOCATION: 42206..42230
; OTHER INFORMATION: 20-841-149.probe
; NAME/KEY: misc_binding
; LOCATION: 45430..45454
; OTHER INFORMATION: 20-842-115.probe
; NAME/KEY: misc_binding
; LOCATION: 77046..77070
; OTHER INFORMATION: 20-853-415.probe
; US-09-750-580-1
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Query Match 40.0%; Score 22; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 32 CGAGATCAGCCTGGCCCAACATG 53
Db 58206 CGAGATCAGCCTGGCCCAACATG 58185
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RESULT 9
US-09-110-116-2/c
; Sequence 2, Application US/09110116
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Patent No. 6013479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Hong  
 ; APPLICANT: Cohan, Victoria L.  
 ; APPLICANT: Stuart, Susan G.  
 ; TITLE OF INVENTION: HUMAN ENR1-LIKE G PROTEIN COUPLED  
 ; TITLE OF INVENTION: RECEPTOR  
 ; FILE REFERENCE: PF-0550 US  
 ; CURRENT APPLICATION NUMBER: US/09/110,116  
 ; CURRENT FILING DATE: 1998-07-02  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 3350  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (3293)...(3293)  
 ; OTHER INFORMATION: a or g or c or t/u, unknown, or other  
 ; OTHER INFORMATION: 429905, EOSINOT03  
 US-09-110-116-2

Query Match 38.2%; Score 21; DB 3; Length 3350;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 33 GAGATCAGCCTGGCCACATG 53  
 |||||  
 Db 3066 GAGATCAGCCTGGCCACATG 3046

RESULT 10  
 US-09-328-174A-1  
 ; Sequence 1, Application US/09328174A  
 ; Patent No. 6448003  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guida, Marco  
 ; APPLICANT: Kurth, Janice  
 ; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase  
 ; TITLE OF INVENTION: (STP2)  
 ; FILE REFERENCE: 4389-6 (formerly SEQ-16P)  
 ; CURRENT APPLICATION NUMBER: US/09/328,174A  
 ; CURRENT FILING DATE: 1999-06-08  
 ; PRIOR APPLICATION NUMBER: 09/328,174  
 ; PRIOR FILING DATE: 1999-06-08  
 ; NUMBER OF SEQ ID NOS: 110  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 8396  
 ; TYPE: DNA  
 ; ORGANISM: H. sapiens  
 US-09-328-174A-1

Query Match 38.2%; Score 21; DB 4; Length 8396;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 33 GAGATCAGCCTGGCCACATG 53  
 |||||  
 Db 4657 GAGATCAGCCTGGCCACATG 4677

RESULT 11  
 US-09-167-681-37  
 ; Sequence 37, Application US/09167681A  
 ; Patent No. 6265361  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weinehilb, M.D., Richard M.  
 ; APPLICANT: Raftogiannis, Rebecca B.  
 ; APPLICANT: Wood, Thomas C.  
 ; APPLICANT: Ottewill, Diane M.  
 ; TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS

FILE REFERENCE: 07039/118001  
 ; CURRENT APPLICATION NUMBER: US/09/167,681A  
 ; CURRENT FILING DATE: 1998-10-07  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 37  
 ; LENGTH: 8397  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (3730)...(3879)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3987)...(4112)  
 ; NAME/KEY: CDS  
 ; LOCATION: (4198)...(4293)  
 ; NAME/KEY: CDS  
 ; LOCATION: (6088)...(6213)  
 ; NAME/KEY: CDS  
 ; LOCATION: (6309)...(6404)  
 ; NAME/KEY: CDS  
 ; LOCATION: (7214)...(7393)  
 ; NAME/KEY: CDS  
 ; LOCATION: (7516)...(7629)  
 US-09-167-681-37

Query Match 38.2%; Score 21; DB 4; Length 8409;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GAGATCAGCCTGGCCACATG 53  
 |||||  
 Db 4658 GAGATCAGCCTGGCCACATG 4678

RESULT 12  
 US-09-851-896-3  
 ; Sequence 3, Application US/09851896  
 ; Patent No. 6410325  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND  
 ; TITLE OF INVENTION: EXPRESSION  
 ; FILE REFERENCE: RTS-0220  
 ; CURRENT APPLICATION NUMBER: US/09/851,896  
 ; CURRENT FILING DATE: 2001-05-08  
 ; NUMBER OF SEQ ID NOS: 89  
 ; SEQ ID NO 3  
 ; LENGTH: 70000  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 US-09-851-896-3

Query Match 38.2%; Score 21; DB 4; Length 70000;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 34 AGATCAGCCTGGCCACATGA 54  
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 Db 33721 AGATCAGCCTGGCCACATGA 33741

RESULT 13  
 US-09-750-580-1  
 ; Sequence 1, Application US/09750580  
 ; Patent No. 6455280  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yen, Frances  
 ; APPLICANT: Denison, Blake  
 ; APPLICANT: Bour, Barbara

APPLICANT: Bihain, Bernard  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Ebbets-Reed, Dana  
APPLICANT: Salter-Cid, Luisa  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH  
FILE REFERENCE: 89 US2.CIP  
CURRENT APPLICATION NUMBER: US/09/750,580  
CURRENT FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 09/599,362  
PRIOR FILING DATE: 2000-06-21  
PRIOR APPLICATION NUMBER: PCT/IB00/0101  
PRIOR FILING DATE: 2000-06-21  
PRIOR APPLICATION NUMBER: PCT/IB99/02058  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: US 49/469/099  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: US 60/113,686  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: US 60/141,032  
PRIOR FILING DATE: 1999-06-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent.pm  
SEQ ID NO 1  
LENGTH: 81001  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 10946..12946  
OTHER INFORMATION: 5'regulatory region  
NAME/KEY: exon  
LOCATION: 12947..12958  
OTHER INFORMATION: exon 1  
NAME/KEY: exon  
LOCATION: 13470..13526  
OTHER INFORMATION: exon 2  
NAME/KEY: exon  
LOCATION: 13641..13752  
OTHER INFORMATION: exon 3  
NAME/KEY: exon  
LOCATION: 14271..15968  
OTHER INFORMATION: exon 4  
NAME/KEY: misc feature  
LOCATION: 15969..17969  
OTHER INFORMATION: 3'regulatory region  
NAME/KEY: allele  
LOCATION: 1239  
OTHER INFORMATION: 20-828-311 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 12347  
OTHER INFORMATION: 17-42-319 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 15241  
OTHER INFORMATION: 17-41-250 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 42218  
OTHER INFORMATION: 20-841-149 : polymorphic base A or G  
NAME/KEY: allele  
LOCATION: 45442  
OTHER INFORMATION: 20-842-115 : polymorphic base A or G  
NAME/KEY: allele  
LOCATION: 77058  
OTHER INFORMATION: 20-853-415 : polymorphic base C or T  
NAME/KEY: primer bind  
LOCATION: 929..949  
OTHER INFORMATION: 20-828.pu  
NAME/KEY: primer bind  
LOCATION: 1357..1377  
OTHER INFORMATION: 20-828.rp complement  
NAME/KEY: primer bind  
LOCATION: 12029..12050  
OTHER INFORMATION: 17-41-250.probe  
OTHER INFORMATION: 17-42.pu  
NAME/KEY: primer bind  
LOCATION: 12581..12603  
OTHER INFORMATION: 17-42.rp complement  
NAME/KEY: primer bind  
LOCATION: 14992..15012  
OTHER INFORMATION: 17-41.pu  
NAME/KEY: primer bind  
LOCATION: 15460..15482  
OTHER INFORMATION: 17-41.rp complement  
NAME/KEY: primer bind  
LOCATION: 42070..42090  
OTHER INFORMATION: 20-841.pu  
NAME/KEY: primer bind  
LOCATION: 42572..42591  
OTHER INFORMATION: 20-841.rp complement  
NAME/KEY: primer bind  
LOCATION: 45328..45347  
OTHER INFORMATION: 20-842.pu  
NAME/KEY: primer bind  
LOCATION: 45863..45883  
OTHER INFORMATION: 20-842.rp complement  
NAME/KEY: primer bind  
LOCATION: 76644..76664  
OTHER INFORMATION: 20-853.pu  
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OTHER INFORMATION: 20-853.rp complement  
NAME/KEY: primer bind  
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; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match      38.2%; Score 21; DB 4; Length 84495;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-09-798-096-10
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

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Job time : 31.153 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 1029858 seqs, 724030393 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	25	45.5	14417	9	US-09-860-670-251
	6	25	45.5	14426	9	US-09-860-670-249
	7	24	43.6	98	9	US-10-074-095-818
	8	24	43.6	98	10	US-09-764-860-818
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C 94	22	40.0	18596	10	US-09-967-768A-119	Sequence 119, App	167	21	38.2	26225	10	US-09-764-869-1276	Sequence 1276, Ap
C 95	22	40.0	20210	9	US-10-125-540-598	Sequence 598, App	C 168	21	38.2	26928	9	US-10-020-141-7	Sequence 7, Appli
C 96	22	40.0	20210	10	US-09-764-870-598	Sequence 598, App	C 169	21	38.2	26928	9	US-10-017-631-1	Sequence 1, Appli
C 97	22	40.0	25950	9	US-10-125-540-597	Sequence 597, App	C 170	21	38.2	26928	10	US-09-880-107-2278	Sequence 2278, A
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C 100	22	40.0	29449	9	US-10-074-045-73	Sequence 73, Appl	C 173	21	38.2	27681	9	US-10-091-504-1998	Sequence 1998, Ap
C 101	22	40.0	31871	9	US-10-092-154-1403	Sequence 1403, Ap	C 174	21	38.2	27681	10	US-09-764-869-1997	Sequence 1997, Ap
C 102	22	40.0	31871	10	US-09-764-847-1403	Sequence 1403, Ap	C 175	21	38.2	27681	10	US-09-764-869-1998	Sequence 1998, Ap
C 103	22	40.0	51719	10	US-09-918-686-2	Sequence 2, Appli	C 176	21	38.2	32169	9	US-10-092-154-1963	Sequence 1963, Ap
C 104	22	40.0	81001	9	US-09-842-364-1	Sequence 1, Appli	C 177	21	38.2	32169	9	US-09-764-891-8605	Sequence 8605, Ap
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C 106	22	40.0	92139	10	US-09-918-686-1	Sequence 1, Appli	C 179	21	38.2	32189	9	US-09-764-891-8604	Sequence 8604, Ap
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C 108	22	40.0	148567	10	US-09-801-8769-3	Sequence 3, Appli	C 181	21	38.2	32190	9	US-09-860-670-255	Sequence 255, App
C 109	22	40.0	203654	10	US-09-820-905-3	Sequence 3, Appli	C 182	21	38.2	32249	9	US-09-860-670-260	Sequence 260, App
C 110	22	40.0	465237	10	US-09-933-267A-1	Sequence 1, Appli	C 183	21	38.2	32249	10	US-09-740-041-3	Sequence 3, Appli
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C 128	21	38.2	1906	10	US-09-739-254-32	Sequence 32, Appl	C 201	20	36.4	369	10	US-09-867-701-678	Sequence 7290, Ap
C 129	21	38.2	1906	10	US-09-904-615-32	Sequence 32, Appl	C 202	20	36.4	377	10	US-09-867-701-7290	Sequence 7290, Ap
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C 131	21	38.2	2349	9	US-09-764-891-6859	Sequence 6859, Ap	C 204	20	36.4	423	10	US-09-867-701-6774	Sequence 6774, Ap
C 132	21	38.2	2455	9	US-10-012-896-881	Sequence 881, App	C 205	20	36.4	423	10	US-09-867-701-10582	Sequence 10582, A
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C 137	21	38.2	2455	9	US-09-895-814-882	Sequence 882, App	C 210	20	36.4	479	9	US-10-198-846-626	Sequence 626, App
C 138	21	38.2	2455	10	US-09-759-143-881	Sequence 881, App	C 211	20	36.4	491	9	US-09-764-891-7969	Sequence 7969, Ap
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C 140	21	38.2	2455	10	US-09-780-669-881	Sequence 881, App	C 213	20	36.4	673	9	US-10-198-846-7740	Sequence 7740, A
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C 144	21	38.2	2549	9	US-10-198-846-13920	Sequence 13920, A	C 217	20	36.4	860	9	US-10-198-846-5928	Sequence 5928, Ap
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C 157	21	38.2	16285	10	US-09-764-847-1369	Sequence 1369, Ap	C 230	20	36.4	7703	9	US-10-073-961-456	Sequence 456, App
C 158	21	38.2	16579	9	US-09-764-891-8443	Sequence 8443, Ap	C 231	20	36.4	7703	10	US-09-764-887-456	Sequence 456, App
C 159	21	38.2	18636	9	US-09-764-862-17	Sequence 17, Appl	C 232	20	36.4	7970	10	US-09-764-887-456	Sequence 456, App
C 160	21	38.2	23934	9	US-09-764-891-7210	Sequence 7210, Ap	C 233	20	36.4	7970	9	US-09-764-968-1357	Sequence 1357, Ap
C 161	21	38.2	23934	9	US-10-074-095-777	Sequence 777, App	C 234	20	36.4	9339	9	US-09-764-891-5385	Sequence 5385, Ap
C 162	21	38.2	23934	10	US-09-764-860-777	Sequence 777, App	C 235	20	36.4	10093	9	US-09-764-891-6310	Sequence 6310, Ap
C 163	21	38.2	23934	10	US-09-764-877-2536	Sequence 2536, App	C 236	20	36.4	10612	10	US-09-764-877-3311	Sequence 3311, Ap
C 164	21	38.2	23934	10	US-09-764-877-2544	Sequence 2544, Ap	C 237	20	36.4	10614	10	US-09-764-877-3313	Sequence 3313, Ap
C 165	21	38.2	25231	9	US-09-764-891-5800	Sequence 5800, Ap	C 238	20	36.4	10901	9	US-09-764-891-5924	Sequence 5924, Ap

C 239	20	36.4	15515	10	US-09-822-860-3	Sequence 3, Appli	19	34.5	2120	9	US-10-123-108-73	Sequence 73, Appl
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C 241	20	36.4	18820	9	US-09-764-891-6452	Sequence 6452, Ap	19	34.5	2120	9	US-10-123-261-73	Sequence 73, Appl
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C 246	20	36.4	20029	9	US-10-092-154-1624	Sequence 1624, Ap	19	34.5	2120	9	US-10-123-903-73	Sequence 73, Appl
C 247	20	36.4	20029	10	US-09-764-847-1624	Sequence 1624, Ap	19	34.5	2120	9	US-10-124-819-73	Sequence 73, Appl
C 248	20	36.4	30676	10	US-09-927-091-8	Sequence 8, Appli	19	34.5	2120	9	US-10-124-822-73	Sequence 73, Appl
C 249	20	36.4	32146	9	US-10-074-095-797	Sequence 797, App	19	34.5	2120	9	US-10-140-925-73	Sequence 73, Appl
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C 251	20	36.4	32148	9	US-09-764-891-6906	Sequence 6906, Ap	19	34.5	2120	9	US-10-121-041-73	Sequence 73, Appl
C 252	20	36.4	32248	9	US-10-074-095-802	Sequence 802, App	19	34.5	2120	9	US-10-121-043-73	Sequence 73, Appl
C 253	20	36.4	32248	10	US-09-764-860-802	Sequence 802, App	19	34.5	2120	9	US-10-121-047-73	Sequence 73, Appl
C 254	20	36.4	32816	10	US-09-729-094-3	Sequence 3, Appli	19	34.5	2120	9	US-10-123-215-73	Sequence 73, Appl
C 255	20	36.4	41936	10	US-09-967-768A-116	Sequence 116, App	19	34.5	2120	9	US-10-123-902-73	Sequence 73, Appl
C 256	20	36.4	44848	9	US-09-988-113-42	Sequence 42, Appl	19	34.5	2120	9	US-10-123-908-73	Sequence 73, Appl
C 257	20	36.4	44848	10	US-09-776-874A-42	Sequence 42, Appl	19	34.5	2120	9	US-10-123-909-73	Sequence 73, Appl
C 258	20	36.4	45845	10	US-09-927-091-6	Sequence 6, Appli	19	34.5	2120	9	US-10-123-910-73	Sequence 73, Appl
C 259	20	36.4	49744	10	US-09-927-091-4	Sequence 4, Appli	19	34.5	2120	9	US-10-124-813-73	Sequence 73, Appl
C 260	20	36.4	52354	10	US-09-742-311-3	Sequence 3, Appli	19	34.5	2120	9	US-10-124-817-73	Sequence 73, Appl
C 261	20	36.4	65608	9	US-09-954-531-180	Sequence 180, App	19	34.5	2120	9	US-10-124-824-73	Sequence 73, Appl
C 262	20	36.4	65608	10	US-09-962-436-292	Sequence 292, App	19	34.5	2120	9	US-10-125-922-73	Sequence 73, Appl
C 263	20	36.4	65608	10	US-09-962-832-119	Sequence 119, App	19	34.5	2120	9	US-10-125-924-73	Sequence 73, Appl
C 264	20	36.4	66686	10	US-09-736-960-86	Sequence 86, Appl	19	34.5	2120	9	US-10-127-829A-73	Sequence 73, Appl
C 265	20	36.4	98865	10	US-09-770-689A-3	Sequence 3, Appli	19	34.5	2120	9	US-10-127-835A-73	Sequence 73, Appl
C 266	20	36.4	139257	9	US-09-920-671-11	Sequence 11, Appl	19	34.5	2120	9	US-10-127-839A-73	Sequence 73, Appl
C 267	20	36.4	170834	10	US-09-935-232-7	Sequence 7, Appli	19	34.5	2120	9	US-10-127-901A-73	Sequence 73, Appl
C 268	20	36.4	235033	9	US-10-301-844-1	Sequence 1, Appli	19	34.5	2120	9	US-10-128-693A-73	Sequence 73, Appl
C 269	20	36.4	237326	9	US-10-301-844-2	Sequence 2, Appli	19	34.5	2120	9	US-10-131-813A-73	Sequence 73, Appl
C 270	19	34.5	97	9	US-09-764-891-8614	Sequence 8614, Ap	19	34.5	2120	9	US-10-131-818A-73	Sequence 73, Appl
C 271	19	34.5	102	10	US-10-073-961-540	Sequence 540, App	19	34.5	2120	9	US-10-131-823A-73	Sequence 73, Appl
C 272	19	34.5	102	10	US-09-764-887-540	Sequence 540, App	19	34.5	2120	9	US-10-131-824A-73	Sequence 73, Appl
C 273	19	34.5	216	10	US-09-764-877-3514	Sequence 3514, Ap	19	34.5	2120	9	US-10-131-830A-73	Sequence 73, Appl
C 274	19	34.5	320	10	US-09-867-701-9832	Sequence 9832, Ap	19	34.5	2120	9	US-10-137-872A-73	Sequence 73, Appl
C 275	19	34.5	353	10	US-09-867-701-3577	Sequence 3577, Ap	19	34.5	2120	9	US-10-140-860-73	Sequence 73, Appl
C 276	19	34.5	370	9	US-09-918-995-37699	Sequence 37699, A	19	34.5	2120	9	US-10-142-417-73	Sequence 73, Appl
C 277	19	34.5	390	9	US-09-764-891-2014	Sequence 2014, Ap	19	34.5	2120	9	US-10-147-502-73	Sequence 73, Appl
C 278	19	34.5	401	9	US-09-918-995-35883	Sequence 35883, A	19	34.5	2120	9	US-10-147-515-73	Sequence 73, Appl
C 279	19	34.5	401	10	US-09-967-701-10043	Sequence 10043, A	19	34.5	2120	9	US-10-147-519-73	Sequence 73, Appl
C 280	19	34.5	410	10	US-09-764-877-3416	Sequence 3416, Ap	19	34.5	2120	9	US-10-152-395-73	Sequence 73, Appl
C 281	19	34.5	411	9	US-09-986-480-104	Sequence 104, App	19	34.5	2120	9	US-10-157-782-73	Sequence 73, Appl
C 282	19	34.5	418	9	US-09-918-995-14847	Sequence 14847, A	19	34.5	2120	9	US-10-121-040-73	Sequence 73, Appl
C 283	19	34.5	418	10	US-09-867-701-3670	Sequence 3670, Ap	19	34.5	2120	9	US-10-121-056-73	Sequence 73, Appl
C 284	19	34.5	420	10	US-09-764-877-689	Sequence 689, App	19	34.5	2120	9	US-10-121-061-73	Sequence 73, Appl
C 285	19	34.5	437	10	US-09-967-701-4628	Sequence 4628, Ap	19	34.5	2120	9	US-10-123-235-73	Sequence 73, Appl
C 286	19	34.5	457	9	US-09-918-995-16149	Sequence 16149, A	19	34.5	2120	9	US-10-124-818-73	Sequence 73, Appl
C 287	19	34.5	517	9	US-09-918-995-36102	Sequence 36102, A	19	34.5	2120	9	US-10-125-926A-73	Sequence 73, Appl
C 288	19	34.5	534	9	US-09-918-995-30665	Sequence 30665, A	19	34.5	2120	9	US-10-125-930A-73	Sequence 73, Appl
C 289	19	34.5	612	9	US-09-764-872-70	Sequence 70, Appl	19	34.5	2120	9	US-10-127-831A-73	Sequence 73, Appl
C 290	19	34.5	1027	9	US-09-764-872-617	Sequence 616, App	19	34.5	2120	9	US-10-127-837A-73	Sequence 73, Appl
C 291	19	34.5	1027	9	US-09-764-872-617	Sequence 617, App	19	34.5	2120	9	US-10-127-838B-73	Sequence 73, Appl
C 292	19	34.5	1383	9	US-09-764-891-8325	Sequence 8325, Ap	19	34.5	2120	9	US-10-127-842A-73	Sequence 73, Appl
C 293	19	34.5	2104	9	US-09-953-133-1	Sequence 1, Appli	19	34.5	2120	9	US-10-127-843A-73	Sequence 73, Appl
C 294	19	34.5	2120	9	US-10-028-072-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-684A-73	Sequence 73, Appl
C 295	19	34.5	2120	9	US-10-121-049-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-686A-73	Sequence 73, Appl
C 296	19	34.5	2120	9	US-10-123-904-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-690A-73	Sequence 73, Appl
C 297	19	34.5	2120	9	US-10-140-470-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 298	19	34.5	2120	9	US-10-175-746-73	Sequence 73, Appl	19	34.5	2120	9	US-10-131-819A-73	Sequence 73, Appl
C 299	19	34.5	2120	9	US-10-176-918-73	Sequence 73, Appl	19	34.5	2120	9	US-10-127-850A-73	Sequence 73, Appl
C 300	19	34.5	2120	9	US-10-176-921-73	Sequence 73, Appl	19	34.5	2120	9	US-10-127-851A-73	Sequence 73, Appl
C 301	19	34.5	2120	9	US-10-137-865-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-684A-73	Sequence 73, Appl
C 302	19	34.5	2120	9	US-10-140-474-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-686A-73	Sequence 73, Appl
C 303	19	34.5	2120	9	US-10-142-431-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-690A-73	Sequence 73, Appl
C 304	19	34.5	2120	9	US-10-143-114-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 305	19	34.5	2120	9	US-10-140-002-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 306	19	34.5	2120	9	US-10-142-419-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 307	19	34.5	2120	9	US-10-123-362-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 308	19	34.5	2120	9	US-10-142-423-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 309	19	34.5	2120	9	US-10-121-050-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 310	19	34.5	2120	9	US-10-141-755-73	Sequence 73, Appl	19	34.5	2120	9	US-10-128-691A-73	Sequence 73, Appl
C 311	19	34.5	2120	9	US-10-143-032-73	Sequence 73, Appl	19	34.5	2120	9	US-10-131-829A-73	Sequence 73, Appl

C 385	19	34.5	2120	9	US-10-131-836A-73	Sequence 73, Appl	C 458	19	34.5	13485	10	US-09-764-870-548	Sequence 548, App
C 386	19	34.5	2120	9	US-10-137-868-73	Sequence 73, Appl	C 459	19	34.5	15295	10	US-09-764-877-3404	Sequence 3404, Ap
C 387	19	34.5	2120	9	US-10-146-729-73	Sequence 73, Appl	C 460	19	34.5	15745	10	US-09-764-877-3336	Sequence 3336, Ap
C 388	19	34.5	2120	9	US-10-146-791-73	Sequence 73, Appl	C 461	19	34.5	17200	10	US-09-764-877-3390	Sequence 3390, Ap
C 389	19	34.5	2120	9	US-10-147-484-73	Sequence 73, Appl	C 462	19	34.5	18878	10	US-09-764-877-3806	Sequence 3806, Ap
C 390	19	34.5	2120	9	US-10-147-482-73	Sequence 73, Appl	C 463	19	34.5	19315	9	US-10-091-438-245	Sequence 245, App
C 391	19	34.5	2120	9	US-10-147-508-73	Sequence 73, Appl	C 464	19	34.5	21358	9	US-09-764-872-816	Sequence 816, App
C 392	19	34.5	2120	9	US-10-147-512-73	Sequence 73, Appl	C 465	19	34.5	21358	9	US-09-764-891-9107	Sequence 9107, Ap
C 393	19	34.5	2120	9	US-10-158-782-73	Sequence 73, Appl	C 466	19	34.5	21470	9	US-10-092-154-1157	Sequence 1157, Ap
C 394	19	34.5	2120	9	US-10-175-735-73	Sequence 73, Appl	C 467	19	34.5	21470	10	US-09-764-847-1157	Sequence 1157, Ap
C 395	19	34.5	2120	9	US-10-123-905-73	Sequence 73, Appl	C 468	19	34.5	21676	9	US-09-764-872-815	Sequence 815, App
C 396	19	34.5	2120	9	US-10-123-907-73	Sequence 73, Appl	C 469	19	34.5	21676	9	US-09-764-891-9106	Sequence 9106, Ap
C 397	19	34.5	2120	9	US-10-124-815-73	Sequence 73, Appl	C 470	19	34.5	21913	9	US-09-764-891-6065	Sequence 6065, Ap
C 398	19	34.5	2120	9	US-10-125-921A-73	Sequence 73, Appl	C 471	19	34.5	21913	9	US-09-764-891-6066	Sequence 6066, Ap
C 399	19	34.5	2120	9	US-10-125-928A-73	Sequence 73, Appl	C 472	19	34.5	21913	9	US-09-764-891-6067	Sequence 6067, Ap
C 400	19	34.5	2120	9	US-10-127-821A-73	Sequence 73, Appl	C 473	19	34.5	23106	9	US-09-863-049A-1	Sequence 1, Appl1
C 401	19	34.5	2120	9	US-10-127-822A-73	Sequence 73, Appl	C 474	19	34.5	23580	9	US-10-074-095-990	Sequence 990, App
C 402	19	34.5	2120	9	US-10-127-824A-73	Sequence 73, Appl	C 475	19	34.5	23580	10	US-09-764-860-990	Sequence 264, App
C 403	19	34.5	2120	9	US-10-127-826A-73	Sequence 73, Appl	C 476	19	34.5	23603	9	US-09-860-670-258	Sequence 258, App
C 404	19	34.5	2120	9	US-10-127-827A-73	Sequence 73, Appl	C 477	19	34.5	23613	9	US-09-860-670-263	Sequence 263, App
C 405	19	34.5	2120	9	US-10-127-828A-73	Sequence 73, Appl	C 478	19	34.5	24218	9	US-10-073-961-602	Sequence 602, App
C 406	19	34.5	2120	9	US-10-127-830A-73	Sequence 73, Appl	C 479	19	34.5	24768	9	US-09-764-887-602	Sequence 602, App
C 407	19	34.5	2120	9	US-10-127-832A-73	Sequence 73, Appl	C 480	19	34.5	24768	10	US-09-764-887-602	Sequence 8034, Ap
C 408	19	34.5	2120	9	US-10-127-833A-73	Sequence 73, Appl	C 481	19	34.5	27062	9	US-09-764-891-8034	Sequence 8303, Ap
C 409	19	34.5	2120	9	US-10-127-834A-73	Sequence 73, Appl	C 482	19	34.5	32134	9	US-09-764-891-6303	Sequence 6303, Ap
C 410	19	34.5	2120	9	US-10-127-836A-73	Sequence 73, Appl	C 483	19	34.5	32148	9	US-09-764-891-6906	Sequence 6906, Ap
C 411	19	34.5	2120	9	US-10-127-841A-73	Sequence 73, Appl	C 484	19	34.5	32184	9	US-09-764-891-8538	Sequence 8538, Ap
C 412	19	34.5	2120	9	US-10-127-844A-73	Sequence 73, Appl	C 485	19	34.5	32191	9	US-09-764-891-6304	Sequence 6304, Ap
C 413	19	34.5	2120	9	US-10-128-687A-73	Sequence 73, Appl	C 486	19	34.5	32204	9	US-09-764-891-6454	Sequence 6454, Ap
C 414	19	34.5	2120	9	US-10-128-688A-73	Sequence 73, Appl	C 487	19	34.5	32204	9	US-09-764-891-8537	Sequence 8537, Ap
C 415	19	34.5	2120	9	US-10-128-689A-73	Sequence 73, Appl	C 488	19	34.5	32367	9	US-10-158-160A-14	Sequence 14, Appl
C 416	19	34.5	2120	9	US-10-128-694A-73	Sequence 73, Appl	C 489	19	34.5	36741	10	US-09-782-378A-12	Sequence 12, Appl
C 417	19	34.5	2120	9	US-10-131-825A-73	Sequence 73, Appl	C 490	19	34.5	53332	9	US-10-424-562-3	Sequence 3, Appl1
C 418	19	34.5	2120	9	US-10-230-417-73	Sequence 73, Appl	C 491	19	34.5	53332	10	US-09-801-861-3	Sequence 3, Appl1
C 419	19	34.5	2120	9	US-10-121-051-73	Sequence 73, Appl	C 492	19	34.5	60153	9	US-10-222-334-7	Sequence 7, Appl1
C 420	19	34.5	2120	9	US-10-131-815A-73	Sequence 73, Appl	C 493	19	34.5	62804	12	US-10-096-960-3	Sequence 3, Appl1
C 421	19	34.5	2120	9	US-10-131-817A-73	Sequence 73, Appl	C 494	19	34.5	62944	10	US-09-954-456-2257	Sequence 2257, Ap
C 422	19	34.5	2120	9	US-10-131-821A-73	Sequence 73, Appl	C 495	19	34.5	73308	10	US-09-954-456-2276	Sequence 2276, Ap
C 423	19	34.5	2120	9	US-10-131-822A-73	Sequence 73, Appl	C 496	19	34.5	98829	9	US-10-017-724-3	Sequence 3, Appl1
C 424	19	34.5	2120	9	US-10-131-828A-73	Sequence 73, Appl	C 497	19	34.5	147309	10	US-09-742-312-3	Sequence 3, Appl1
C 425	19	34.5	2120	9	US-10-131-835A-73	Sequence 73, Appl	C 498	19	34.5	254366	9	US-09-967-768A-314	Sequence 314, App
C 426	19	34.5	2120	9	US-10-131-836A-73	Sequence 73, Appl	C 499	19	34.5	326014	10	US-09-932-871-3	Sequence 3, Appl1
C 427	19	34.5	2120	9	US-10-137-869A-73	Sequence 73, Appl	C 500	19	34.5	465237	10	US-09-731-231A-3	Sequence 1, Appl1
C 428	19	34.5	2120	9	US-10-147-523-73	Sequence 73, Appl	C 501	19	34.5	465237	9	US-09-933-267A-1	Sequence 1, Appl1
C 429	19	34.5	2120	9	US-10-158-785-73	Sequence 73, Appl	C 502	19	34.5	1503841	9	US-09-946-807-1	Sequence 1, Appl1
C 430	19	34.5	2120	9	US-10-123-912-73	Sequence 73, Appl	C 503	19	34.5	1503841	10	US-09-946-807-1	Sequence 1, Appl1
C 431	19	34.5	2120	9	US-10-123-912-73	Sequence 73, Appl	C 504	19	34.5	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C 432	19	34.5	2120	9	US-10-192-007-73	Sequence 73, Appl	C 505	18	32.7	129	9	US-09-795-668-1	Sequence 557, App
C 433	19	34.5	2120	9	US-10-194-359-73	Sequence 73, Appl	C 506	18	32.7	129	9	US-10-073-961-557	Sequence 557, App
C 434	19	34.5	2594	10	US-09-822-849A-338	Sequence 338, App	C 507	18	32.7	129	9	US-09-764-887-557	Sequence 557, App
C 435	19	34.5	2907	10	US-09-954-456-318	Sequence 318, App	C 508	18	32.7	254	10	US-09-867-701-1718	Sequence 1718, Ap
C 436	19	34.5	2907	10	US-09-954-456-823	Sequence 823, App	C 509	18	32.7	299	10	US-09-867-701-9327	Sequence 9327, Ap
C 437	19	34.5	2907	10	US-09-954-456-1226	Sequence 1226, Ap	C 510	18	32.7	334	10	US-09-867-701-6897	Sequence 6897, Ap
C 438	19	34.5	2907	10	US-09-880-107-2318	Sequence 2318, Ap	C 511	18	32.7	349	10	US-09-867-701-416	Sequence 416, App
C 439	19	34.5	3116	9	US-09-764-872-585	Sequence 585, App	C 512	18	32.7	375	9	US-09-803-719-1151	Sequence 1151, Ap
C 440	19	34.5	3336	9	US-10-118-783-1	Sequence 1, Appl1	C 513	18	32.7	385	10	US-09-867-701-236	Sequence 236, App
C 441	19	34.5	3336	9	US-10-118-783-2	Sequence 2, Appl1	C 514	18	32.7	410	10	US-09-867-701-444	Sequence 444, App
C 442	19	34.5	5080	9	US-10-092-154-1197	Sequence 1197, Ap	C 515	18	32.7	422	10	US-09-867-701-7383	Sequence 7383, Ap
C 443	19	34.5	5080	9	US-10-092-154-1198	Sequence 1198, Ap	C 516	18	32.7	430	9	US-09-918-995-16743	Sequence 16743, A
C 444	19	34.5	5080	10	US-09-764-847-1197	Sequence 1197, Ap	C 517	18	32.7	433	9	US-09-918-995-37132	Sequence 37132, A
C 445	19	34.5	5080	10	US-09-764-847-1198	Sequence 1198, Ap	C 518	18	32.7	434	9	US-09-918-995-28768	Sequence 28768, A
C 446	19	34.5	5797	9	US-09-764-891-6093	Sequence 6093, Ap	C 519	18	32.7	440	10	US-09-918-995-4317	Sequence 4317, Ap
C 447	19	34.5	5987	9	US-10-118-783-3	Sequence 3, Appl1	C 520	18	32.7	443	10	US-09-867-701-1719	Sequence 1719, Ap
C 448	19	34.5	6990	9	US-10-118-783-23	Sequence 23, Appl1	C 521	18	32.7	447	10	US-09-867-701-430	Sequence 430, App
C 449	19	34.5	7133	9	US-10-198-846-13766	Sequence 13766, A	C 522	18	32.7	455	9	US-09-918-995-9772	Sequence 9772, Ap
C 450	19	34.5	7389	9	US-09-764-868-1448	Sequence 1448, Ap	C 523	18	32.7	459	9	US-09-918-995-11365	Sequence 11365, A
C 451	19	34.5	10126	10	US-09-764-877-2194	Sequence 2194, Ap	C 524	18	32.7	467	9	US-09-918-995-26473	Sequence 26473, A
C 452	19	34.5	10377	9	US-09-764-891-6453	Sequence 6453, Ap	C 525	18	32.7	484	9	US-09-918-995-30630	Sequence 30630, A
C 453	19	34.5	12754	9	US-09-984-827-5	Sequence 5, Appl1	C 526	18	32.7	486	9	US-10-158-846-2363	Sequence 2363, Ap
C 454	19	34.5	12771	10	US-09-764-891-5777	Sequence 5777, Ap	C 527	18	32.7	489	10	US-09-783-590-11928	Sequence 11928, A
C 455	19	34.5	13223	9	US-09-764-877-5777	Sequence 5777, Ap	C 528	18	32.7	502	9	US-09-918-995-20295	Sequence 20295, A
C 456	19	34.5	13223	9	US-10-074-045-67	Sequence 67, Appl	C 529	18	32.7	505	9	US-09-918-995-22293	Sequence 22293, A
C 457	19	34.5	13485	9	US-10-125-540-548	Sequence 548, App	C 530	18	32.7	506	9	US-09-918-995-3126	Sequence 3126, Ap

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c 535	18	32.7	646	9	US-10-198-846-8147	Sequence 8147, App	c 608	18	32.7	113604	9	US-10-227-195A-2	Sequence 2, Appli
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c 538	18	32.7	950	10	US-09-954-456-1228	Sequence 1228, App	c 611	18	32.7	176373	9	US-10-095-407-17	Sequence 17, Appl
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c 573	18	32.7	8879	9	US-10-092-154-1402	Sequence 1402, App	c 646	17	30.9	468	9	US-09-918-995-32510	Sequence 32510, A
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c 728	17	30.9	5602	10	US-09-764-887-616	Sequence 616, App	c 800	17	30.9	17792	9	US-10-091-504-1599	Sequence 1599, Ap
c 729	17	30.9	5786	9	US-10-079-854-240	Sequence 240, App	c 801	17	30.9	17792	10	US-09-764-869-1599	Sequence 1599, Ap
c 730	17	30.9	5786	10	US-09-764-878-240	Sequence 240, App	c 802	17	30.9	17965	9	US-09-764-891-8198	Sequence 8198, Ap
c 731	17	30.9	6398	9	US-10-079-854-272	Sequence 272, App	c 803	17	30.9	17965	10	US-09-768-781-5	Sequence 5, Appli
c 732	17	30.9	6398	9	US-10-079-854-273	Sequence 273, App	c 804	17	30.9	18000	10	US-09-800-631-17	Sequence 17, Appl
c 733	17	30.9	6398	9	US-10-074-095-951	Sequence 951, App	c 805	17	30.9	18000	9	US-10-092-154-1682	Sequence 1682, Ap
c 734	17	30.9	6398	9	US-10-074-095-952	Sequence 952, App	c 806	17	30.9	18692	10	US-09-764-847-1682	Sequence 1682, Ap
c 735	17	30.9	6398	10	US-09-764-878-272	Sequence 272, App	c 807	17	30.9	19000	9	US-10-109-084-3	Sequence 3, Appli
c 736	17	30.9	6398	10	US-09-764-878-273	Sequence 273, App	c 808	17	30.9	19167	9	US-09-764-891-8028	Sequence 8028, Ap
c 737	17	30.9	6398	10	US-09-764-860-951	Sequence 951, App	c 809	17	30.9	19616	10	US-09-764-877-3220	Sequence 3220, Ap
c 738	17	30.9	6398	10	US-09-764-860-952	Sequence 952, App	c 810	17	30.9	20029	9	US-10-092-154-1624	Sequence 1624, Ap
c 739	17	30.9	6534	9	US-09-764-891-5454	Sequence 5454, Ap	c 811	17	30.9	20029	10	US-09-764-847-1624	Sequence 1624, Ap
c 740	17	30.9	6660	10	US-09-764-877-2529	Sequence 2529, Ap	c 812	17	30.9	20530	9	US-09-764-891-8252	Sequence 8252, Ap
c 741	17	30.9	6964	9	US-09-816-653A-5	GENERAL INFORMAT	c 813	17	30.9	20966	9	US-10-277-032-3	Sequence 3, Appli
c 742	17	30.9	7588	9	US-09-764-891-3724	Sequence 3724, Ap	c 814	17	30.9	20966	10	US-10-231-814-7	Sequence 7, Appli
c 743	17	30.9	7687	9	US-09-764-891-7346	Sequence 7346, Ap	c 815	17	30.9	20966	9	US-09-776-976-7	Sequence 7, Appli
c 744	17	30.9	7739	10	US-09-764-877-3189	Sequence 3189, Ap	c 816	17	30.9	20966	10	US-09-758-055-7	Sequence 7, Appli
c 745	17	30.9	7809	9	US-09-764-891-6094	Sequence 6094, Ap	c 817	17	30.9	20966	10	US-09-909-547-7	Sequence 7, Appli
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c 747	17	30.9	8575	9	US-09-764-891-8707	Sequence 8707, Ap	c 819	17	30.9	21606	9	US-10-091-504-1733	Sequence 1733, Ap
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	17	30.9					c 822	17	30.9	21761	9	US-10-092-154-1680	Sequence 1680, Ap



c 823	17	30.9	21761	10	US-09-764-847-1680	Sequence 1680, Ap	896	17	30.9	32219	10	US-09-764-869-2016	Sequence 2016, Ap
824	17	30.9	22255	9	US-09-976-740-51	Sequence 51, Appl	897	17	30.9	32248	9	US-10-074-095-802	Sequence 802, App
825	17	30.9	22255	12	US-10-023-529-51	Sequence 51, Appl	898	17	30.9	32248	9	US-09-764-860-802	Sequence 802, App
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c 827	17	30.9	22452	9	US-09-764-868-1487	Sequence 1487, Ap	c 900	17	30.9	32249	9	US-09-764-891-5759	Sequence 5759, Ap
c 828	17	30.9	22452	9	US-09-764-868-1489	Sequence 1489, Ap	c 901	17	30.9	32249	9	US-09-764-891-7619	Sequence 7619, Ap
c 829	17	30.9	22484	10	US-09-875-114-2	Sequence 2, Appli	c 902	17	30.9	32249	10	US-09-764-878-202	Sequence 202, App
c 830	17	30.9	22484	10	US-09-880-107-3341	Sequence 3341, Ap	c 903	17	30.9	32249	10	US-09-954-456-1110	Sequence 1110, App
c 831	17	30.9	22645	9	US-09-764-891-7673	Sequence 7673, Ap	c 904	17	30.9	32641	10	US-09-954-456-1110	Sequence 1110, App
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c 834	17	30.9	23433	10	US-09-927-091-7	Sequence 7, Appli	c 907	17	30.9	32641	9	US-10-135-687-3	Sequence 3, Appli
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c 836	17	30.9	24533	9	US-09-764-868-1349	Sequence 1349, Ap	c 909	17	30.9	32641	10	US-09-954-456-292	Sequence 292, App
c 837	17	30.9	24881	10	US-09-817-184-3	Sequence 4, Appli	c 910	17	30.9	32641	10	US-09-954-456-529	Sequence 529, App
c 838	17	30.9	25377	9	US-10-061-119-4	Sequence 4, Appli	c 911	17	30.9	32641	10	US-09-880-107-3950	Sequence 3950, App
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c 840	17	30.9	26006	9	US-09-764-891-6285	Sequence 1963, Ap	c 913	17	30.9	32641	12	US-10-025-187-3	Sequence 3, Appli
c 841	17	30.9	26006	10	US-09-764-864-1638	Sequence 1638, Ap	c 914	17	30.9	32641	10	US-09-820-003A-3	Sequence 3, Appli
c 842	17	30.9	26013	9	US-10-091-504-1961	Sequence 1961, Ap	c 915	17	30.9	32641	9	US-10-274-873-3	Sequence 3, Appli
c 843	17	30.9	26013	9	US-09-764-891-6283	Sequence 6283, Ap	c 916	17	30.9	32641	9	US-09-816-093-3	Sequence 3, Appli
c 844	17	30.9	26013	10	US-09-764-869-1961	Sequence 1961, Ap	c 917	17	30.9	32641	9	US-10-282-048-3	Sequence 3, Appli
c 845	17	30.9	26013	10	US-09-764-864-1636	Sequence 1636, Ap	c 918	17	30.9	32641	9	US-10-152-724A-24	Sequence 24, Appli
c 846	17	30.9	26018	9	US-10-091-504-1962	Sequence 1962, Ap	c 919	17	30.9	32641	10	US-09-816-685-3	Sequence 3, Appli
c 847	17	30.9	26018	9	US-09-764-891-6284	Sequence 6284, Ap	c 920	17	30.9	32641	10	US-09-954-456-292	Sequence 292, App
c 848	17	30.9	26018	10	US-09-764-869-1962	Sequence 1962, Ap	c 921	17	30.9	32641	10	US-09-954-456-529	Sequence 529, App
c 849	17	30.9	26018	10	US-09-764-864-1637	Sequence 1637, Ap	c 922	17	30.9	32641	10	US-09-880-107-3950	Sequence 3950, App
c 850	17	30.9	26657	10	US-09-810-673A-3	Sequence 3, Appli	c 923	17	30.9	32641	10	US-10-060-332-3	Sequence 3, Appli
c 851	17	30.9	27332	9	US-10-092-154-1555	Sequence 1555, Ap	c 924	17	30.9	32641	9	US-10-025-187-3	Sequence 3, Appli
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c 855	17	30.9	27681	9	US-10-091-504-1997	Sequence 1997, Ap	c 928	17	30.9	32641	9	US-09-816-093-3	Sequence 3, Appli
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c 857	17	30.9	27681	10	US-09-764-869-1997	Sequence 1997, Ap	c 930	17	30.9	32641	9	US-10-152-724A-23	Sequence 23, Appli
c 858	17	30.9	27681	10	US-09-764-869-1998	Sequence 1998, Ap	c 931	17	30.9	32641	9	US-09-747-810-1	Sequence 1, Appli
c 859	17	30.9	28001	9	US-10-193-295-3	Sequence 3, Appli	c 932	17	30.9	32641	9	US-10-224-562-3	Sequence 3, Appli
c 860	17	30.9	28313	10	US-09-764-877-3194	Sequence 3194, Ap	c 933	17	30.9	32641	10	US-09-801-861-3	Sequence 3, Appli
c 861	17	30.9	28313	10	US-09-764-877-3194	Sequence 3194, Ap	c 934	17	30.9	32641	10	US-09-801-861-3	Sequence 3, Appli
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c 865	17	30.9	30625	10	US-09-927-091-5	Sequence 5, Appli	c 938	17	30.9	32641	9	US-09-804-472-3	Sequence 3, Appli
c 866	17	30.9	31474	9	US-09-764-891-8149	Sequence 8149, Ap	c 939	17	30.9	32641	9	US-09-859-888-3	Sequence 3, Appli
c 867	17	30.9	31994	9	US-10-091-548-71	Sequence 71, Appli	c 940	17	30.9	32641	10	US-09-854-883-243	Sequence 243, App
c 868	17	30.9	31994	9	US-10-091-548-71	Sequence 71, Appli	c 941	17	30.9	32641	10	US-09-880-107-3949	Sequence 3949, Ap
c 869	17	30.9	31994	9	US-10-074-095-599	Sequence 599, App	c 942	17	30.9	32641	10	US-09-880-107-3428	Sequence 3428, Ap
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c 871	17	30.9	32134	9	US-09-764-891-6303	Sequence 6303, Ap	c 944	17	30.9	32641	10	US-10-300-827-3	Sequence 3, Appli
c 872	17	30.9	32134	9	US-09-764-891-6763	Sequence 6763, Ap	c 945	17	30.9	32641	9	US-09-803-661-3	Sequence 3, Appli
c 873	17	30.9	32146	9	US-10-074-095-797	Sequence 797, App	c 946	17	30.9	32641	9	US-10-237-195A-1	Sequence 1, Appli
c 874	17	30.9	32146	10	US-09-764-860-797	Sequence 797, App	c 947	17	30.9	32641	10	US-10-227-195A-2	Sequence 2, Appli
c 875	17	30.9	32152	9	US-09-764-872-518	Sequence 518, App	c 948	17	30.9	32641	10	US-09-818-512-3	Sequence 3, Appli
c 876	17	30.9	32152	9	US-10-072-349-328	Sequence 328, App	c 949	17	30.9	32641	9	US-09-729-920-3	Sequence 3, Appli
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c 878	17	30.9	32173	9	US-09-764-891-6246	Sequence 6246, Ap	c 951	17	30.9	32641	10	US-09-731-231A-3	Sequence 3, Appli
c 879	17	30.9	32187	9	US-10-102-627-109	Sequence 109, App	c 952	17	30.9	32641	9	US-09-949-654-3	Sequence 3, Appli
c 880	17	30.9	32190	9	US-10-079-854-201	Sequence 201, App	c 953	17	30.9	32641	9	US-09-901-136-3	Sequence 3, Appli
c 881	17	30.9	32190	10	US-09-764-878-201	Sequence 201, App	c 954	17	30.9	32641	10	US-09-844-653-5	Sequence 5, Appli
c 882	17	30.9	32191	9	US-09-764-891-6304	Sequence 6304, Ap	c 955	16	29.1	84	9	US-09-263-959-1	Sequence 1, Appli
c 883	17	30.9	32191	10	US-09-764-877-3374	Sequence 3374, Ap	c 956	16	29.1	84	9	US-09-764-872-885	Sequence 885, App
c 884	17	30.9	32192	9	US-09-764-891-9791	Sequence 9791, Ap	c 957	16	29.1	84	9	US-09-764-872-886	Sequence 886, App
c 885	17	30.9	32192	10	US-09-764-877-3657	Sequence 3657, Ap	c 958	16	29.1	84	9	US-09-764-872-887	Sequence 887, App
c 886	17	30.9	32193	9	US-10-079-854-200	Sequence 200, App	c 959	16	29.1	84	9	US-09-764-891-9880	Sequence 9880, App
c 887	17	30.9	32193	10	US-09-764-878-200	Sequence 200, App	c 960	16	29.1	84	10	US-09-764-877-3676	Sequence 3676, App
c 888	17	30.9	32195	9	US-10-102-627-92	Sequence 92, Appli	c 961	16	29.1	86	9	US-10-073-961-563	Sequence 563, App
c 889	17	30.9	32195	10	US-10-091-504-2017	Sequence 2017, Ap	c 962	16	29.1	86	10	US-09-764-887-563	Sequence 563, App
c 890	17	30.9	32195	10	US-09-764-869-2017	Sequence 2017, Ap	c 963	16	29.1	87	9	US-09-764-891-5536	Sequence 5536, App
c 891	17	30.9	32204	9	US-09-764-872-517	Sequence 517, App	c 964	16	29.1	87	9	US-09-764-891-5537	Sequence 5537, App
c 892	17	30.9	32204	9	US-10-072-349-327	Sequence 327, App	c 965	16	29.1	87	9	US-09-764-891-10026	Sequence 10026, A
c 893	17	30.9	32204	10	US-09-764-855-327	Sequence 327, App	c 966	16	29.1	87	9	US-10-074-095-962	Sequence 962, App
c 894	17	30.9	32216	9	US-09-764-891-9613	Sequence 9613, Ap	c 967	16	29.1	87	10	US-09-764-860-962	Sequence 962, App
c 895	17	30.9	32219	9	US-10-091-504-2016	Sequence 2016, Ap	c 968	16	29.1	87	10	US-09-764-877-3775	Sequence 3775, Ap

c 969 16 29.1 89 9 US-10-073-961-538  
 c 970 16 29.1 89 10 US-09-764-887-538  
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 Sequence 6894, App  
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 Sequence 1674, App

## ALIGNMENTS

RESULT 1  
 US-09-918-995-22754  
 ; Sequence 22754, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 22754  
 ; LENGTH: 490  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(490)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-22754

Query Match 49.1%; Score 27; DB 9; Length 490;  
 Best Local Similarity 100.0%; Pred.No. 1.5e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGACGGCAGACCTTCAGGTCAGGA 28  
 Db 409 AGGACGGCAGACCTTCAGGTCAGGA 435

RESULT 2  
 US-09-867-701-795

; Sequence 795, Application US/09867701  
 ; Patent No. US2002013237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 795  
 ; LENGTH: 218  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
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 US-09-867-701-795

Query Match 45.5%; Score 25; DB 10; Length 218;  
 Best Local Similarity 100.0%; Pred.No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATGA 54  
 Db 53 TTCGAGATCAGCTGGCCACATGA 77

## RESULT 3

US-09-918-995-23432  
 ; Sequence 23432, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 23432  
 ; LENGTH: 506  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
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 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-23432

Query Match 45.5%; Score 25; DB 9; Length 506;  
 Best Local Similarity 100.0%; Pred.No. 0.00018;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATGA 54  
 Db 286 TTCGAGATCAGCTGGCCACATGA 310

## RESULT 4

US-09-748-107-3  
 ; Sequence 3, Application US/09748107  
 ; Patent No. US20020028915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEI, Ming-Hui et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CLO00784  
; CURRENT APPLICATION NUMBER: US/09/748,107  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 10708  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(10708)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-748-107-3

Query Match 45.5%; Score 25; DB 10; Length 10708;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6117 TTCGAGATCAGCCTGGCCCAACATGA 6141

## RESULT 5

US-09-860-670-251/c  
; Sequence 251, Application US/09860670  
; Patent No. US20020165137A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA12791  
; CURRENT APPLICATION NUMBER: US/09/860,670  
; CURRENT FILING DATE: 2001-05-21  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 251  
; LENGTH: 14417  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-860-670-251

Query Match 45.5%; Score 25; DB 9; Length 14417;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATGA 54  
|||||  
Db 10166 TTCGAGATCAGCCTGGCCCAACATGA 10142

## RESULT 6

US-09-860-670-249/c  
; Sequence 249, Application US/09860670  
; Patent No. US20020165137A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA12791  
; CURRENT APPLICATION NUMBER: US/09/860,670  
; CURRENT FILING DATE: 2001-05-21  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 249  
; LENGTH: 14426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-860-670-249

Query Match 45.5%; Score 25; DB 9; Length 14426;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATGA 54  
|||||  
Db 10175 TTCGAGATCAGCCTGGCCCAACATGA 10151

## RESULT 7

US-10-074-095-818/c  
; Sequence 818, Application US/10074095  
; Publication No. US2003007704A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008C1  
; CURRENT APPLICATION NUMBER: US/10/074,095  
; CURRENT FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: 09/764,860  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
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; PRIOR FILING DATE: 2000-08-22  
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; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
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; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/251,869  
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; PRIOR APPLICATION NUMBER: 60/235,834  
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; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
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; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
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; PRIOR APPLICATION NUMBER: 60/224,519  
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; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/249,299  
; PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/236,327  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/241,785  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/244,617  
;; PRIOR FILING DATE: 2000-11-01  
;; PRIOR APPLICATION NUMBER: 60/225,268  
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;; PRIOR APPLICATION NUMBER: 60/229,344  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/234,997  
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;; PRIOR APPLICATION NUMBER: 60/229,343  
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;; PRIOR APPLICATION NUMBER: 60/237,040  
;; PRIOR FILING DATE: 2000-10-02  
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;; PRIOR APPLICATION NUMBER: 60/241,787  
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;; PRIOR APPLICATION NUMBER: 60/227,182  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/225,214  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/235,836  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: 60/230,438

;; PRIOR FILING DATE: 2000-09-06  
;; PRIOR APPLICATION NUMBER: 60/215,135  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: 60/225,266  
;; PRIOR FILING DATE: 2000-08-14  
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;; PRIOR APPLICATION NUMBER: 60/241,786  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,221  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08

Query Match 43.6%; Score 24; DB 9; Length 98;  
Best Local Similarity 100.0%; Pred.No. 0.00084;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 TTGAGATCAGCTGGCCACATG 53

Db 42 TTGAGATCAGCTGGCCACATG 19

## RESULT 8

US-10-074-095-819/c  
; Sequence 819, Application US/10074095  
; Publication No. US2003007704A1

## GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC008C1

; CURRENT APPLICATION NUMBER: US/10/074,095

; CURRENT FILING DATE: 2002-02-14

; PRIOR APPLICATION NUMBER: 09/766,860

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: 60/214,886

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/217,487

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,758

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/220,963

; PRIOR FILING DATE: 2000-07-26

; PRIOR APPLICATION NUMBER: 60/217,496

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,447

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/218,290

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/225,757

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/226,868

; PRIOR FILING DATE: 2000-08-22

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; PRIOR FILING DATE: 2000-07-07

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; PRIOR FILING DATE: 2000-08-14

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; PRIOR APPLICATION NUMBER: 60/236,327

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/241,785

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; PRIOR FILING DATE: 2000-11-01

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; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
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; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08

Query Match 43.6%; Score 24; DB 9; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATG 53  
|||  
Db 42 TTCGAGATCAGCTGGCCACATG 19

## RESULT 9

US-09-764-860-818/c  
; Sequence 818, Application US/09764860  
; Patent No. US20020094953A1  
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT APPLICATION NUMBER: US/09/764,860  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 818  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-860-818

Query Match 43.6%; Score 24; DB 10; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATG 53  
|||  
Db 42 TTCGAGATCAGCTGGCCACATG 19

## RESULT 10

US-09-764-860-819/c  
; Sequence 819, Application US/09764860  
; Patent No. US20020094953A1  
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT APPLICATION NUMBER: US/09/764,860  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 819  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-860-819

Query Match 43.6%; Score 24; DB 10; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCTGGCCACATG 53  
|||  
Db 42 TTCGAGATCAGCTGGCCACATG 19

## RESULT 11

US-09-764-891-5685  
; Sequence 5685, Application US/09764891  
; Publication No. US20030077808A1  
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC006  
; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5685  
; LENGTH: 379  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (46)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-891-5685

Query Match 43.6%; Score 24; DB 9; Length 379;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53  
Db 18 TTCGAGATCAGCCTGGCCCAACATG 41

## RESULT 12

US-09-918-995-3449  
; Sequence 3449, Application US/09918995  
; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3449

; LENGTH: 392

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-3449

Query Match 43.6%; Score 24; DB 9; Length 392;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53  
Db 41 TTCGAGATCAGCCTGGCCCAACATG 64

## RESULT 13

US-09-867-701-7253  
; Sequence 7253, Application US/09867701

; Patent No. US20020132237A1

; GENERAL INFORMATION:

; APPLICANT: Aglate, Paul A.

; APPLICANT: Jones, Robert

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.497

; CURRENT APPLICATION NUMBER: US/09/867,701

; CURRENT FILING DATE: 2001-05-29

; NUMBER OF SEQ ID NOS: 10912

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7253

; LENGTH: 431

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-867-701-7253

Query Match 43.6%; Score 24; DB 10; Length 431;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53  
Db 321 TTCGAGATCAGCCTGGCCCAACATG 344

## RESULT 14

US-09-867-701-10214/c  
; Sequence 10214, Application US/09867701

; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10214  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-10214

Query Match 43.6%; Score 24; DB 10; Length 433;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53  
Db 223 TTCGAGATCAGCCTGGCCCAACATG 200

## RESULT 15

US-09-918-995-26320  
; Sequence 26320, Application US/09918995  
; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26320

; LENGTH: 498

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(498)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-26320

Query Match 43.6%; Score 24; DB 9; Length 498;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TTCGAGATCAGCCTGGCCCAACATG 53  
Db 187 TTCGAGATCAGCCTGGCCCAACATG 210

Search completed: June 17, 2003, 09:58:44  
Job time : 25.8144 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 62.5 Seconds  
(without alignments)  
14252.028 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_4365\_4419

Perfect score: 55

Sequence: 1 gaggcaggcagacacttga.....atcagctggccaacatgag 55

- Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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8: em\_htc:\*  
9: gb\_est1:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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108	50.9	28	13	14	BQ331585
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121	24	43.6	381	12	BF875939	CMO-ET016	C 194	24	43.6	472	17	AQ797824
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125	24	43.6	388	17	AQ095261	HS 3027_A	C 198	24	43.6	476	9	AA468416
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143	24	43.6	409	17	AQ119443	HS 2171_B	C 216	24	43.6	508	10	AW819483
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151	24	43.6	417	9	AI524515	to37f08.x	C 224	24	43.6	522	17	AQ532619
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193	24	4										

226	24	43.6	535	17	AQ118074	HS_3001_A	299	24	43.6	864	12	BG110162
227	24	43.6	536	17	AZ254463	UP_351-10	300	24	43.6	865	17	AQ740087
C 228	24	43.6	537	9	AUI144139	AUI144139	C 301	24	43.6	866	17	AQ743930
C 229	24	43.6	542	14	BM999729	UI-H-DIO-	C 302	24	43.6	867	17	AQ894479
C 230	24	43.6	543	12	BG250044	602362129	C 303	24	43.6	868	17	BQ976789
C 231	24	43.6	545	9	AUI146155	AUI146155	C 304	24	43.6	869	17	AQ738714
C 232	24	43.6	547	17	AQ90957	HS_32115_B	C 305	24	43.6	894	17	AQ738714
C 233	24	43.6	547	17	AQ934879	AQ934879	C 306	24	43.6	909	12	BG746234
C 234	24	43.6	547	17	AQ353250	CITBI-EI-	C 307	24	43.6	932	12	BF982349
C 235	24	43.6	549	12	BF530520	602071770	C 308	24	43.6	953	12	BG675453
C 236	24	43.6	552	17	AQ218D10P	AL480155 T. brucei	C 309	24	43.6	959	9	AL043979
C 237	24	43.6	556	17	AQ391019	CITBI-EI-	C 310	24	43.6	1006	12	BG746082
C 238	24	43.6	557	17	AQ561005	AQ561005 HS_5342_B	C 311	24	43.6	1050	12	BG167427
C 239	24	43.6	559	14	BM874128	laa01c10.	C 312	24	43.6	1074	14	BM807220
C 240	24	43.6	562	17	AQ580881	RPCI-11-4	C 313	24	43.6	1108	14	BM802547
C 241	24	43.6	563	14	BM706294	UI-B-DWO-	C 314	24	43.6	1267	11	BC014134
C 242	24	43.6	564	13	BM559468	AGENCOURT	C 315	24	43.6	1738	11	BC014399
C 243	24	43.6	565	13	BM555830	AGENCOURT	C 316	24	43.6	142	10	BE180038
C 244	24	43.6	565	17	AQ482258S	RPCI-11-2	C 317	24	43.6	150	17	BL5246
C 245	24	43.6	569	9	AUI148206	AUI148206	C 318	24	43.6	194	10	BE174114
C 246	24	43.6	576	10	AW249541	AQ249541	C 319	24	43.6	196	13	BI041962
C 247	24	43.6	576	17	AQ528927	RPCI-11-4	C 320	24	43.6	226	14	T96639
C 248	24	43.6	581	17	B86746	B86746 RPCI11-2401	C 321	24	43.6	237	9	AA911529
C 249	24	43.6	586	17	AQ320497	RPCI11-150	C 322	24	43.6	246	9	A1287706
C 250	24	43.6	594	12	BG571816	602593150	C 323	24	43.6	250	13	BI004309
C 251	24	43.6	599	10	BE150678	RC1-HT026	C 324	24	43.6	253	12	BF842017
C 252	24	43.6	604	13	BI548829	BI548829 603196679	C 325	24	43.6	258	14	AA811772
C 253	24	43.6	608	17	B68414	CIT-HSP-202	C 326	24	43.6	261	14	R93649
C 254	24	43.6	614	9	AA552907	AA552907 nR60312.8	C 327	24	43.6	264	9	AA737155
C 255	24	43.6	617	10	AV759972	AV759972	C 328	24	43.6	264	14	R93572
C 256	24	43.6	623	17	AQ380505	RPCI11-16	C 329	24	43.6	264	14	R93374
C 257	24	43.6	628	14	BM991214	UI-H-DIO-	C 330	24	43.6	268	9	A1560307
C 258	24	43.6	629	17	AQ560385	AQ560385 HS_2077_B	C 331	24	43.6	282	13	BI061081
C 259	24	43.6	631	9	AA056108	zF55d03.r	C 332	24	43.6	282	13	BI055714
C 260	24	43.6	631	13	BM504006	BM504006 1998e08.y	C 333	24	43.6	290	13	BI055714
C 261	24	43.6	631	17	AG150345	Pan trogl	C 334	24	43.6	303	9	AA533412
C 262	24	43.6	635	10	AW747980	AW747980 QV0-BT004	C 335	24	43.6	306	12	BF819214
C 263	24	43.6	637	17	AG102493	Pan trogl	C 336	24	43.6	309	17	E44601
C 264	24	43.6	652	17	AQ348813	RPCI11-10	C 337	24	43.6	318	9	AA353985
C 265	24	43.6	656	10	AW820619	AW820619 RCO-ST029	C 338	24	43.6	320	12	BG057766
C 266	24	43.6	658	9	AA126519	AA126519 zR85d12.8	C 339	24	43.6	325	9	AA405517
C 267	24	43.6	660	9	AL705934	AL705934 DRFPZP686L	C 340	24	43.6	327	9	AA405517
C 268	24	43.6	664	10	BE178471	BE178471 RC3-HT060	C 341	24	43.6	334	9	AA834474
C 269	24	43.6	665	17	AG150986	AG150986 Pan trogl	C 342	24	43.6	335	9	AA584150
C 270	24	43.6	672	17	AG092869	AG092869 Pan trogl	C 343	24	43.6	343	10	AW834434
C 271	24	43.6	684	17	AG166450	AG166450 Pan trogl	C 344	24	43.6	346	10	AW834430
C 272	24	43.6	685	17	AG109125	AG109125 Pan trogl	C 345	24	43.6	350	9	AA527741
C 273	24	43.6	686	17	AG118963	AG118963 Pan trogl	C 346	24	43.6	350	9	AA527741
C 274	24	43.6	690	12	BE910659	BE910659 601502643	C 347	24	43.6	351	14	R14355
C 275	24	43.6	691	17	AG1186132	AG1186132 Pan trogl	C 348	24	43.6	351	14	R14355
C 276	24	43.6	693	17	AG114428	AG114428 Pan trogl	C 349	24	43.6	357	10	BF146697
C 277	24	43.6	699	17	AG095566	AG095566 Pan trogl	C 350	24	43.6	366	17	AQ099316
C 278	24	43.6	700	17	AQ013879	AQ013879 RPCI11-24	C 351	24	43.6	369	17	AQ263757
C 279	24	43.6	702	17	AG062195	AG062195 Pan trogl	C 352	24	43.6	371	9	AA761254
C 280	24	43.6	706	17	AG186101	AG186101 Pan trogl	C 353	24	43.6	374	10	AW846599
C 281	24	43.6	707	17	AG094472	AG094472 Pan trogl	C 354	24	43.6	375	17	AQ412819
C 282	24	43.6	715	17	AG118483	AG118483 Pan trogl	C 355	24	43.6	378	9	A1535902
C 283	24	43.6	721	12	BG540436	BG540436 602568750	C 356	24	43.6	382	9	AA806789
C 284	24	43.6	728	9	AL596676	AL596676 DRFPZP451N	C 357	24	43.6	382	9	AA568433
C 285	24	43.6	730	14	BQ183112	BQ183112 UI-H-EUO-	C 358	24	43.6	386	14	H62292
C 286	24	43.6	733	17	B92010	CIT-HSP-217	C 359	24	43.6	388	10	BE088635
C 287	24	43.6	736	10	AV721604	AV721604 AV721604	C 360	24	43.6	390	14	R98443
C 288	24	43.6	746	17	AG031300	AG031300 Pan trogl	C 361	24	43.6	401	9	AA084782
C 289	24	43.6	761	17	B95257	B95257 CIT-HSP-217	C 362	24	43.6	403	12	BF881703
C 290	24	43.6	772	17	AQ029113	AQ029113 Pan trogl	C 363	24	43.6	403	14	R33331
C 291	24	43.6	773	17	AQ740481	AQ740481 HS_5504_A	C 364	24	43.6	405	12	BF875880
C 292	24	43.6	776	14	BQ000500	BQ000500 UI-H-DPO-	C 365	24	43.6	405	17	AQ218752
C 293	24	43.6	784	10	EQ005056	EQ005056 AV757526	C 366	24	43.6	408	9	AA584559
C 294	24	43.6	785	13	BM007944	BM007944 603617666	C 367	24	43.6	424	14	H81284
C 295	24	43.6	788	13	BQ212207	BQ212207 AGENCOURT	C 368	24	43.6	424	14	H81284
C 296	24	43.6	803	17	AQ986115	AQ986115 HS_3072_B	C 369	24	43.6	431	9	AA722336
C 297	24	43.6	811	17	AQ780945	AQ780945 HS_3138_B	C 370	24	43.6	436	12	BF123921
C 298	24	43.6	846	12	BE739933	BE739933 601556191	C 371	24	43.6	437	10	AW834471
C 299	24	43.6					C 372	24	43.6	438	9	AE061279
C 300	24	43.6					C 373	24	43.6	441	9	A1963771

C 372	23	41.8	448	17	AQ634562	AO634562	RPCI-11-4	C 445	23	41.8	687	12	BG718011	BG718011	602696017
C 373	23	41.8	449	10	AV721585	AV721585	AV721585	C 446	23	41.8	689	14	BQ021292	BQ021292	UI-H-DH1-
C 374	23	41.8	450	17	AQ412211	AQ412211	RPCI-11-1	C 447	23	41.8	691	17	AQ835107	AQ835107	HS_4822_A
C 375	23	41.8	452	17	AQ663990	AQ663990	HS_2277_B	C 448	23	41.8	692	17	AG173673	AG173673	Pan trogl
C 376	23	41.8	455	9	AA523834	AA523834	NI50906.S	C 449	23	41.8	695	17	AQ344988	AQ344988	RPCI-11-11
C 377	23	41.8	456	17	AQ263210	AQ263210	CITBI-E1-	C 450	23	41.8	701	17	AG1764198	AG1764198	AV764198
C 378	23	41.8	459	14	BQ181460	BQ181460	UI-H-EUO-	C 451	23	41.8	701	17	AG014803	AG014803	Homo sapi
C 379	23	41.8	463	17	AQ021152	AQ021152	CIT-HSP-2	C 452	23	41.8	706	17	AG014804	AG014804	Homo sapi
C 380	23	41.8	467	17	AQ527122	AQ527122	CITBI-E1-	C 453	23	41.8	712	17	AG177809	AG177809	Pan trogl
C 381	23	41.8	468	14	N22428	N22428	YW39606.S1	C 454	23	41.8	719	14	BM721278	BM721278	UI-E-BO1-
C 382	23	41.8	476	9	AA227360	AA227360	ZI17B04.r	C 455	23	41.8	720	17	AQ395438	AQ395438	CITBI-E1-
C 383	23	41.8	476	10	AW269690	AW269690	XV55D04.X	C 456	23	41.8	740	13	BI517589	BI517589	603041887
C 384	23	41.8	476	14	H58653	H58653	YR20A06.S1	C 457	23	41.8	741	17	AG173270	AG173270	Pan trogl
C 385	23	41.8	476	14	W04193	W04193	za57e10.r1	C 458	23	41.8	751	12	BF669330	BF669330	602120614
C 386	23	41.8	479	17	AQ286120	AQ286120	RPCI-11-89	C 459	23	41.8	772	10	AV761968	AV761968	AV761968
C 387	23	41.8	491	17	AQ828509	AQ828509	HS_5355_B	C 460	23	41.8	775	9	AL700165	AL700165	DKFZp686J
C 388	23	41.8	496	14	H63390	H63390	YR53B02.S1	C 461	23	41.8	804	17	AQ752317	AQ752317	HS_5565_B
C 389	23	41.8	497	17	AQ522229	AQ522229	HS_5221_A	C 462	23	41.8	855	17	AQ746225	AQ746225	HS_2276_A
C 390	23	41.8	498	17	AQ583170	AQ583170	RPCI-11-4	C 463	23	41.8	872	12	BF382089	BF382089	601814829
C 391	23	41.8	502	17	AQ172790	AQ172790	HS_3195_B	C 464	23	41.8	891	14	BQ220253	BQ220253	AGENCOURT
C 392	23	41.8	504	17	AQ175961	AQ175961	HS_3214_B	C 465	23	41.8	901	12	BF674663	BF674663	602137887
C 393	23	41.8	518	13	BG998514	BG998514	PM4-HTI30	C 466	23	41.8	942	9	AL515364	AL515364	AL515364
C 394	23	41.8	518	17	AQ331615	AQ331615	HS_5006_A	C 467	23	41.8	966	12	BG387516	BG387516	602412327
C 395	23	41.8	520	12	BF853910	BF853910	MR3-EN008	C 468	23	41.8	969	14	BQ720750	BQ720750	AGENCOURT
C 396	23	41.8	520	17	AQ251736	AQ251736	HS_3202_B	C 469	23	41.8	989	14	BQ223101	BQ223101	AGENCOURT
C 397	23	41.8	525	9	AA461163	AA461163	zx70A06.S	C 470	22	40.0	100	10	AW809210	AW809210	MR4-ST011
C 398	23	41.8	525	12	BF751908	BF751908	RC3-EN003	C 471	22	40.0	145	10	AW809262	AW809262	MR4-ST011
C 399	23	41.8	526	12	BF699338	BF699338	602125906	C 472	22	40.0	145	10	AW809283	AW809283	MR4-ST011
C 400	23	41.8	527	17	AQ542658	AQ542658	RPCI-11-3	C 473	22	40.0	190	10	BE178921	BE178921	RC3-HT061
C 401	23	41.8	528	17	AQ314944	AQ314944	RPCI-11-94	C 474	22	40.0	218	10	AW440677	AW440677	hc88C03.X
C 402	23	41.8	534	17	AQ277751	AQ277751	CITBI-E1-	C 475	22	40.0	221	9	AI377441	AI377441	tc23F01.X
C 403	23	41.8	535	9	A1912588	A1912588	wt1d10.X	C 476	22	40.0	224	10	AW833129	AW833129	RC3-TT000
C 404	23	41.8	537	17	AQ708354	AQ708354	HS_5569_A	C 477	22	40.0	229	14	R97049	R97049	YQ74905.S1
C 405	23	41.8	550	14	BQ287956	BQ287956	IK37F07.X	C 478	22	40.0	254	14	N72436	N72436	YV40909.r1
C 406	23	41.8	552	12	BF850673	BF850673	PM4-EN006	C 479	22	40.0	272	13	BI028338	BI028338	CM4-MT028
C 407	23	41.8	552	17	B48639	B48639	RPCI-11-2M15	C 480	22	40.0	282	17	AQ424457	AQ424457	CITBI-E1-
C 408	23	41.8	556	9	AL134615	AL134615	DKFZp547F	C 481	22	40.0	293	10	AW801998	AW801998	IL5-UM007
C 409	23	41.8	557	12	BG289272	BG289272	602384280	C 482	22	40.0	298	13	BI026936	BI026936	CM3-MT029
C 410	23	41.8	566	9	AU158610	AU158610	Human	C 483	22	40.0	307	9	AA699307	AA699307	zi32h07.S
C 411	23	41.8	573	17	AQ307838	AQ307838	HS_2199_A	C 484	22	40.0	329	12	BF945347	BF945347	PMO-NN117
C 412	23	41.8	573	17	AQ415110	AQ415110	RPCI-11-2	C 485	22	40.0	356	10	AW890526	AW890526	QV4-NT004
C 413	23	41.8	575	9	AL692058	AL692058	DKFZp313M	C 486	22	40.0	356	10	AW890454	AW890454	QV4-NT004
C 414	23	41.8	577	17	AZ516938	AZ516938	RPCI-11-8	C 487	22	40.0	363	13	BI003322	BI003322	PMO-HN007
C 415	23	41.8	580	10	AW394122	AW394122	MR2-TT001	C 488	22	40.0	367	10	AW088656	AW088656	xdl0G08.X
C 416	23	41.8	581	10	AW248498	AW248498	2820490.3	C 489	22	40.0	367	12	BF900888	BF900888	IL2-MT017
C 417	23	41.8	582	13	BG996815	BG996815	PMO-HT116	C 490	22	40.0	368	10	AW693769	AW693769	AV693769
C 418	23	41.8	582	17	AQ427274	AQ427274	CITBI-E1-	C 491	22	40.0	370	10	AW695089	AW695089	AV695089
C 419	23	41.8	594	12	BF130220	BF130220	601818246	C 492	22	40.0	375	10	AW689521	AW689521	AV689521
C 420	23	41.8	594	17	AG016678	AG016678	Homo sapi	C 493	22	40.0	376	12	BG896294	BG896294	HOA29-1-A
C 421	23	41.8	597	12	BG777139	BG777139	602664355	C 494	22	40.0	377	9	AA705566	AA705566	zj92G12.S
C 422	23	41.8	597	14	W27004	W27004	19h3 Human	C 495	22	40.0	377	10	AA695098	AA695098	AV695098
C 423	23	41.8	617	9	AL037258	AL037258	DKFZp564A	C 496	22	40.0	377	10	AW814002	AW814002	RC6-ST019
C 424	23	41.8	627	14	BQ417413	BQ417413	IK37F07.Y	C 497	22	40.0	380	10	AW695096	AW695096	AV695096
C 425	23	41.8	629	10	AW977942	AW977942	EST390051	C 498	22	40.0	381	10	AV692912	AV692912	AV692912
C 426	23	41.8	635	17	AG017087	AG017087	Homo sapi	C 499	22	40.0	381	13	BI003337	BI003337	PMO-HN007
C 427	23	41.8	642	17	AG084074	AG084074	Pan trogl	C 500	22	40.0	384	9	AI202789	AI202789	qi39b10.X
C 428	23	41.8	642	17	AG178478	AG178478	Pan trogl	C 501	22	40.0	389	9	AI053562	AI053562	qi68e04.X
C 429	23	41.8	645	17	AG136634	AG136634	Pan trogl	C 502	22	40.0	391	9	AI253439	AI253439	ap85h07.X
C 430	23	41.8	648	10	AW993287	AW993287	RC2-EN003	C 503	22	40.0	395	17	AQ060869	AQ060869	CIT-HSP-2
C 431	23	41.8	655	12	BG720278	BG720278	602692341	C 504	22	40.0	397	14	H49353	H49353	YQ18d11.S1
C 432	23	41.8	657	17	AG017098	AG017098	Homo sapi	C 505	22	40.0	399	12	BF763656	BF763656	CMO-CS004
C 433	23	41.8	660	17	AG157820	AG157820	Pan trogl	C 506	22	40.0	411	9	AA676553	AA676553	zi38d09.S
C 434	23	41.8	664	17	AG107524	AG107524	Pan trogl	C 507	22	40.0	415	9	AA508070	AA508070	ng93a04.S
C 435	23	41.8	665	14	BQ672640	BQ672640	AGENCOURT	C 508	22	40.0	416	17	AQ212371	AQ212371	HS_3002_B
C 436	23	41.8	665	17	AG084035	AG084035	Pan trogl	C 509	22	40.0	417	13	BI026661	BI026661	PMI-MT019
C 437	23	41.8	667	12	BF669424	BF669424	602120124	C 510	22	40.0	425	10	AW833911	AW833911	QV0-TT000
C 438	23	41.8	670	10	AV752038	AV752038	AV752038	C 511	22	40.0	426	9	AA648957	AA648957	ns30G05.S
C 439	23	41.8	671	13	BI597240	BI597240	603250517	C 512	22	40.0	428	17	AQ278208	AQ278208	CITBI-E1-
C 440	23	41.8	672	12	BG492997	BG492997	602537443	C 513	22	40.0	429	17	AQ493975	AQ493975	HS_5134_B
C 441	23	41.8	672	14	BQ000216	BQ000216	UI-H-DIO-	C 514	22	40.0	433	10	AV683048	AV683048	AV683048
C 442	23	41.8	676	17	AQ630943	AQ630943	RPCI-11-4	C 515	22	40.0	433	10	AV698172	AV698172	AV698172
C 443	23	41.8	677	17	AQ284240	AQ284240	RPCI-11-79	C 516	22	40.0	433	10	AV698174	AV698174	AV698174
C 444	23	41.8	685	17	AG014842	AG014842	Homo sapi	C 517	22	40.0	433	10	AV698212	AV698212	AV698212

C 518	22	40.0	435	9	AA262463	AA262463 zsl6h08.r	591	21	38.2	158	12	BF805831	BF805831 QV4-C1015
C 519	22	40.0	439	10	AW195152	AW195152 xh66f03.x	C 592	21	38.2	163	13	BI016061	BI016061 PMO-ET025
C 520	22	40.0	444	10	BE144030	BE144030 MKO-HT016	593	21	38.2	168	10	AW893063	AW893063 CM3-NN000
C 521	22	40.0	446	9	A1620103	A1620103 tu92e11.x	594	21	38.2	172	10	BE004691	BE004691 CM1-BN011
C 522	22	40.0	462	14	H61613	H61613 YR23b01.r1	595	21	38.2	173	12	BF858536	BF858536 RCL-F7019
C 523	22	40.0	464	17	AQ266993	AQ266993 RPCI11-71	596	21	38.2	192	9	AA434346	AA434346 aa83a11.r
C 524	22	40.0	474	17	AQ474017	AQ474017 CITBI-E1	C 597	21	38.2	193	12	BG013063	BG013063 PM1-GN030
C 525	22	40.0	470	14	H89771	H89771 yu82b01.r1	598	21	38.2	197	17	B65546	B65546 CIT-HSP-202
C 526	22	40.0	476	17	AQ318934	AQ318934 RPCI11-10	599	21	38.2	207	13	BI036762	BI036762 RCG-NT015
C 527	22	40.0	477	13	BI010330	BI010330 MR2-EN009	600	21	38.2	207	14	F23326	F23326 HSPD13217 H
C 528	22	40.0	477	13	BI010330	BI010330 MR2-EN009	601	21	38.2	210	9	AA371898	AA371898 ESR83754
C 529	22	40.0	480	10	BE246739	BE246739 TCEAPD44	C 602	21	38.2	219	13	EG991589	EG991589 MR3-HT113
C 530	22	40.0	480	14	BQ363256	BQ363256 MR3-ST019	C 603	21	38.2	225	9	A1950671	A1950671 wx52g10.x
C 531	22	40.0	484	17	AQ833576	AQ833576 HS 5304.B	C 604	21	38.2	229	12	BF872623	BF872623 IL3-ET011
C 532	22	40.0	489	17	AQ476669	AQ476669 CITBI-E1	605	21	38.2	229	12	BF874288	BF874288 IL3-ET011
C 533	22	40.0	491	12	BF821084	BF821084 MR1-RT004	606	21	38.2	231	14	F18187	F18187 HSPD02762 H
C 534	22	40.0	493	17	AQ354205	AQ354205 CITBI-E1	C 607	21	38.2	235	9	AA809413	AA809413 ob71f08.s
C 535	22	40.0	495	17	AQ036334	AQ036334 CIT-HSP-2	C 608	21	38.2	241	12	EG54636	EG54636 l042c06.x
C 536	22	40.0	496	9	AI100747	AI100747 z191h04.r	C 609	21	38.2	244	12	BF858528	BF858528 RCL-F7019
C 537	22	40.0	501	10	AW820917	AW820917 RC2-ST030	610	21	38.2	249	17	AQ194922	AQ194922 RPCI11-59
C 538	22	40.0	502	17	AQ140180	AQ140180 HS 3109.B	C 611	21	38.2	250	9	AA077870	AA077870 7H13G09 C
C 539	22	40.0	511	14	W02850	W02850 za05b06.r1	612	21	38.2	252	17	AQ263585	AQ263585 CITBI-E1
C 540	22	40.0	518	10	AW813432	AW813432 MR3-ST019	613	21	38.2	252	17	AQ280701	AQ280701 CITBI-E1
C 541	22	40.0	525	12	BE878288	BE878288 601A8005	C 614	21	38.2	253	9	AA680253	AA680253 ac86b08.s
C 542	22	40.0	534	17	AQ481386	AQ481386 RPCI-11-2	C 615	21	38.2	254	9	A1535853	A1535853 jun2.F02r
C 543	22	40.0	544	17	AQ318992	AQ318992 RPCI11-10	C 616	21	38.2	259	14	BQ353144	BQ353144 PMO-HT091
C 544	22	40.0	546	9	AA088714	AA088714 z189a12.r	617	21	38.2	259	17	AQ088982	AQ088982 HS 2200 B
C 545	22	40.0	547	9	AL702622	AL702622 DKF2p686K	C 618	21	38.2	263	9	A1242994	A1242994 qh46h12.x
C 546	22	40.0	548	17	AQ314262	AQ314262 RPCI11-96	C 619	21	38.2	265	17	AQ362933	AQ362933 CITBI-E1
C 547	22	40.0	551	17	AQ356084	AQ356084 RPCI-11-4	620	21	38.2	267	12	BF907766	BF907766 IL2-UT007
C 548	22	40.0	563	17	AV427704	AV427704 CITBI-E1	C 621	21	38.2	270	13	BI020263	BI020263 IL3-MT026
C 549	22	40.0	575	10	AV747043	AV747043 AV747043	C 622	21	38.2	270	14	H40191	H40191 yps59e05.r1
C 550	22	40.0	591	14	BM819135	BM819135 K-EST0086	623	21	38.2	271	9	AA339780	AA339780 EST44919
C 551	22	40.0	592	17	AQ625967	AQ625967 CITBI-E1	C 624	21	38.2	272	9	AU147947	AU147947 AU147947
C 552	22	40.0	598	17	AQ712466	AQ712466 HS 2118.A	625	21	38.2	272	12	BF921835	BF921835 CM3-NT017
C 553	22	40.0	604	10	AW851224	AW851224 IL3-CT022	626	21	38.2	273	17	AQ417534	AQ417534 RPCI-11-1
C 554	22	40.0	604	10	AW851361	AW851361 IL3-CT022	627	21	38.2	274	10	AW085882	AW085882 xc60c06.x
C 555	22	40.0	613	13	BI115316	BI115316 602863111	628	21	38.2	275	17	AQ103532	AQ103532 HS 3070.A
C 556	22	40.0	634	10	BE156176	BE156176 QV0-HT036	C 629	21	38.2	279	9	AA224238	AA224238 zr14g10.s
C 557	22	40.0	642	12	BG482973	BG482973 602502986	630	21	38.2	281	17	AQ461035	AQ461035 HS 5183.A
C 558	22	40.0	647	17	AG104223	AG104223 Pan trogl	C 631	21	38.2	286	10	AW884576	AW884576 QV3-OT006
C 559	22	40.0	650	12	EG570337	EG570337 602590764	632	21	38.2	288	9	AA868763	AA868763 ak52f08.s
C 560	22	40.0	662	10	BE156181	BE156181 QV0-HT036	633	21	38.2	291	9	AA374958	AA374958 EST87225
C 561	22	40.0	663	17	AQ351794	AQ351794 CITBI-E1	C 634	21	38.2	292	17	AQ634620	AQ634620 RPCI-11-4
C 562	22	40.0	668	17	AG033573	AG033573 Pan trogl	635	21	38.2	298	9	AA610702	AA610702 np92a07.s
C 563	22	40.0	672	17	AQ345321	AQ345321 RPCI11-12	C 636	21	38.2	302	9	AA366269	AA366269 ESR77198
C 564	22	40.0	692	17	AG180755	AG180755 Pan trogl	C 637	21	38.2	303	10	AW078904	AW078904 xl19e06.x
C 565	22	40.0	698	10	AV696231	AV696231 AV696231	C 638	21	38.2	304	9	AA480783	AA480783 ne86c12.s
C 566	22	40.0	701	17	AG011324	AG011324 Homo sapi	639	21	38.2	305	17	AQ276159	AQ276159 CITBI-E1
C 567	22	40.0	702	17	AQ343621	AQ343621 RPCI11-12	640	21	38.2	310	9	AA092605	AA092605 l16269.se
C 568	22	40.0	703	10	AV697319	AV697319 AV697319	C 641	21	38.2	310	13	BG995013	BG995013 MR4-HT105
C 569	22	40.0	704	10	AV683192	AV683192 AV683192	C 642	21	38.2	311	9	A1198718	A1198718 gf78b02.x
C 570	22	40.0	708	10	AV684276	AV684276 AV684276	643	21	38.2	313	10	AV754619	AV754619 AV754619
C 571	22	40.0	708	17	AQ740332	AQ740332 HS 5501.A	C 644	21	38.2	315	9	A1300628	A1300628 q021c11.x
C 572	22	40.0	712	12	EG569919	EG569919 602590562	C 645	21	38.2	324	9	A1343421	A1343421 nc19d08.s
C 573	22	40.0	713	10	AV696227	AV696227 AV696227	646	21	38.2	324	9	AA226620	AA226620 nc19d08.s
C 574	22	40.0	716	17	AG011336	AG011336 Homo sapi	C 647	21	38.2	331	9	A1147087	A1147087 ok33e12.s
C 575	22	40.0	717	10	AV697321	AV697321 AV697321	C 648	21	38.2	332	13	BG977421	BG977421 PM1-C1015
C 576	22	40.0	725	17	AG011323	AG011323 Homo sapi	C 649	21	38.2	332	17	AQ531074	AQ531074 RPCI-11-3
C 577	22	40.0	734	17	AG0698315	AG0698315 AV698315	650	21	38.2	335	14	M78032	M78032 EST01619 H1
C 578	22	40.0	734	17	AG102918	AG102918 Pan trogl	651	21	38.2	338	17	AQ088667	AQ088667 HS 22335.B
C 579	22	40.0	735	17	AG144447	AG144447 Pan trogl	C 652	21	38.2	340	14	H93453	H93453 yu57a12.r1
C 580	22	40.0	753	17	AQ896801	AQ896801 HS 3184.A	C 653	21	38.2	346	10	AV732537	AV732537 AV732537
C 581	22	40.0	890	14	BQ230601	BQ230601 AGENCOURT	C 654	21	38.2	353	17	AQ552922	AQ552922 RPCI-11-4
C 582	22	40.0	908	12	EG181036	EG181036 602329141	C 655	21	38.2	355	12	BF842194	BF842194 RCG-HT084
C 583	22	40.0	942	13	BI113842	BI113842 602861073	656	21	38.2	356	12	BF903107	BF903107 CM3-WT019
C 584	22	40.0	1011	14	BQ943906	BQ943906 AGENCOURT	C 657	21	38.2	357	14	H91361	H91361 yu87e03.r1
C 585	22	40.0	1712	11	AF119914	AF119914 Homo sapi	C 658	21	38.2	357	14	R64046	R64046 y122b04.r1
C 586	21	38.2	107	9	AA564523	AA564523 nh21e12.s	659	21	38.2	358	12	BF871414	BF871414 IL3-ET011
C 587	21	38.2	119	13	BG985326	BG985326 PMO-CN015	660	21	38.2	358	17	AQ665179	AQ665179 HS 5344.B
C 588	21	38.2	127	12	BF856443	BF856443 RCO-FN020	661	21	38.2	359	9	AA640359	AA640359 nr21h12.s
C 589	21	38.2	127	14	BQ345849	BQ345849 PMO-NT031	C 662	21	38.2	361	12	BF897181	BF897181 IL2-MT017
C 590	21	38.2	155	10	BE085073	BE085073 RCS-BT066	663	21	38.2	361	17	AQ111390	AQ111390 CIT-HSP-2

664	21	38.2	363	17	AQ084492	AQ084492 HS 2252.A	737	21	38.2	443	17	BH141050	BH141050 UP 310-11
665	21	38.2	365	17	AQ349192	AQ349192 RC111-13	738	21	38.2	443	17	AQ589759	AQ589759 HS 2117.B
666	21	38.2	367	14	EQ328821	EQ328821 QV4-EN004	739	21	38.2	444	13	BI481020	BI481020 HZPE-087
667	21	38.2	367	14	H54457	H54457 YQ91907.s1	740	21	38.2	444	17	AQ218824	AQ218824 HS 2004.A
668	21	38.2	368	17	AQ132644	AQ132644 HS 3057.A	741	21	38.2	445	9	AI038726	AI038726 ox35f10.s
669	21	38.2	371	9	A1699049	A1699049 tx74d06.x	742	21	38.2	445	9	AA460924	AA460924 xz61b09.s
670	21	38.2	372	9	AA347382	AA347382 EST53673	743	21	38.2	446	9	AL700830	AL700830 DKZP6861
671	21	38.2	373	9	AA230159	AA230159 nc38d10.s	744	21	38.2	447	9	AI433833	AI433833 t117a07.x
672	21	38.2	375	17	B93239	B93239 CIT-HSP-217	745	21	38.2	448	17	BH367106	BH367106 UP_295-16
673	21	38.2	376	10	AW276741	AW276741 xp65c09.x	746	21	38.2	449	9	AI471480	AI471480 ta20g06.x
674	21	38.2	378	9	A1224619	A1224619 qw36g09.x	747	21	38.2	451	9	AI096395	AI096395 qb91g08.x
675	21	38.2	379	9	A1494488	A1494488 qz16d03.x	748	21	38.2	451	9	AI650702	AI650702 wb35f10.x
676	21	38.2	379	17	B90423	B90423 CIT-HSP-216	749	21	38.2	453	17	AQ020765	AQ020765 CIT-HSP-2
677	21	38.2	382	9	AA569315	AA569315 nm31h05.s	750	21	38.2	454	10	AW834472	AW834472 MR2-TT001
678	21	38.2	383	17	AQ214890	AQ214890 HS 3059.B	751	21	38.2	455	17	AQ242743	AQ242743 HS 2058.B
679	21	38.2	384	12	BF915728	BF915728 MR3-UT012	752	21	38.2	456	14	R97987	R97987 YQ75b01.s1
680	21	38.2	384	14	H511993	H511993 YQ32902.r1	753	21	38.2	457	17	AQ040970	AQ040970 CIT-HSP-2
681	21	38.2	384	14	T26396	T26396 AB164F4R In	754	21	38.2	458	9	AI791137	AI791137 ab95c08.x
682	21	38.2	385	14	BQ693971	BQ693971 1000114.H	755	21	38.2	460	9	AA158787	AA158787 zo63c11.s
683	21	38.2	386	9	AA714733	AA714733 nw30a08.s	756	21	38.2	462	9	AA658863	AA658863 nt84b07.s
684	21	38.2	386	17	AQ342425	AQ342425 RC111-11	757	21	38.2	463	14	H30475	H30475 yo58c01.r1
685	21	38.2	386	17	AQ411300	AQ411300 HS 5071.B	758	21	38.2	463	17	AQ765103	AQ765103 HS 3153.B
686	21	38.2	387	14	F23264	F23264 HSPD13207.H	759	21	38.2	463	17	AQ637211	AQ637211 RPCI-11-4
687	21	38.2	389	9	AA525522	AA525522 ni33d09.s	760	21	38.2	465	17	AA721998	AA721998 zh17e05.s
688	21	38.2	390	10	AV655267	AV655267 AV655267	761	21	38.2	469	17	AQ729762	AQ729762 HS 2133.A
689	21	38.2	391	14	R99851	R99851 YQ69h11.r1	762	21	38.2	470	17	AQ524022	AQ524022 HS 5224.A
690	21	38.2	392	14	EQ946252	EQ946252 AGENCOURT	763	21	38.2	473	14	R99852	R99852 YQ69h11.s1
691	21	38.2	393	13	BI049547	BI049547 IL5-GN024	764	21	38.2	473	17	AQ168881	AQ168881 HS 3213.A
692	21	38.2	393	17	AQ093299	AQ093299 HS 3018.A	765	21	38.2	473	17	AQ588668	AQ588668 CITBI-E1-
693	21	38.2	394	17	AQ630254	AQ630254 RPCI-11-4	766	21	38.2	475	17	B50249	B50249 CIT-HSP-247
694	21	38.2	395	17	AQ531108	AQ531108 RPCI-11-3	767	21	38.2	476	17	AQ147453	AQ147453 HS 3070.A
695	21	38.2	396	17	AQ166650	AQ166650 HS 3148.A	768	21	38.2	477	12	BG164052	BG164052 G02341071
696	21	38.2	398	9	AA400668	AA400668 zv09g11.s	769	21	38.2	477	13	BI013263	BI013263 PM4-ET015
697	21	38.2	398	17	AQ495244	AQ495244 HS 5143.B	770	21	38.2	480	17	R98221	R98221 YQ75b01.r1
698	21	38.2	400	9	AA350087	AA350087 EST57440	771	21	38.2	481	14	B46148	B46148 HS -1058-B2-
699	21	38.2	401	10	AA080057	AA080057 xe48b07.x	772	21	38.2	482	14	N26037	N26037 YX89c01.s1
700	21	38.2	402	9	AA806405	AA806405 oc37b12.s	773	21	38.2	482	17	AQ712614	AQ712614 HS 2134.A
701	21	38.2	402	9	AA827756	AA827756 ob59g01.s	774	21	38.2	483	13	BM312571	BM312571 ig76c08.y
702	21	38.2	403	17	AQ153556	AQ153556 HS 2242.B	775	21	38.2	483	17	AQ734019	AQ734019 HS 2151.A
703	21	38.2	404	12	BF934706	BF934706 IL2-NT020	776	21	38.2	484	14	N67821	N67821 za04h11.s1
704	21	38.2	406	14	N24668	N24668 YX90f11.s1	777	21	38.2	484	17	AQ393054	AQ393054 CITBI-E1-
705	21	38.2	407	17	AQ889852	AQ889852 HS 2199.B	778	21	38.2	487	17	B72461	B72461 RPCI-11-8P13
706	21	38.2	408	13	BI024433	BI024433 CM3-MT029	779	21	38.2	492	12	BE888651	BE888651 G01513046
707	21	38.2	409	10	AV759911	AV759911 AV759911	780	21	38.2	495	17	AQ531096	AQ531096 RPCI-11-3
708	21	38.2	410	9	AA640990	AA640990 nr27g08.r	781	21	38.2	496	10	AW156911	AW156911 au89e03.x
709	21	38.2	411	9	AA461227	AA461227 xz61b09.r	782	21	38.2	499	13	BM142609	BM142609 QV3-KT001
710	21	38.2	411	10	AAW300650	AAW300650 xk03d12.x	783	21	38.2	500	12	BF736906	BF736906 QV3-KT001
711	21	38.2	414	9	A1242633	A1242633 qu37d09.x	784	21	38.2	501	14	N74620	N74620 za55b06.s1
712	21	38.2	415	17	B63136	B63136 CIT978SK-A-	785	21	38.2	501	17	AQ680133	AQ680133 HS 2153.B
713	21	38.2	417	9	A1304840	A1304840 q063h12.x	786	21	38.2	501	17	AQ417519	AQ417519 RPCI-11-1
714	21	38.2	417	12	BF741641	BF741641 CM4-HB002	787	21	38.2	503	14	N70251	N70251 za55c10.s1
715	21	38.2	419	17	AQ039353	AQ039353 CIT-HSP-2	788	21	38.2	503	17	AQ272945	AQ272945 HS 5438.B
716	21	38.2	420	10	AAW571685	AAW571685 xx36c04.x	789	21	38.2	503	17	AQ437756	AQ437756 HS 5056.B
717	21	38.2	424	9	AA074096	AA074096 zf78a06.s	790	21	38.2	504	14	BQ025859	BQ025859 UT-1-BB1p
718	21	38.2	424	10	AA659386	AA659386 AV659386	791	21	38.2	504	17	BH152879	BH152879 UP 297-17
719	21	38.2	424	14	H99483	H99483 YX25c02.s1	792	21	38.2	506	17	AQ590149	AQ590149 HS 2126.A
720	21	38.2	425	17	AQ116554	AQ116554 HS 3011.B	793	21	38.2	508	14	H81519	H81519 yu61h04.r1
721	21	38.2	425	17	AQ147452	AQ147452 HS 3070.A	794	21	38.2	508	17	AQ622943	AQ622943 HS 5351.A
722	21	38.2	426	9	AA693988	AA693988 zi48a09.s	795	21	38.2	509	17	A1523959	A1523959 tg98f09.x
723	21	38.2	426	17	AQ787447	AQ787447 HS 3224.B	796	21	38.2	509	10	AV718842	AV718842 AV718842
724	21	38.2	429	14	H93454	H93454 yu57a12.s1	797	21	38.2	509	17	AQ062552	AQ062552 CIT-HSP-2
725	21	38.2	430	17	AQ059328	AQ059328 CIT-HSP-2	798	21	38.2	509	17	AQ771989	AQ771989 HS 5413.B
726	21	38.2	430	17	AQ589714	AQ589714 HS 2117.B	799	21	38.2	509	17	AQ264678	AQ264678 CITBI-E1-
727	21	38.2	432	9	AA135488	AA135488 zo28g06.s	800	21	38.2	513	9	AA171399	AA171399 zp33a05.s
728	21	38.2	432	9	A1700365	A1700365 wd07b04.x	801	21	38.2	514	17	AQ721134	AQ721134 HS 5557.A
729	21	38.2	432	10	AAW977899	AAW977899 EST390008	802	21	38.2	516	17	AQ214501	AQ214501 HS 3243.B
730	21	38.2	433	17	AQ311458	AQ311458 CITBI-E1-	803	21	38.2	517	17	AQ581110	AQ581110 RPCI-11-4
731	21	38.2	436	10	AAW854903	AAW854903 PM0-CT026	804	21	38.2	518	17	AQ691287	AQ691287 HS 5358.A
732	21	38.2	440	9	A1004740	A1004740 ou04f03.x	805	21	38.2	518	17	AQ760344	AQ760344 HS 3028.A
733	21	38.2	440	17	AQ088547	AQ088547 HS 3000.A	806	21	38.2	520	17	AQ880778	AQ880778 HS 5059.A
734	21	38.2	441	17	AQ227371	AQ227371 HS 2017.B	807	21	38.2	520	17	AQ186785	AQ186785 HS 3109.B
735	21	38.2	442	17	B89067	B89067 CIT-HSP-217	808	21	38.2	525	10	AAW375925	AAW375925 RC2-CT020
736	21	38.2	443	17	B65515	B65515 CIT-HSP-202	809	21	38.2	525	14	BQ640757	BQ640757 hb32g10.y

810	21	38.2	532	17	AQ019256	CIT-HSP-2	AQ019256	CIT-HSP-2	883	21	38.2	682	17	AG075285	AG075285	Pan trogl
811	21	38.2	536	13	B1017697	MR4-ET013	B1017697	MR4-ET013	884	21	38.2	684	17	AG170364	AG170364	Pan trogl
812	21	38.2	539	9	A10191278	ow62b10.x	A10191278	ow62b10.x	885	21	38.2	687	17	AG154132	AG154132	Pan trogl
813	21	38.2	539	17	AQ429382	CITBI-E1-	AQ429382	CITBI-E1-	886	21	38.2	688	17	AG062661	AG062661	Pan trogl
814	21	38.2	540	17	AQ679599	HS 5346-A	AQ679599	HS 5346-A	887	21	38.2	692	10	BE397160	BE397160	601290852
815	21	38.2	541	10	BE390700	601286877	BE390700	601286877	888	21	38.2	696	17	AG159631	AG159631	Pan trogl
816	21	38.2	541	17	AQ719752	HS 5544-A	AQ719752	HS 5544-A	889	21	38.2	698	17	AG092502	AG092502	Pan trogl
817	21	38.2	543	10	AW376024	RC2-CT020	AW376024	RC2-CT020	890	21	38.2	704	17	AG085773	AG085773	Pan trogl
818	21	38.2	545	10	AW835295	QVO-LT001	AW835295	QVO-LT001	891	21	38.2	709	17	AQ379867	AQ379867	RP111-16
819	21	38.2	546	9	A1903466	RC-BT029-	A1903466	RC-BT029-	892	21	38.2	710	17	AG002493	AG002493	Homo sapi
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821	21	38.2	549	17	AQ673632	HS 5481-B	AQ673632	HS 5481-B	894	21	38.2	711	17	AG144362	AG144362	Pan trogl
822	21	38.2	550	17	AQ779553	HS 3001-A	AQ779553	HS 3001-A	895	21	38.2	714	14	BM979083	BM979083	UI-CF-DU1
823	21	38.2	553	13	B1014701	QVI-ET018	B1014701	QVI-ET018	896	21	38.2	728	17	AG139892	AG139892	Pan trogl
824	21	38.2	560	9	AA207152	zq84b04.s	AA207152	zq84b04.s	897	21	38.2	729	9	A1133721	A1133721	HA2346 Hu
825	21	38.2	561	10	AW851451	IL3-CT022	AW851451	IL3-CT022	898	21	38.2	730	17	AV708236	AV708236	AV708236
826	21	38.2	561	17	AQ391161	CITBI-E1-	AQ391161	CITBI-E1-	899	21	38.2	736	17	AG104187	AG104187	Pan trogl
827	21	38.2	562	17	AQ313801	RC111-94	AQ313801	RC111-94	900	21	38.2	737	17	AQ888919	AQ888919	HS 3100-A
828	21	38.2	565	17	AQ231371	HS 2027-B	AQ231371	HS 2027-B	901	21	38.2	742	12	BG402743	BG402743	602418407
829	21	38.2	566	17	AQ514219	HS 5184-B	AQ514219	HS 5184-B	902	21	38.2	745	17	AG031599	AG031599	Pan trogl
830	21	38.2	566	17	AQ542989	RPCI-11-3	AQ542989	RPCI-11-3	903	21	38.2	746	12	BE877847	BE877847	601489324
831	21	38.2	569	13	B1439601	IC28C09-X	B1439601	IC28C09-X	904	21	38.2	756	10	BE538447	BE538447	601068292
832	21	38.2	571	17	AQ568449	HS 5302-B	AQ568449	HS 5302-B	905	21	38.2	760	9	AL046084	AL046084	DKFZp434H
833	21	38.2	576	12	BF913268	IL3-UT011	BF913268	IL3-UT011	906	21	38.2	763	9	AL042931	AL042931	DKFZp434K
834	21	38.2	582	17	AQ632117	RPCI-11-4	AQ632117	RPCI-11-4	907	21	38.2	766	17	AQ749899	AQ749899	HS 5573-A
835	21	38.2	584	17	AQ552982	RPCI-11-3	AQ552982	RPCI-11-3	908	21	38.2	768	9	AI903408	AI903408	RC-BT029-
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838	21	38.2	592	17	AQ771958	HS 5413-B	AQ771958	HS 5413-B	911	21	38.2	776	13	BI333658	BI333658	602999118
839	21	38.2	593	12	EG484873	602505572	EG484873	602505572	912	21	38.2	788	13	BI870254	BI870254	603393756
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841	21	38.2	596	10	AV716708	AV716708	AV716708	AV716708	914	21	38.2	793	17	AQ989824	AQ989824	HS 3130-A
842	21	38.2	598	10	AW833160	RC3-TT000	AW833160	RC3-TT000	915	21	38.2	798	12	BG818715	BG818715	602779031
843	21	38.2	599	17	AQ562894	HS 2069-B	AQ562894	HS 2069-B	916	21	38.2	815	9	AL515221	AL515221	AL515221
844	21	38.2	602	17	B58317	CIT-HSP-201	B58317	CIT-HSP-201	917	21	38.2	815	12	EG400842	EG400842	602464065
845	21	38.2	606	17	AQ263107	CITBI-E1-	AQ263107	CITBI-E1-	918	21	38.2	840	9	AL698166	AL698166	DKFZp686L
846	21	38.2	606	17	AQ508672	RPCI-11-3	AQ508672	RPCI-11-3	919	21	38.2	853	12	BI107777	BI107777	602779986
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851	21	38.2	621	17	AQ881021	HS 5127-B	AQ881021	HS 5127-B	924	21	38.2	918	12	BG403431	BG403431	602419116
852	21	38.2	623	10	AW833135	RC3-TT000	AW833135	RC3-TT000	925	21	38.2	921	14	BQ718465	BQ718465	AGENCOURT
853	21	38.2	625	9	AL523643	AL523643	AL523643	AL523643	926	21	38.2	924	13	BI772030	BI772030	603058885
854	21	38.2	627	14	BQ712185	AGENCOURT	BQ712185	AGENCOURT	927	21	38.2	927	17	AQ743709	AQ743709	HS 5507-A
855	21	38.2	631	17	AQ237934	RPCI11-64	AQ237934	RPCI11-64	928	21	38.2	931	12	BF031034	BF031034	601558911
856	21	38.2	635	17	AG133268	Pan trogl	AG133268	Pan trogl	929	21	38.2	941	14	BQ710423	BQ710423	AGENCOURT
857	21	38.2	636	17	AG066329	Pan trogl	AG066329	Pan trogl	930	21	38.2	955	14	BQ999033	BQ999033	AGENCOURT
858	21	38.2	638	13	BM007682	603617112	BM007682	603617112	931	21	38.2	976	14	BQ956832	BQ956832	AGENCOURT
859	21	38.2	638	17	AQ768775	HS 3160-B	AQ768775	HS 3160-B	932	21	38.2	985	14	BQ883445	BQ883445	AGENCOURT
860	21	38.2	643	17	AG122019	Pan trogl	AG122019	Pan trogl	933	21	38.2	1002	13	BM473164	BM473164	AGENCOURT
861	21	38.2	644	14	BQ613996	IL02C01-X	BQ613996	IL02C01-X	934	21	38.2	1012	12	BF526552	BF526552	602070862
862	21	38.2	644	17	AG017589	Homo sapi	AG017589	Homo sapi	935	21	38.2	1032	13	BM562790	BM562790	AGENCOURT
863	21	38.2	644	17	AG017592	Homo sapi	AG017592	Homo sapi	936	21	38.2	1154	12	BM112891	BM112891	602285093
864	21	38.2	648	12	BG484168	602504782	BG484168	602504782	937	21	38.2	1236	14	BQ432831	BQ432831	AGENCOURT
865	21	38.2	649	17	AG017591	Homo sapi	AG017591	Homo sapi	938	21	38.2	1520	13	BM581118	BM581118	AGENCOURT
866	21	38.2	649	17	AG017593	Homo sapi	AG017593	Homo sapi	939	21	38.2	2871	11	BC026029	BC026029	Homo sapi
867	21	38.2	649	17	AG064568	Pan trogl	AG064568	Pan trogl	940	21	38.2	108	10	BE244605	BE244605	TCBAP2E08
868	21	38.2	650	17	AQ320779	RPCI11-92	AQ320779	RPCI11-92	941	21	38.2	111	10	BE173891	BE173891	CM0-HF056
869	21	38.2	654	17	AG169335	Pan trogl	AG169335	Pan trogl	942	21	38.2	119	17	AQ477175	AQ477175	CITBI-E1-
870	21	38.2	655	17	AQ284316	RPCI11-79	AQ284316	RPCI11-79	943	21	38.2	140	12	BF901310	BF901310	IL2-MT017
871	21	38.2	658	17	AG088933	Pan trogl	AG088933	Pan trogl	944	21	38.2	160	13	BI030697	BI030697	IL5-MT026
872	21	38.2	660	14	BQ020061	UI-H-ED0-	BQ020061	UI-H-ED0-	945	21	38.2	173	13	BI029484	BI029484	IL5-MT026
873	21	38.2	662	17	AG149255	Pan trogl	AG149255	Pan trogl	946	21	38.2	180	14	PO5220	PO5220	HSC04B121 n
874	21	38.2	662	17	AG182637	Pan trogl	AG182637	Pan trogl	947	21	38.2	191	9	AI255015	AI255015	qV48d12.x
875	21	38.2	663	17	AG080702	Pan trogl	AG080702	Pan trogl	948	21	38.2	192	9	AI255004	AI255004	qV48c12.x
876	21	38.2	664	17	AQ062179	Pan trogl	AQ062179	Pan trogl	949	21	38.2	196	13	BI003351	BI003351	PM0-HN007
877	21	38.2	668	17	AQ261203	CITBI-E1-	AQ261203	CITBI-E1-	950	21	38.2	201	9	AA218911	AA218911	zq15f05.s
878	21	38.2	671	9	AA630096	ab95c08.s	AA630096	ab95c08.s	951	21	38.2	209	10	AW864296	AW864296	PM4-SN001
879	21	38.2	672	17	AQ110663	CIT-HSP-2	AQ110663	CIT-HSP-2	952	21	38.2	212	9	AL044042	AL044042	DKFZp434K
880	21	38.2	673	13	BI160652	60285072	BI160652	60285072	953	21	38.2	215	12	BF923476	BF923476	IL0-MT023
881	21	38.2	675	17	AQ378745	RPCI11-15	AQ378745	RPCI11-15	954	21	38.2	230	12	BF996130	BF996130	RC3-GN004
882	21	38.2	680	10	AV700695	AV700695	AV700695	AV700695	955	21	38.2	231	9	AA528570	AA528570	nf01h03.s



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956 20 36.4 232 10 AW022221 df34e11.y
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961 20 36.4 242 12 BF827975 MR2-BT0003
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963 20 36.4 244 13 BI015158 MR4-ET014
964 20 36.4 245 10 AW817652 RC2-ST025
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966 20 36.4 256 9 AA806212 oe29e01.s
967 20 36.4 273 9 AA669706 ac23c11.s
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990 20 36.4 314 17 AQ091805 HS 2208.A
991 20 36.4 316 12 BF80764 QV3-ET017
992 20 36.4 324 9 AA745191 nw15f10.s
993 20 36.4 327 17 AQ087044 HS 2236.A
994 20 36.4 329 12 BF900875 IL2-WT017
995 20 36.4 329 17 B02544 CSRL-155F2
996 20 36.4 330 9 AI039565 ox37f05.s
997 20 36.4 335 17 AQ388265 RPC111-14
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## ALIGNMENTS

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LOCUS 60240986P1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4537892 5',
DEFINITION mRNA sequence.
ACCESSION BG284780
VERSION BG284780.1 GI:13036079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 388)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DFP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10463 row: 1 column: 21
High quality sequence stop: 388.
FEATURES
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pcMV-SPORE6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 118 a 96 c 107 g 67 t
ORIGIN
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Query Match 65.5%; Score 36; DB 12; Length 388;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 141 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 176
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RESULT 2
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DEFINITION IMAGE:3078210 5', mRNA sequence.
ACCESSION AW503185
VERSION AW503185.1 GI:7118344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio-llnl.gov/bbrp/image/image.html
The following repetitive elements were found in this cDNA
sequence:
7-205, >ALU 123-412, >ALU
Seq primer: M13 Forward.
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/lab_host="DH10B (LTI)"
/note="vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI;
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(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
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BASE COUNT      103 a 108 c 124 g 77 t
ORIGIN
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Db 188 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 223

RESULT 3
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DEFINITION RPCI-11-460L9-TV RPCI-11 Homo sapiens genomic clone RPCI-11-460L9,
            DNA sequence.
ACCESSION  AQ582126
VERSION     AQ582126.1 GI:5009236
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 574)
AUTHORS     Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
TITLE       Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
JOURNAL     Unpublished (1997)
COMMENT     Other GSSs: RPCI-11-460L9.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@jeng.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
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BASE COUNT      176 a 127 c 116 g 155 t
ORIGIN
    Query Match      65.5%; Score 36; DB 17; Length 574;
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    Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 239 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 274

RESULT 4
AU119400
LOCUS      AU119400          814 bp      mRNA      linear      EST 01-AUG-2002
DEFINITION HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project
            5'- & 3'-end one pass sequencing: Helix

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DEFINITION AU119400 HEMBA1 Homo sapiens cDNA clone HEMBA1005720 5', mRNA
            sequence.
ACCESSION  AU119400
VERSION     AU119400.1 GI:10934635
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 814)
AUTHORS     Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
TITLE       HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
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BASE COUNT      218 a 186 c 225 g 181 t
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 5.2e-07;
    Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 53
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Db 583 TGAGGTCAGGAATTCGAGATCAGCTGGCCCAACATG 618

RESULT 5
AU119141
LOCUS      AU119141          824 bp      mRNA      linear      EST 01-AUG-2002
DEFINITION AU119141 HEMBA1 Homo sapiens cDNA clone HEMBA1005123 5', mRNA
            sequence.
ACCESSION  AU119141
VERSION     AU119141.1 GI:10934376
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 824)
AUTHORS     Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
TITLE       HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix

```

Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

# FEATURES

Location/Qualifiers

1. .824  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="HEMBA1005123"  
/clone\_lib="HEMBA1"  
/tissue\_type="whole embryo, mainly head"  
/dev\_stages="embryo, 10 weeks"  
/notes="Vector: pME185FL3"  
185 c 226 g 183 t 3 others

BASE COUNT

227 a 185 c 226 g 183 t 3 others

## ORIGIN

Query Match 65.5%; Score 36; DB 9; Length 824;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 53  
|||||  
Db 583 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 618  
|||||

RESULT 6  
LOCUS BQ643665 933 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8302262 NIH\_MGC\_100 Homo sapiens cDNA clone IMAGE:6271131

5', mRNA sequence.  
ACCESSION BQ643665  
VERSION BQ643665.1 GI:21767837

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 933)  
NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

TITLE Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

JOURNAL Tissue Procurement: CGAP (Stanford)  
cDNA Library Preparation: Rubin Laboratory

COMMENT cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LNCM2447 row: g column: 04  
High quality sequence stop: 432.

Location/Qualifiers

1. .933  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6271131"  
/clone\_lib="NIH\_MGC\_100"  
/tissue\_type="hepatocellular carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

# FEATURES

source

BASE COUNT 257 a 204 c 244 g 226 t 2 others

## ORIGIN

Query Match 65.5%; Score 36; DB 14; Length 933;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 53  
|||||  
Db 624 TGAGGTGAGGAATTCGAGATCAGCTGGCCCAACATG 659  
|||||

RESULT 7  
LOCUS AQ460151 528 bp DNA linear GSS 23-APR-1999  
DEFINITION HS 5125\_B2\_C04\_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=701 Col=8 Row=F, DNA sequence.

ACCESSION AQ460151  
VERSION AQ460151.1 GI:4638791

KEYWORDS GSS.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 528)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., and Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

AUTHORS Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

TITLE Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL 93380589

MEDLINE Contact: Mahairas GG, Wallace JC, Hood L

COMMENT High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618  
Fax: (206) 616-3887

Email: [jwallace@u.washington.edu](mailto:jwallace@u.washington.edu)  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong ([pieter@dejong.med.buffalo.edu](mailto:pieter@dejong.med.buffalo.edu)). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>) or from Resear h Genetics ([inforesgen.com](http://inforesgen.com)). BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 701 row: F column: 8  
Seq primer: T7  
Class: BAC ends

High quality sequence stop: 528.  
Location/Qualifiers

1. .528  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="plate=701 Col=8 Row=F"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/sex="male"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

BASE COUNT 168 a 113 c 138 g 107 t 2 others

ORIGIN

Query Match 58.2%; Score 32; DB 17; Length 528;  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGGTGAGGAATTCGAGATCAGCTGGCCCA 49  
|||||  
Db 193 TGAGGTGAGGAATTCGAGATCAGCTGGCCCA 224  
|||||

RESULT 8  
LOCUS AQ298954 569 bp DNA linear GSS 15-DEC-1998  
DEFINITION HS 3171\_B2\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=12 Row=N, DNA sequence.

```

ACCESSION AQ298954
VERSION AQ298954.1 GI:4016133
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 569)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 9380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3171 row: N column: 12
Class: BAC ends
High quality sequence stop: 569.
Location/Qualifiers
1..569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="3171 Col=N"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="Male"
/note="Organ: sperm; Vector: pBelOAC11; BAC Clones in
E-Coli 'DH10B'"

BASE COUNT 165 a 113 c 143 g 140 t 8 others
ORIGIN

Query Match 58.2%; Score 32; DB 17; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GTCAGGAATTCGAGATCAGCTGCCCAACATG 53
|||||
Db 172 GTCAGGAATTCGAGATCAGCTGCCCAACATG 203
|||||

RESULT 9
BE279465/c
LOCUS BE279465 751 bp mRNA linear EST 13-JUL-2000
DEFINITION 601158078F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504906 5',
mRNA sequence.
ACCESSION BE279465
VERSION BE279465.1 GI:9154458
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM80 row: k column: 19
High quality sequence stop: 618.

FEATURES
source
1..751
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3504906"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 148 a 109 c 112 g 96 t  
ORIGIN

Query Match 56.4%; Score 31; DB 12; Length 465;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGTTCAGGAATTCGAGATCAGCTGGCCA 48  
Db 369 TGAGTTCAGGAATTCGAGATCAGCTGGCCA 399

RESULT 11  
AW834360/c  
LOCUS  
DEFINITION MR2-TT0013-211199-017-a08 TT0013 Homo sapiens CDNA, mRNA sequence.  
ACCESSION AW834360  
VERSION AW834360.1 GI:7928334  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 361)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.U. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR2-TT0013-211199-017-a08&t3=1999-11-21&t4=1)

Seq primer: puc 18 forward  
High quality sequence start: 26  
High quality sequence stop: 124.

Location/Qualifiers

1. 361  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="TT0013"  
/dev\_stages="Adult"

/note="Organ: testis; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 91 a 98 c 84 g 88 t

ORIGIN

Query Match 54.5%; Score 30; DB 10; Length 361;  
Best Local Similarity 100.0%; Pred. No. 0.00034;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CACTTCAGGTCAGGAATTCGAGATCAGCCT 43  
Db 78 CACTTCAGGTCAGGAATTCGAGATCAGCCT 49

RESULT 12

BE395693

LOCUS

DEFINITION BE395693

ACCESSION BE395693

VERSION BE395693.1 GI:9341058

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 625)

AUTHORS NIH-MGC

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@nci.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1C320 row: j column: 24

High quality sequence stop: 614.

Location/Qualifiers

1. 625

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="NIH-MGC\_44"

/tissue\_type="endometrium, adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 168 a 140 c 179 g 138 t

ORIGIN

Query Match 52.7%; Score 29; DB 10; Length 625;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGAGTTCAGGAATTCGAGATCAGCCTGGC 46

Db 549 TGAGTTCAGGAATTCGAGATCAGCCTGGC 577

RESULT 13

BQ331585

LOCUS

DEFINITION BQ331585

ACCESSION BQ331585

VERSION BQ331585.1 GI:20972750

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 108)

## AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM3&t2=PM3-ET0262-070501-017-e04.l&t3=2001-05-07&t4=1>)

Seq primer: pUC18 forward.

Location/Qualifiers

## FEATURES

source

```
1..108
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0262"
/dev_stage="Adult"
/notes="Organ: lung_tumor; Vector: puc18; Site:1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
```

BASE COUNT 31 a 27 c 31 g 19 t

## ORIGIN

```
Query Match 50.9%; Score 28; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

## Qy

26 GGAATTCGAGATCAGCTGGCCACATG 53

|||||

## Db

22 GGAATTCGAGATCAGCTGGCCACATG 49

## RESULT 14

## AQ467676

## LOCUS

DEFINITION HS 5203 B1 A05 SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic\_clone Plate=779 Col=9 Row=B, DNA sequence.

## ACCESSION

## AQ467676

## VERSION

## AQ467676.1

## KEYWORDS

## GSS.

## SOURCE

## human.

## ORGANISM

## Homo sapiens

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## 1 (bases 1 to 175)

## Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

## Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

## Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

## 99380589

## COMMENT

## Contact: Mahairas GG, Wallace JC, Hood L

## High Throughput Sequencing Center

## University of Washington

## 401 Queen Anne Avenue North, Seattle, WA 98109, USA

## Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

<http://www.htsc.washington.edu>

Plate: 779 row: B column: 9

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 175.

Location/Qualifiers

## FEATURES

source

```
1..175
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/notes="vector: pBAC3.6; Site:1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
```

BASE COUNT 52 a 38 c 46 g 39 t

## ORIGIN

```
Query Match 50.9%; Score 28; DB 17; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

## Qy

1 GAGCAGGCGAGCAGCTTGGTTCAGGA 28

|||||

## Db

104 GAGCAGGCGAGCAGCTTGGTTCAGGA 131

## RESULT 15

## AQ412104/c

## LOCUS

DEFINITION RPCI-11-198P7.TV RPCI-11 Homo sapiens genomic clone RPCI-11-198P7, DNA sequence.

## ACCESSION

## AQ412104

## VERSION

## AQ412104.1

## KEYWORDS

## GSS.

## SOURCE

## human.

## ORGANISM

## Homo sapiens

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## 1 (bases 1 to 302)

## Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

## Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

## Map Building

## Unpublished (1997)

## Contact: Shaying Zhao, William Nierman, Mark Adams

## Department of Eukaryotic Genomics

## The Institute for Genomic Research

## 9712 Medical Center Dr., Rockville, MD 20850

## Tel: 301 838 0200

## Fax: 301 838 0208

## Email: hbe@tigr.org

## Clones are derived from the human BAC library RPCI-11. For BAC

## library availability, please contact Pieter de Jong

## (pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

## Research Genet cs (info@resgen.com). BAC end search page:

[http://www.tigr.org/tdb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html).

## Seq primer: T7

## Class: BAC ends.

## Location/Qualifiers

## 1..302

## /organism="Homo sapiens"

## /db\_xref="GDB:7576014"

```

/db_xref="taxon:9606"
/clone="RPCI-11-198P7"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC11 Human Male BAC Library"
BASE COUNT      82 a      71 c      60 g      89 t
ORIGIN

```

```

Query Match      50.9%; Score 28; DB 17; Length 302;
Best Local Similarity 100.0%; Pred.No: 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GAGCAGGCAGACACTTGAGGTCAGGA 28
      |||||
Db     141 GAGCAGGCAGACACTTGAGGTCAGGA 114

```

Search completed: June 17, 2003, 06:23:23  
Job time : 116.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 42.3809 Seconds  
(without alignments)  
15794.017 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_4451\_4473

Perfect score: 23

Sequence: 1 cagccagcagtcgtgacagtggt 23

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	9108	9	AF123653 Homo sapi
2	23	100.0	173264	2	AC025853 Homo sapi
3	23	100.0	177568	9	Z97055 Human DNA s
C 4	22	95.7	1821	9	AB046623 Macaca fa
5	22	95.7	2787	9	AB052149 Macaca fa
C 6	22	95.7	4913	9	AL451072 Human DNA
7	22	95.7	39151	9	AP000535 Homo sapi
8	22	95.7	39668	9	AP000536 Homo sapi
9	22	95.7	40102	9	AC010647 Homo sapi
10	22	95.7	41159	9	AC004755 Homo sapi
11	22	95.7	41576	9	HSN128A12
12	22	95.7	44767	9	AL669893 Human DNA
C 13	22	95.7	54154	9	AL583845 Human DNA
14	22	95.7	56652	2	AC027427 Homo sapi
15	22	95.7	62833	2	AC107942 Homo sapi
16	22	95.7	68035	9	AL158199 Human DNA
17	22	95.7	69415	2	AC107916 Homo sapi
18	22	95.7	70384	2	AC084263 Homo sapi
19	22	95.7	77027	9	AL161792 Human DNA
C 20	22	95.7	77237	2	AC022599 Homo sapi
21	22	95.7	79018	9	AL627107 Human DNA
C 22	22	95.7	82732	9	AL512347 Human DNA
C 23	22	95.7	83750	9	AL359390 Human DNA
24	22	95.7	84657	9	AL136378 Human DNA
25	22	95.7	85490	2	AC022957 Homo sapi
26	22	95.7	87636	9	AL139039 Human DNA
C 27	22	95.7	89429	2	AL356304 Homo sapi
28	22	95.7	96669	9	AC055720 Homo sapi
29	22	95.7	96717	9	AL359182 Human DNA
C 30	22	95.7	102714	9	AP000692 Homo sapi
31	22	95.7	104660	9	AP000347 Homo sapi
32	22	95.7	110000	2	AC008576 <sup>1</sup> Continuation (2 of
33	22	95.7	110000	2	AC008576 <sup>2</sup> Continuation (3 of
C 34	22	95.7	110000	2	AC09517 <sup>2</sup> Continuation (3 of
C 35	22	95.7	111122	9	AC097105 Homo sapi
C 36	22	95.7	111187	2	AC009283 Homo sapi
37	22	95.7	111370	9	AC067815 Homo sapi
38	22	95.7	114600	9	HS477H23 Human DNA
C 39	22	95.7	115371	9	AC004918 Homo sapi
C 40	22	95.7	117000	9	AC117475 Homo sapi
C 41	22	95.7	117628	9	AC008891 Homo sapi
42	22	95.7	120029	2	HSJ282H10 Human DNA
C 43	22	95.7	122889	9	HSDA204F4 Human DNA
C 44	22	95.7	124540	9	AL353600 Human DNA
C 45	22	95.7	125780	9	CNS01DWK Human chr
C 46	22	95.7	130753	9	HS510L9 Homo sapi
C 47	22	95.7	134362	2	AC084853 Homo sapi
C 48	22	95.7	134577	2	AC015680 Homo sapi
C 49	22	95.7	135417	9	HSJ41217 Human DNA
50	22	95.7	136327	2	AC005845 Homo sapi
C 51	22	95.7	137077	9	AC007562 Homo sapi
52	22	95.7	137682	9	AC023274 Homo sapi
53	22	95.7	138817	2	AC090148 Homo sapi
54	22	95.7	140335	9	AC018645 Homo sapi
C 55	22	95.7	141220	2	AC024238 Homo sapi
56	22	95.7	141450	9	CNS05TBX Human chr
C 57	22	95.7	143968	9	AL138744 Human DNA
58	22	95.7	145726	2	AC021807 Homo sapi
59	22	95.7	145966	9	AC006451 Homo sapi
60	22	95.7	146698	2	AC105039 Homo sapi
61	22	95.7	146877	2	AC026487 Homo sapi
C 62	22	95.7	147492	9	AL358781 Human DNA
63	22	95.7	147974	2	AC076970 Homo sapi
C 64	22	95.7	148876	9	AC011455 Homo sapi
65	22	95.7	149546	9	AC087256 Homo sapi

66	22	95.7	150937	9	AL445243	Human DNA	139	22	95.7	210957	2	AL392188	Homo sapi
67	22	95.7	152876	2	AC099488	Homo sapi	140	22	95.7	211748	9	AC010146	Homo sapi
68	22	95.7	152966	9	AL359713	Human DNA	c 141	22	95.7	212505	2	AC027220	Homo sapi
69	22	95.7	154939	9	AC022537	Homo sapi	c 142	22	95.7	215962	2	AC010615	Homo sapi
70	22	95.7	155296	9	AL359175	Human DNA	c 143	22	95.7	217117	2	AC0116438	Homo sapi
71	22	95.7	155526	2	AC013371	Homo sapi	c 144	22	95.7	225428	2	AC115115	Homo sapi
72	22	95.7	155702	9	AC013271	Homo sapi	c 145	22	95.7	226035	9	CNS01DXV	Human chr
73	22	95.7	155786	2	AC027721	Homo sapi	c 146	22	95.7	263839	2	AC117380	Homo sapi
74	22	95.7	156955	9	AL157886	Human DNA	c 147	22	95.7	284671	2	AC106710	Homo sapi
75	22	95.7	157921	2	AC027726	Homo sapi	c 148	22	95.7	305000	9	HSDPA	Homo sapi
76	22	95.7	157968	2	AC023438	Homo sapi	c 149	22	95.7	340000	9	AP001725	Homo sapi
77	22	95.7	159384	2	AL356110	Homo sapi	150	21	91.3	51	6	AX159173	Sequence
78	22	95.7	159859	2	AC074010	Homo sapi	151	21	91.3	51	6	AX159174	Sequence
79	22	95.7	161487	2	AC119571	Pan trogl	c 152	21	91.3	170	6	AX322336	Sequence
80	22	95.7	161494	9	AC110495	Homo sapi	153	21	91.3	401	6	AX270245	Sequence
81	22	95.7	161699	9	AC113435	Pan trogl	154	21	91.3	401	6	AX270246	Sequence
82	22	95.7	162208	9	AC073321	Homo sapi	155	21	91.3	401	6	AX270247	Sequence
83	22	95.7	164423	2	AC026828	Homo sapi	156	21	91.3	401	6	AX270248	Sequence
84	22	95.7	164916	9	AC021305	Homo sapi	157	21	91.3	401	6	AX271776	Sequence
85	22	95.7	165090	9	AC010655	Homo sapi	158	21	91.3	401	6	AX271777	Sequence
86	22	95.7	165854	9	AC073043	Homo sapi	159	21	91.3	401	6	AX271778	Sequence
87	22	95.7	166164	2	AC023388	Homo sapi	160	21	91.3	401	6	AX271779	Sequence
88	22	95.7	166186	2	AC109815	Homo sapi	161	21	91.3	441	11	HUMUT5200A	Human STS U
89	22	95.7	167021	9	AC079414	Homo sapi	162	21	91.3	463	11	HUMUT5408	Human chrom
90	22	95.7	167195	9	AC009044	Homo sapi	163	21	91.3	476	9	AF512806	Homo sapi
91	22	95.7	168227	9	AC021868	Homo sapi	164	21	91.3	527	6	AX388834	Sequence
92	22	95.7	169342	9	AL136991	Human DNA	165	21	91.3	558	6	AX389815	Sequence
93	22	95.7	170026	2	AC013627	Homo sapi	166	21	91.3	558	6	AX391031	Sequence
94	22	95.7	170520	2	AL358172	Homo sapi	167	21	91.3	581	6	AX390832	Sequence
95	22	95.7	171360	2	AC068543	Homo sapi	c 168	21	91.3	581	11	G63668	SHGC-141466
96	22	95.7	171731	2	AC091659	Papio cyn	c 169	21	91.3	1552	9	BC0097023	Homo sapi
97	22	95.7	172573	9	AC007276	Homo sapi	c 170	21	91.3	1561	9	BC007023	Homo sapi
98	22	95.7	173135	9	AC092018	Homo sapi	c 171	21	91.3	1675	9	AK097604	Homo sapi
99	22	95.7	173456	9	AL158198	Human DNA	c 172	21	91.3	1764	9	AK092844	Homo sapi
100	22	95.7	174826	9	AC116562	Homo sapi	c 173	21	91.3	1879	9	AK021739	Homo sapi
101	22	95.7	175064	2	AC012230	Homo sapi	c 174	21	91.3	2049	9	AK094063	Homo sapi
102	22	95.7	175236	2	AC108938	Homo sapi	c 175	21	91.3	2107	9	AB050434	Macaca fa
103	22	95.7	175339	9	AC005772	Homo sapi	c 176	21	91.3	2130	9	F187967S01	Homo sapi
104	22	95.7	175403	9	AC093268	Homo sapi	c 177	21	91.3	2443	9	AK055262	Homo sapi
105	22	95.7	175935	2	AC024074	Homo sapi	c 178	21	91.3	2580	9	AK094213	Homo sapi
106	22	95.7	175952	9	AL391872	Human DNA	c 179	21	91.3	2611	9	AK074364	Homo sapi
107	22	95.7	176182	9	AC018845	Homo sapi	c 180	21	91.3	2783	9	D50134	Homo sapien
108	22	95.7	176544	2	AL138877	Homo sapi	c 181	21	91.3	2852	9	AK092611	Homo sapi
109	22	95.7	178500	2	AL359926	Homo sapi	c 182	21	91.3	2893	9	BC020558	Homo sapi
110	22	95.7	178771	2	AF267168	Homo sapi	c 183	21	91.3	2968	9	HSU52154	Human G pro
111	22	95.7	179040	2	AC022732	Homo sapi	c 184	21	91.3	2975	9	BC008816	Homo sapi
112	22	95.7	179064	9	AL353807	Human DNA	c 185	21	91.3	2975	9	BC011631	Homo sapi
113	22	95.7	181302	9	AC091619	Papio cyn	c 186	21	91.3	3085	9	HUML14D	Human mRNA
114	22	95.7	182178	9	AL138711	Human DNA	c 187	21	91.3	3172	6	AX330716	Sequence
115	22	95.7	182617	9	AC007731	Homo sapi	c 188	21	91.3	3172	6	AX331138	Sequence
116	22	95.7	184560	2	AC021124	Homo sapi	c 189	21	91.3	3172	6	HSU23942	Human lanes
117	22	95.7	185279	9	AC007338	Homo sapi	c 190	21	91.3	3180	9	HSM900699	Homo sapi
118	22	95.7	188023	10	AL645543	Mouse DNA	c 191	21	91.3	3324	9	AK090602	Homo sapi
119	22	95.7	188622	9	AL359258	Human DNA	c 192	21	91.3	3514	9	AK091323	Homo sapi
120	22	95.7	188736	9	CNS00MG	Human chr	c 193	21	91.3	3521	9	HUM36DC22	Homo sapien
121	22	95.7	188833	9	HS268H5	Human DNA	c 194	21	91.3	4337	9	AK096349	Homo sapi
122	22	95.7	189317	9	HSJ190J20	Human DNA	c 195	21	91.3	4463	9	HUMGUSBA	Human beta-
123	22	95.7	189610	9	AC104301	Homo sapi	c 196	21	91.3	4734	9	HSPD54CG7	Homo sapi
124	22	95.7	190998	9	AC019181	Homo sapi	c 197	21	91.3	5119	9	AF082937	Homo sapi
125	22	95.7	191774	2	AC025648	Homo sapi	c 198	21	91.3	5759	9	HUMFEN1GNA	Human fibri
126	22	95.7	192592	9	AC005500	Homo sapi	c 199	21	91.3	5880	9	AB070559	Homo sapi
127	22	95.7	192670	9	AC008592	Homo sapi	c 200	21	91.3	6222	9	AY028318S2	Homo sapi
128	22	95.7	195634	9	AC013464	Homo sapi	c 201	21	91.3	6283	9	AY033055S2	Homo sapi
129	22	95.7	196541	2	AC091622	Pan trogl	c 202	21	91.3	6306	9	AY028320S2	Homo sapi
130	22	95.7	196817	9	AC019209	Homo sapi	c 203	21	91.3	9839	9	HSA295622	Homo sapi
131	22	95.7	196993	9	CNS01D7T	Human chr	c 204	21	91.3	10315	9	AC104526	Homo sapi
132	22	95.7	197310	2	AF254981	Homo sapi	c 205	21	91.3	10318	9	AL662877	Human DNA
133	22	95.7	197455	9	AC005701	Homo sapi	c 206	21	91.3	12206	9	HSJ69F7A	Human DNA s
134	22	95.7	197932	2	AC020715	Homo sapi	c 207	21	91.3	12293	6	AX409505	Sequence
135	22	95.7	201365	2	AC120051	Homo sapi	c 208	21	91.3	12293	9	HUMC201	Homo sapien
136	22	95.7	202768	2	AC092345	Homo sapi	c 209	21	91.3	13288	9	AC119795	Homo sapi
137	22	95.7	206399	2	AC090376	Homo sapi	c 210	21	91.3	15469	2	AC009067	Homo sapi
138	22	95.7	207767	2	AP001497	Homo sapi	c 211	21	91.3	16090	9	AL354812	Human DNA



C 212	21	91.3	16342	9	HSN85E10	268758 Human DNA s	C 285	21	91.3	40451	9	AL139802	Human DNA
C 213	21	91.3	17429	9	AL445253	AL445253 Human DNA	C 286	21	91.3	40491	9	AC002116	Human DNA
C 214	21	91.3	18228	9	AL772153	AL772153 Human DNA	C 287	21	91.3	40883	9	AC005776	Homo sapi
C 215	21	91.3	20125	9	AC094079	AC094079 Homo sapi	C 288	21	91.3	40962	2	AC006189	Homo sapi
C 216	21	91.3	20539	9	HS349E10	AL022341 Human DNA	C 289	21	91.3	41219	2	AC005382	Homo sapi
C 217	21	91.3	20938	9	AL589942	AL589942 Human DNA	C 290	21	91.3	41300	2	AC003097	Homo sapi
C 218	21	91.3	21249	2	AC004105	AC004105 Homo sapi	C 291	21	91.3	41518	9	AC010515	Homo sapi
C 219	21	91.3	22050	9	AC087243	AC087243 Homo sapi	C 292	21	91.3	41572	9	AC006132	Homo sapi
C 220	21	91.3	24019	9	AL359184	AL359184 Human DNA	C 293	21	91.3	41630	9	AC005785	Homo sapi
C 221	21	91.3	24747	9	AL136990	AL136990 Human DNA	C 294	21	91.3	41669	9	AL138821	Human DNA
C 222	21	91.3	24869	2	AC083996	AC083996 Homo sapi	C 295	21	91.3	42301	9	AC005944	Homo sapi
C 223	21	91.3	24935	9	AC092423	AC092423 Homo sapi	C 296	21	91.3	42304	9	AL355881	Human DNA s
C 224	21	91.3	25031	9	HSJ917C11	AL078642 Human DNA	C 297	21	91.3	42749	9	HSU42H12	Human DNA s
C 225	21	91.3	26226	9	AL136180	AL136180 Homo sapi	C 298	21	91.3	42863	9	AB065617	Homo sapi
C 226	21	91.3	26356	9	AC092001	AC092001 Homo sapi	C 299	21	91.3	42863	9	AB065617	Homo sapi
C 227	21	91.3	26855	2	AL391984	AL391984 Homo sapi	C 300	21	91.3	43058	6	AX332810	Sequence
C 228	21	91.3	27182	9	AC007093	AC007093 Homo sapi	C 301	21	91.3	43058	6	AX333047	Sequence
C 229	21	91.3	27213	9	AP000291	AP000291 Homo sapi	C 302	21	91.3	43058	6	AX411306	Sequence
C 230	21	91.3	27927	9	AC103879	AC103879 Homo sapi	C 303	21	91.3	43058	9	HSJG1	Human DNA s
C 231	21	91.3	28428	9	AY057059S2	AY057060 Homo sapi	C 304	21	91.3	43527	9	AC006293	Homo sapi
C 232	21	91.3	28519	9	AL512565	AL512565 Homo sapi	C 305	21	91.3	43661	9	AC004493	Homo sapi
C 233	21	91.3	29021	9	AL356477	AL356477 Human DNA	C 306	21	91.3	43735	9	AC108209	Homo sapi
C 234	21	91.3	29103	9	HSJ165D7	Z58273 Human DNA s	C 307	21	91.3	43746	9	AC093641	Homo sapi
C 235	21	91.3	31501	9	HSJG216	AC006216 Homo sapi	C 308	21	91.3	44118	9	AC006165	Homo sapi
C 236	21	91.3	31671	9	AC009977	AC009977 Homo sapi	C 309	21	91.3	44621	9	AP001873	Homo sapi
C 237	21	91.3	31686	9	AC117422	AC117422 Homo sapi	C 310	21	91.3	45292	9	AC114957	Homo sapi
C 238	21	91.3	32360	9	AL607067	AL607067 Human DNA	C 311	21	91.3	45911	9	AC005688	Homo sapi
C 239	21	91.3	32360	9	AC005339	AC005339 Homo sapi	C 312	21	91.3	45980	2	U82206	Homo sapien
C 240	21	91.3	32887	9	AC118535	AC118535 Homo sapi	C 313	21	91.3	46166	2	AC104253	Homo sapi
C 241	21	91.3	33795	6	AX409537	AX409537 Sequence	C 314	21	91.3	46251	9	AD000671	Homo sapi
C 242	21	91.3	33795	9	AF253417	AF253417 Homo sapi	C 315	21	91.3	46324	9	AC093818	Homo sapi
C 243	21	91.3	33917	9	AC004410	AC004410 Homo sapi	C 316	21	91.3	46894	9	AC114729	Homo sapi
C 244	21	91.3	33931	9	AC022156	AC022156 Homo sapi	C 317	21	91.3	46912	9	AC011557	Homo sapi
C 245	21	91.3	34068	9	HS312E8	AL032819 Human DNA	C 318	21	91.3	47673	2	AC083879	Homo sapi
C 246	21	91.3	34359	9	AL596307	AL596307 Human DNA	C 319	21	91.3	47834	9	HSJ834A16	Human DNA
C 247	21	91.3	34507	9	AL591895	AL591895 Homo sapi	C 320	21	91.3	48133	9	AL359700	Human DNA
C 248	21	91.3	35001	9	AP002892	AP002892 Homo sapi	C 321	21	91.3	48289	9	AC067729	Homo sapi
C 249	21	91.3	35120	9	AL590112	AL590112 Human DNA	C 322	21	91.3	48522	2	AC105112	Homo sapi
C 250	21	91.3	35587	9	AC005763	AC005763 Homo sapi	C 323	21	91.3	48623	2	AC130469	Homo sapi
C 251	21	91.3	35688	9	AC073417	AC073417 Homo sapi	C 324	21	91.3	48677	9	AC108465	Homo sapi
C 252	21	91.3	35730	9	HSN74G7	Z69715 Human DNA s	C 325	21	91.3	48698	9	AL592171	Human DNA
C 253	21	91.3	36029	9	U73479	U73479 Homo sapien	C 326	21	91.3	48860	9	AL136461	Human DNA
C 254	21	91.3	36413	2	AC097272	AC097272 Hylobates	C 327	21	91.3	49151	2	AC068148	Homo sapi
C 255	21	91.3	36428	9	AC110000	AC110000 Homo sapi	C 328	21	91.3	49362	2	AL355875	Human DNA
C 256	21	91.3	36431	9	AC068499	AC068499 Homo sapi	C 329	21	91.3	49831	9	AC104063	Homo sapi
C 257	21	91.3	36437	9	HSU138B7	Z78422 Human DNA s	C 330	21	91.3	51700	9	AL157763	Human DNA
C 258	21	91.3	36534	9	U73167	U73167 Homo sapien	C 331	21	91.3	51705	9	AC092589	Homo sapi
C 259	21	91.3	36552	9	HSU90094	U90094 Human chrom	C 332	21	91.3	51953	2	AC083779	Homo sapi
C 260	21	91.3	36558	9	HSU81834	U81834 Human cosm	C 333	21	91.3	52273	2	AC068690	Homo sapi
C 261	21	91.3	36565	9	HSU73648	U73648 Human chrom	C 334	21	91.3	52597	2	HSJ421120	Human DNA
C 262	21	91.3	36594	9	HUMTPA	K03021 Human tissu	C 335	21	91.3	52737	2	AC007800	Homo sapi
C 263	21	91.3	37219	9	HSN11D4	Z68285 Human DNA s	C 336	21	91.3	52813	9	AC010991	Homo sapi
C 264	21	91.3	37239	9	AC096549	AC096549 Homo sapi	C 337	21	91.3	52847	9	AL356121	Human DNA
C 265	21	91.3	37448	9	AC006138	AC006138 Homo sapi	C 338	21	91.3	53035	2	AC104987	Homo sapi
C 266	21	91.3	37693	9	AP000522	AP000522 Homo sapi	C 339	21	91.3	53249	2	AC092688	Homo sapi
C 267	21	91.3	37852	9	AC124902	AC124902 Homo sapi	C 340	21	91.3	53542	6	AX247730	Sequence
C 268	21	91.3	37991	9	AC005101	AC005101 Homo sapi	C 341	21	91.3	53823	2	AC091642	Homo sapi
C 269	21	91.3	38080	9	HS429E7	AL031722 Human DNA	C 342	21	91.3	53987	2	AC091943	Homo sapi
C 270	21	91.3	38134	9	AC000040	AC000040 Homo sapi	C 343	21	91.3	54375	9	AC011377	Homo sapi
C 271	21	91.3	38250	2	AC012006	AC012006 Homo sapi	C 344	21	91.3	54395	2	AC011297	Homo sapi
C 272	21	91.3	38491	9	AC006049	AC006049 Homo sapi	C 345	21	91.3	54498	2	AC023815	Homo sapi
C 273	21	91.3	38684	2	AC108461	AC108461 Homo sapi	C 346	21	91.3	55448	9	AC084353	Homo sapi
C 274	21	91.3	38852	9	AC006261	AC006261 Homo sapi	C 347	21	91.3	56641	2	AL138833	Homo sapi
C 275	21	91.3	38974	2	AL450315	AL450315 Homo sapi	C 348	21	91.3	56716	2	AC105047	Homo sapi
C 276	21	91.3	39000	9	HSN86D4	Z82250 Human DNA s	C 349	21	91.3	56822	2	AC091084	Homo sapi
C 277	21	91.3	39132	9	AC005515	AC005515 Homo sapi	C 350	21	91.3	56827	9	HSJHC3A5	Human DNA s
C 278	21	91.3	39514	9	AC005594	AC005594 Homo sapi	C 351	21	91.3	56913	9	HS67C13	Sequence
C 279	21	91.3	39838	9	AC007766	AC007766 Homo sapi	C 352	21	91.3	57108	2	AC130297	Homo sapi
C 280	21	91.3	39856	9	AF241735	AF241735 Homo sapi	C 353	21	91.3	57121	2	AC084255	Homo sapi
C 281	21	91.3	39923	9	AL627082	AL627082 Human DNA	C 354	21	91.3	57821	9	AC073595	Homo sapi
C 282	21	91.3	40179	9	AC004036	AC004036 Homo sapi	C 355	21	91.3	58917	9	AC004819	Homo sapi
C 283	21	91.3	40351	9	AC005620	AC005620 Homo sapi	C 356	21	91.3	59065	6	ARI83260	Sequence
C 284	21	91.3	40439	9	AF442963	AF442963 Homo sapi	C 357	21	91.3	59406	9	AP001171	Homo sapi

358	21	91.3	59427	9	AC079882	AC079882 Homo sapi	431	21	91.3	71903	9	AL607035	Human DNA
359	21	91.3	59586	9	HS449017	Z98749 Human DNA s	C 432	21	91.3	72022	2	AC084430	Homo sapi
360	21	91.3	60149	9	AL135925	AL135925 Homo sapi	C 433	21	91.3	72305	2	AC076975	Homo sapi
361	21	91.3	60455	9	AP000264	AP000264 Homo sapi	C 434	21	91.3	72402	2	AL389924	Human DNA
362	21	91.3	60694	2	AC087827	AC087827 Homo sapi	C 435	21	91.3	72485	2	AC083792	Homo sapi
363	21	91.3	60725	9	AL669983	AL669983 Homo sapi	C 436	21	91.3	72533	2	AC127543	Homo sapi
364	21	91.3	60834	2	AC087472	AC087472 Homo sapi	C 437	21	91.3	72665	2	AC026981	Homo sapi
365	21	91.3	60901	9	AL160406	AL160406 Homo sapi	C 438	21	91.3	72665	2	AC026981	Homo sapi
366	21	91.3	61079	9	AC105202	AC105202 Homo sapi	C 439	21	91.3	72978	9	AL359759	Human DNA
367	21	91.3	61228	9	AC106706	AC106706 Homo sapi	C 440	21	91.3	73386	2	AC129501	Homo sapi
368	21	91.3	61913	9	AL671966	AL671966 Homo sapi	C 441	21	91.3	73469	2	AC117575	Mus muscu
369	21	91.3	61991	2	AC131282	AC131282 Homo sapi	C 442	21	91.3	73503	2	AC013586	Homo sapi
370	21	91.3	62078	2	AC013711	AC013711 Homo sapi	C 443	21	91.3	74102	9	AL356316	Human DNA
371	21	91.3	62078	2	AC013711	AC013711 Homo sapi	C 444	21	91.3	74129	2	AC073167	Homo sapi
372	21	91.3	62147	9	AC093251	AC093251 Homo sapi	C 445	21	91.3	74274	2	AC087717	Homo sapi
373	21	91.3	62287	2	AC115104	AC115104 Homo sapi	C 446	21	91.3	74581	9	AL391235	Human DNA
374	21	91.3	62288	9	AC005571	AC005571 Homo sapi	C 447	21	91.3	75184	9	AC005218	Homo sapi
375	21	91.3	62464	2	AC131572	AC131572 Homo sapi	C 448	21	91.3	75326	2	AC026999	Homo sapi
376	21	91.3	62747	2	AC087475	AC087475 Homo sapi	C 449	21	91.3	75440	9	AP000786	Homo sapi
377	21	91.3	63006	9	AL451166	AL451166 Homo sapi	C 450	21	91.3	75523	9	AL627233	Human DNA
378	21	91.3	63029	2	AC131288	AC131288 Homo sapi	C 451	21	91.3	76848	9	AC003041	Homo sapi
379	21	91.3	63090	9	AC087320	AC087320 Homo sapi	C 452	21	91.3	76982	9	AL731542	Human DNA
380	21	91.3	63522	2	AC040937	AC040937 Homo sapi	C 453	21	91.3	77239	9	AL583844	Human DNA
381	21	91.3	63528	2	AC091196	AC091196 Homo sapi	C 454	21	91.3	77322	2	AC021334	Homo sapi
382	21	91.3	63749	9	AC004694	AC004694 Homo sapi	C 455	21	91.3	77331	9	AL354983	Human DNA
383	21	91.3	63797	2	AC127453	AC127453 Homo sapi	C 456	21	91.3	77663	2	AL357131	Continuation (4 of
384	21	91.3	63955	9	AC108151	AC108151 Homo sapi	C 457	21	91.3	77691	9	AL120118	Homo sapi
385	21	91.3	64080	9	AL133217	AL133217 Human DNA	C 458	21	91.3	77702	9	AL138743	Human DNA
386	21	91.3	64323	9	AL356976	AL356976 Homo sapi	C 459	21	91.3	78359	9	AF314199S7	
387	21	91.3	64650	2	AC068864	AC068864 Homo sapi	C 460	21	91.3	78359	9	AL112518	Homo sapi
388	21	91.3	64931	9	AC128716	AC128716 Homo sapi	C 461	21	91.3	78467	9	AC008078	Homo sapi
389	21	91.3	64952	9	AL359745	AL359745 Homo sapi	C 462	21	91.3	78643	9	AC004964	Homo sapi
390	21	91.3	65111	2	AC055857	AC055857 Homo sapi	C 463	21	91.3	79223	9	AL391114	Human DNA
391	21	91.3	65237	2	AC105208	AC105208 Homo sapi	C 464	21	91.3	79227	9	HS148E22	Human DNA
392	21	91.3	65356	2	AC090990	AC090990 Homo sapi	C 465	21	91.3	79319	9	AL512274	Human DNA
393	21	91.3	65413	2	AC116019	AC116019 Homo sapi	C 466	21	91.3	79422	2	AC022750	Homo sapi
394	21	91.3	65608	6	AX330738	AX330738 Sequence	C 467	21	91.3	79600	2	AL353657	Human DNA
395	21	91.3	65608	6	AX332242	AX332242 Sequence	C 468	21	91.3	80039	2	AC021290	Homo sapi
396	21	91.3	65608	6	AX335496	AX335496 Sequence	C 469	21	91.3	80119	2	AC111152	Homo sapi
397	21	91.3	65608	9	HS062293	U62293 Human LIM-k	C 470	21	91.3	80272	2	HSJ491C16	
398	21	91.3	65821	2	AC087461	AC087461 Homo sapi	C 471	21	91.3	80318	2	AC016300	Homo sapi
399	21	91.3	66148	2	AC110017	AC110017 Homo sapi	C 472	21	91.3	80363	2	AC025805	Homo sapi
400	21	91.3	66235	2	AC016226	AC016226 Homo sapi	C 473	21	91.3	80515	9	AC011992	Homo sapi
401	21	91.3	66575	2	AC130324	AC130324 Homo sapi	C 474	21	91.3	80547	9	AC007382	Homo sapi
402	21	91.3	66981	2	AC023178	AC023178 Homo sapi	C 475	21	91.3	80565	9	AL357374	Human DNA
403	21	91.3	67046	9	HS063721	U63721 Human elast	C 476	21	91.3	81001	6	AX063464	Sequence
404	21	91.3	67150	9	AC021651	AC021651 Homo sapi	C 477	21	91.3	81001	6	AX469876	Sequence
405	21	91.3	67326	2	AC073034	AC073034 Homo sapi	C 478	21	91.3	81674	9	HS722E9	Human DNA
406	21	91.3	67392	9	AC107220	AC107220 Homo sapi	C 479	21	91.3	81768	9	AL662825	Human DNA
407	21	91.3	67462	2	AC091595	AC091595 Homo sapi	C 480	21	91.3	81974	9	HS931E15	Human DNA
408	21	91.3	67674	2	AC090641	AC090641 Homo sapi	C 481	21	91.3	81974	9	HSJ363M2	Human DNA
409	21	91.3	67709	9	AC104830	AC104830 Homo sapi	C 482	21	91.3	82279	2	AC010464	Homo sapi
410	21	91.3	67713	2	AC102796	AC102796 Homo sapi	C 483	21	91.3	82316	9	AL354726	Human DNA
411	21	91.3	68091	2	AC124094	AC124094 Homo sapi	C 484	21	91.3	82374	9	AL355001	Human DNA
412	21	91.3	68509	2	HSY313F4	Continuation (4 of	C 485	21	91.3	82700	2	AC015635	Homo sapi
413	21	91.3	68554	2	AC090387	Continuation (4 of	C 486	21	91.3	82806	9	AC007111	Homo sapi
414	21	91.3	68582	9	AB017652	AB017652 Homo sapi	C 487	21	91.3	82827	9	AC079395	Homo sapi
415	21	91.3	68582	9	AP000464	AP000464 Homo sapi	C 488	21	91.3	82938	9	AC079250	Homo sapi
416	21	91.3	68607	2	AC103887	AC103887 Homo sapi	C 489	21	91.3	83153	2	AC011417	Homo sapi
417	21	91.3	68843	9	AL450427	AL450427 Human DNA	C 490	21	91.3	83552	9	AL157759	Human DNA
418	21	91.3	68914	2	AC024970	AC024970 Homo sapi	C 491	21	91.3	83705	9	AC025766	Homo sapi
419	21	91.3	69028	9	AC087493	AC087493 Homo sapi	C 492	21	91.3	83820	9	AL133264	Human DNA
420	21	91.3	69051	2	AC073171	AC073171 Homo sapi	C 493	21	91.3	83951	9	AL354824	Human DNA
421	21	91.3	69165	2	AC023465	AC023465 Homo sapi	C 494	21	91.3	84176	9	AL590782	Human DNA
422	21	91.3	69678	9	AC091573	AC091573 Homo sapi	C 495	21	91.3	84364	9	HS522J7	Z98885 Human DNA s
423	21	91.3	69901	9	HS694E4	AL031255 Human DNA	C 496	21	91.3	84477	2	AC015827	Human DNA
424	21	91.3	69918	9	AL441988	AL441988 Human DNA	C 497	21	91.3	84570	9	AL359552	Human DNA
425	21	91.3	70043	9	AL157776	AL157776 Human DNA	C 498	21	91.3	84678	2	AC087464	Homo sapi
426	21	91.3	70621	9	AL713971	AL713971 Human DNA	C 499	21	91.3	84679	2	AC022571	Homo sapi
427	21	91.3	70849	2	AC090139	AC090139 Homo sapi	C 500	21	91.3	84881	9	AL390726	Human DNA
428	21	91.3	71117	9	HSJ132F21	AL079335 Human DNA	C 501	21	91.3	84971	9	AC092271	Homo sapi
429	21	91.3	71353	9	AF104455	AF104455 Homo sapi	C 502	21	91.3	85275	9	AC092180	Homo sapi
430	21	91.3	71864	2	AC103852	AC103852 Homo sapi	C 503	21	91.3	85275	9	AC092180	Homo sapi

504	21	91.3	85382	9	AL390793	Human DNA	577	21	91.3	96308	9	CNS08C90	AL749540	Human chr
505	21	91.3	85420	9	AC004672	Homo sapi	578	21	91.3	96387	2	HSJ600024	AL080247	Homo sapi
506	21	91.3	85500	9	HS199H16	Human DNA	579	21	91.3	96444	9	HSJ738116	AL049867	Human DNA
507	21	91.3	85550	9	AC104466	Homo sapi	580	21	91.3	96482	9	AC096739	AC096739	Homo sapi
508	21	91.3	85818	9	AL161640	Human DNA	581	21	91.3	96489	9	AC011395	AC011395	Homo sapi
509	21	91.3	85942	9	AC091971	Homo sapi	582	21	91.3	96559	9	AC079347	AC079347	Homo sapi
510	21	91.3	85977	9	AC094085	Homo sapi	583	21	91.3	96638	9	AC092545	AC092545	Homo sapi
511	21	91.3	86057	9	AC092112	Homo sapi	584	21	91.3	96951	9	AC026433	AC026433	Homo sapi
512	21	91.3	86077	9	AC073971	Homo sapi	585	21	91.3	96975	9	AC004975	AC004975	Homo sapi
513	21	91.3	86769	9	HSAP003626	Homo sapi	586	21	91.3	96978	9	AC024075	AC024075	Homo sapi
514	21	91.3	86825	9	AC006967	Homo sapi	587	21	91.3	97037	9	AC004973	AC004973	Homo sapi
515	21	91.3	87000	9	AC097103	Homo sapi	588	21	91.3	97112	9	AL353631	AL353631	Human DNA
516	21	91.3	87076	9	AC005918	Homo sapi	589	21	91.3	97129	9	HS292H14	AL008710	Human DNA
517	21	91.3	87323	9	AC006373	Homo sapi	590	21	91.3	97254	2	AC079517 <sup>4</sup>	Continuation (5 of	
518	21	91.3	87350	2	AC009752	Homo sapi	591	21	91.3	97495	9	AC093014	AC093014	Homo sapi
519	21	91.3	87917	2	AC016261	Homo sapi	592	21	91.3	97556	9	AC079781	AC079781	Homo sapi
520	21	91.3	87973	2	AC009185	Homo sapi	593	21	91.3	97700	9	AL136079	AL136079	Human DNA
521	21	91.3	88347	2	AC104981	Homo sapi	594	21	91.3	97835	9	HS292E10	HS292E10	Human DNA
522	21	91.3	88520	9	AC097503	Homo sapi	595	21	91.3	98261	2	AL355676	AL355676	Homo sapi
523	21	91.3	88528	9	AL356857	Human DNA	596	21	91.3	98404	2	AL355676	AL355676	Homo sapi
524	21	91.3	89153	9	AC026714	Homo sapi	597	21	91.3	98433	9	AC006365	AC006365	Homo sapi
525	21	91.3	89214	9	AC093309	Homo sapi	598	21	91.3	98638	9	CNS05TDO	AL356806	Human chr
526	21	91.3	89603	9	HSU63834	Human K.I.T p	599	21	91.3	98804	2	AC106723 <sup>3</sup>	Continuation (4 of	
527	21	91.3	89871	9	AC092207	Homo sapi	600	21	91.3	98835	9	AC073195	AC073195	Homo sapi
528	21	91.3	90136	9	HS330012	Human DNA	601	21	91.3	98935	9	AC004935	AC004935	Homo sapi
529	21	91.3	90150	9	AC068576	Homo sapi	602	21	91.3	98955	9	AC008886	AC008886	Homo sapi
530	21	91.3	90244	9	AB023051	Homo sapi	603	21	91.3	99036	9	AC005773	AC005773	Homo sapi
531	21	91.3	90256	9	AP001582	Homo sapi	604	21	91.3	99227	9	AC114737	AC114737	Homo sapi
532	21	91.3	90331	9	AL353682	Human DNA	605	21	91.3	99370	9	AC005057	AC005057	Homo sapi
533	21	91.3	90422	9	AC023880	Homo sapi	606	21	91.3	99521	2	AC127700	AC127700	Homo sapi
534	21	91.3	90430	9	AC003100	Homo sapi	607	21	91.3	99611	9	AL591519	AL591519	Human DNA
535	21	91.3	90476	9	AC015910	Homo sapi	608	21	91.3	99859	2	AC025368	AC025368	Homo sapi
536	21	91.3	90815	9	AC002559	Homo sapi	609	21	91.3	99886	9	HS598F2	AL021579	Human DNA
537	21	91.3	90820	2	AC111155	Homo sapi	610	21	91.3	99995	9	AC010480	AC010480	Homo sapi
538	21	91.3	91071	2	AC022589	Homo sapi	611	21	91.3	100000	9	AP000035	AP000035	Homo sapi
539	21	91.3	91311	9	AC011230	Homo sapi	612	21	91.3	100000	9	AP000043	AP000043	Homo sapi
540	21	91.3	91323	9	AC106901	Homo sapi	613	21	91.3	100000	9	AP000101	AP000101	Homo sapi
541	21	91.3	91692	9	AC084253	Homo sapi	614	21	91.3	100000	9	AP000111	AP000111	Homo sapi
542	21	91.3	91832	2	AC114546	Homo sapi	615	21	91.3	100000	9	AP000177	AP000177	Homo sapi
543	21	91.3	91842	9	AC008392	Homo sapi	616	21	91.3	100000	9	AP000187	AP000187	Homo sapi
544	21	91.3	92068	2	AL672077	Homo sapi	617	21	91.3	100000	9	AP000210	AP000210	Homo sapi
545	21	91.3	92242	9	AF216668	Homo sapi	618	21	91.3	100000	9	AP000502	AP000502	Homo sapi
546	21	91.3	92460	9	AL136228	Human DNA	619	21	91.3	100000	9	AP000513	AP000513	Homo sapi
547	21	91.3	92472	9	HS181C9	Human DNA	620	21	91.3	100000	17	AP000132	AP000132	Homo sapi
548	21	91.3	92487	9	AC068280	Homo sapi	621	21	91.3	100116	9	AL591178	AL591178	Human DNA
549	21	91.3	92636	9	AC005251	Homo sapi	622	21	91.3	100133	9	AC113342	AC113342	Homo sapi
550	21	91.3	92644	2	AF186995	Homo sapi	623	21	91.3	100139	9	AC021752	AC021752	Homo sapi
551	21	91.3	92807	9	HS1137F22	Human DNA	624	21	91.3	100139	9	AC021752	AC021752	Homo sapi
552	21	91.3	92858	2	AC024959	Homo sapi	625	21	91.3	100267	9	HSMEHC3W36A	HSMEHC3W36A	Homo sapi
553	21	91.3	92969	9	HSJ687F11	Human DNA	626	21	91.3	100493	2	AP002020	AP002020	Homo sapi
554	21	91.3	93033	2	AP000644	Homo sapi	627	21	91.3	100506	2	AP002020	AP002020	Homo sapi
555	21	91.3	93395	2	AC087882	Homo sapi	628	21	91.3	100521	9	AC119397	AC119397	Homo sapi
556	21	91.3	93403	9	AC073261	Homo sapi	629	21	91.3	100531	2	AC093215	AC093215	Homo sapi
557	21	91.3	93431	9	HUU95737	Human Chrom	630	21	91.3	100701	9	AC005911	AC005911	Homo sapi
558	21	91.3	93519	9	AC130458	Homo sapi	631	21	91.3	100791	9	CNS01R18	AL163011	Human chr
559	21	91.3	94224	9	HS661120	Human DNA	632	21	91.3	100808	9	AC108081	AC108081	Homo sapi
560	21	91.3	94296	2	AL160261	Homo sapi	633	21	91.3	101036	9	AC008711	AC008711	Homo sapi
561	21	91.3	94385	2	AL356673	Homo sapi	634	21	91.3	101077	2	AC024051	AC024051	Homo sapi
562	21	91.3	95084	9	AC010385	Homo sapi	635	21	91.3	101370	9	AC003962	AC003962	Homo sapi
563	21	91.3	95097	9	AL133232	Human DNA	636	21	91.3	101507	9	AP000359	AP000359	Homo sapi
564	21	91.3	95241	9	HS398B19	Human DNA	637	21	91.3	101652	9	AC079754	AC079754	Homo sapi
565	21	91.3	95345	9	AC007029	Homo sapi	638	21	91.3	101728	9	HS109088	AL033524	Human DNA
566	21	91.3	95375	9	HS228A9	Human DNA	639	21	91.3	101768	9	AC006465	AC006465	Homo sapi
567	21	91.3	95546	9	AC022816	Homo sapi	640	21	91.3	101880	9	AC021089	AC021089	Homo sapi
568	21	91.3	95648	9	AC090214	Homo sapi	641	21	91.3	101937	9	AC010221	AC010221	Homo sapi
569	21	91.3	95681	9	AL157890	Human DNA	642	21	91.3	102105	9	AL136166	AL136166	Human DNA
570	21	91.3	95926	9	AC106752	Homo sapi	643	21	91.3	102351	2	AL138848	AL138848	Homo sapi
571	21	91.3	95983	9	AC004874	Homo sapi	644	21	91.3	102370	9	HSJ976013	AL117354	Human DNA
572	21	91.3	96000	2	AC079684	Homo sapi	645	21	91.3	102446	9	AL662849	AL662849	Human DNA
573	21	91.3	96002	2	AC109326	Homo sapi	646	21	91.3	102718	9	AC107628	AC107628	Homo sapi
574	21	91.3	96146	9	AC095052	Homo sapi	647	21	91.3	102892	9	AL359813	AL359813	Human DNA
575	21	91.3	96280	9	AC006968	Homo sapi	648	21	91.3	102910	9	AF254822	AF254822	Homo sapi
576	21	91.3	96308	9	AF190465	Homo sapi	649	21	91.3	103009	9	AC087225	AC087225	Homo sapi

c 650	21	91.3 103023	9	AP000747	AP000747 Homo sapi	c 723	21	91.3 110000	2	AL683889_4	Continuation (5 of
c 651	21	91.3 103108	2	AC008718	AC008718 Homo sapi	724	21	91.3 110000	2	AL732359_0	AL732359 Homo sapi
c 652	21	91.3 103327	9	AL662830	AL662830 Human DNA	725	21	91.3 110000	2	AP002753_0	AP002753 Homo sapi
c 653	21	91.3 103370	9	AL61656	AL61656 Human DNA	726	21	91.3 110000	2	AP002753_1	Continuation (2 of
c 654	21	91.3 103476	9	AC123912	AC123912 Homo sapi	727	21	91.3 110000	2	AC024562_3	Continuation (4 of
c 655	21	91.3 103667	9	AL357073	AL357073 Human DNA	728	21	91.3 110000	9	AC005079_1	Continuation (2 of
c 656	21	91.3 103699	9	AC034305	AC034305 Homo sapi	c 729	21	91.3 110000	9	AF440620_2	Continuation (3 of
c 657	21	91.3 103765	9	AC096743	AC096743 Homo sapi	730	21	91.3 110000	9	AF491780_09	Continuation (10 of
c 658	21	91.3 103829	9	AP000665	AP000665 Homo sapi	731	21	91.3 110025	9	AP003699_	AP003699 Homo sapi
c 659	21	91.3 104285	9	AC091729	AC091729 Homo sapi	732	21	91.3 110042	9	AL590788	AL590788 Human DNA
c 660	21	91.3 104289	2	HS104D14	AL035554 Homo sapi	c 733	21	91.3 110129	9	AC008956	AC008956 Homo sapi
c 661	21	91.3 104307	2	AL591845	AL591845 Human DNA	734	21	91.3 110130	9	AL360268	AL360268 Human DNA
c 662	21	91.3 104581	2	AF267908	AF267908 Homo sapi	735	21	91.3 110184	9	AC020906	AC020906 Homo sapi
c 663	21	91.3 104600	9	AP001166	AP001166 Homo sapi	c 736	21	91.3 110599	2	AC079343	AC079343 Homo sapi
c 664	21	91.3 104770	9	HSJ245M18	AL078584 Human DNA	737	21	91.3 110900	9	HSJ392M17	AL043843 Human DNA
c 665	21	91.3 104853	9	AC117444	AC117444 Homo sapi	c 738	21	91.3 111104	9	AC117389	AC117389 Homo sapi
c 666	21	91.3 104926	9	AC010168	AC010168 Homo sapi	c 739	21	91.3 111191	2	AC127525	AC127525 Homo sapi
c 667	21	91.3 104972	9	AC025176	AC025176 Homo sapi	c 740	21	91.3 111249	9	AP000343	AP000343 Homo sapi
c 668	21	91.3 105040	9	AC011229	AC011229 Homo sapi	c 741	21	91.3 111328	9	AP002755	AP002755 Homo sapi
c 669	21	91.3 105207	9	AC011594	AC011594 Homo sapi	c 742	21	91.3 111500	9	AC121344	AC121344 Homo sapi
c 670	21	91.3 105288	9	AC012330	AC012330 Homo sapi	c 743	21	91.3 111517	9	AC074366	AC074366 Homo sapi
c 671	21	91.3 105489	9	AC093894	AC093894 Homo sapi	c 744	21	91.3 111641	2	HS232N11	AL031656 Human DNA
c 672	21	91.3 105960	9	HS209A6	AL035401 Human DNA	c 745	21	91.3 111688	2	AC105020	AC105020 Homo sapi
c 673	21	91.3 106117	9	AC103564	AC103564 Homo sapi	c 746	21	91.3 111862	2	AL139143	AL139143 Homo sapi
c 674	21	91.3 106123	9	AL158015	AL158015 Human DNA	c 747	21	91.3 111996	9	AC093388	AC093388 Homo sapi
c 675	21	91.3 106208	2	AC130466	AC130466 Homo sapi	c 748	21	91.3 112031	9	AL445487	AL445487 Human DNA
c 676	21	91.3 106246	9	AC108721	AC108721 Homo sapi	c 749	21	91.3 112067	9	AC091485	AC091485 Homo sapi
c 677	21	91.3 106514	9	AC079463	AC079463 Homo sapi	c 750	21	91.3 112067	9	AC008894	AC008894 Homo sapi
c 678	21	91.3 106648	2	AC004588	AC004588 Homo sapi	c 751	21	91.3 112067	9	AC008894	AC008894 Homo sapi
c 679	21	91.3 106650	9	AC007708	AC007708 Homo sapi	c 752	21	91.3 112208	9	AC093313	AC093313 Homo sapi
c 680	21	91.3 106696	9	HUAC003661	AC003661 Homo sapi	c 753	21	91.3 112309	2	AC003025	AC003025 Human Chr
c 681	21	91.3 106735	2	AC011381	AC011381 Homo sapi	c 754	21	91.3 112389	2	AC073598	AC073598 Homo sapi
c 682	21	91.3 106859	9	AL512626	AL512626 Human DNA	c 755	21	91.3 112501	9	AC092953	AC092953 Homo sapi
c 683	21	91.3 106859	9	AL512626	AL512626 Human DNA	c 756	21	91.3 112646	9	AC010240	AC010240 Homo sapi
c 684	21	91.3 106868	2	AC003023	AC003023 Homo sapi	c 757	21	91.3 112659	9	AC010677	AC010677 Homo sapi
c 685	21	91.3 107104	9	HS1179L24	AL096708 Human DNA	c 758	21	91.3 112697	2	AP005367	AP005367 Homo sapi
c 686	21	91.3 107226	9	AC010618	AC010618 Homo sapi	c 759	21	91.3 112748	2	AC007242	AC007242 Homo sapi
c 687	21	91.3 107427	9	HS481A17	Z82212 Human DNA s	c 760	21	91.3 112902	2	AC034211	AC034211 Homo sapi
c 688	21	91.3 107462	2	AC068208	AC068208 Homo sapi	c 761	21	91.3 113020	2	HS394I7	AL021585 Homo sapi
c 689	21	91.3 107467	9	HS958B3	Z93023 Homo sapien	c 762	21	91.3 113036	9	AL158160	AL158160 Human DNA
c 690	21	91.3 107558	2	AC093252	AC093252 Homo sapi	c 763	21	91.3 113202	9	HSJ397H23	AL021972 Human DNA
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c 692	21	91.3 107627	9	AL513218	AL513218 Human DNA	c 765	21	91.3 113252	2	AC004408	AC004408 Homo sapi
c 693	21	91.3 107895	9	AC078929	AC078929 Homo sapi	c 766	21	91.3 113253	2	AC092356	AC092356 Homo sapi
c 694	21	91.3 107921	9	AC112654	AC112654 Homo sapi	c 767	21	91.3 113420	9	AL360006	AL360006 Human DNA
c 695	21	91.3 108205	9	AL138758	AL138758 Human DNA	c 768	21	91.3 113530	9	AC073216	AC073216 Homo sapi
c 696	21	91.3 108336	9	AF216670	AF216670 Homo sapi	c 769	21	91.3 113613	9	AC097524	AC097524 Homo sapi
c 697	21	91.3 108408	2	AC022210	AC022210 Homo sapi	c 770	21	91.3 113687	9	AC069281	AC069281 Homo sapi
c 698	21	91.3 108511	9	AC011418	AC011418 Homo sapi	c 771	21	91.3 113687	9	AC069281	AC069281 Homo sapi
c 699	21	91.3 108813	9	AL138718	AL138718 Human DNA	c 772	21	91.3 113743	9	AC072023	AC072023 Homo sapi
c 700	21	91.3 108841	9	AL359185	AL359185 Human DNA	c 773	21	91.3 113810	9	AC068292	AC068292 Homo sapi
c 701	21	91.3 108865	9	HSJ345E4	AL132661 Human DNA	c 774	21	91.3 113916	9	HUAC003007	AC003007 Human Chr
c 702	21	91.3 108934	9	AL358453	AL358453 Human DNA	c 775	21	91.3 113929	9	AF196969	AF196969 Homo sapi
c 703	21	91.3 109098	2	AF295013	AF295013 Homo sapi	c 776	21	91.3 113980	2	AP001540	AP001540 Homo sapi
c 704	21	91.3 109134	9	AC024571	AC024571 Homo sapi	c 777	21	91.3 113991	9	AC096742	AC096742 Homo sapi
c 705	21	91.3 109149	2	AP000681	AP000681 Homo sapi	c 778	21	91.3 114026	9	AL365201	AL365201 Human DNA
c 706	21	91.3 109296	9	AC083949	AC083949 Homo sapi	c 779	21	91.3 114191	9	AL451007	AL451007 Human DNA
c 707	21	91.3 109445	9	AC008946	AC008946 Homo sapi	c 780	21	91.3 114202	2	AC103829	AC103829 Homo sapi
c 708	21	91.3 109523	2	AL844527	AL844527 Homo sapi	c 781	21	91.3 114349	9	AP000920	AP000920 Homo sapi
c 709	21	91.3 109646	9	HSJHCTB822	AP019413 Homo sapi	c 782	21	91.3 114438	2	AC010356	AC010356 Homo sapi
c 710	21	91.3 109666	9	AP000838	AP000838 Homo sapi	c 783	21	91.3 114517	9	AL158152	AL158152 Human DNA
c 711	21	91.3 109933	2	AC093285	AC093285 Homo sapi	c 784	21	91.3 114657	9	AC097711	AC097711 Homo sapi
c 712	21	91.3 109933	2	AC093285	AC093285 Homo sapi	c 785	21	91.3 114713	9	HSJ3763G1	AL109843 Human DNA
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c 714	21	91.3 110000	2	AC091528_2	Continuation (3 of	c 787	21	91.3 114846	9	HS257I20	AL021878 Human DNA
c 715	21	91.3 110000	2	AC011600_0	AC011600 Homo sapi	c 788	21	91.3 114972	9	AC016617	AC016617 Homo sapi
c 716	21	91.3 110000	2	AC106723_0	AC106723 Homo sapi	c 789	21	91.3 115174	9	AC106028	AC106028 Homo sapi
c 717	21	91.3 110000	2	AC125232_1	Continuation (2 of	c 790	21	91.3 115199	9	AC003695	AC003695 Homo sapi
c 718	21	91.3 110000	2	AC125232_2	Continuation (3 of	c 791	21	91.3 115408	2	AC068848	AC068848 Homo sapi
c 719	21	91.3 110000	2	AL139235_0	AL139235 Homo sapi	c 792	21	91.3 115515	9	HSJ1056H1	AL118505 Human DNA
c 720	21	91.3 110000	2	AL359456_0	AL359456 Homo sapi	c 793	21	91.3 115583	9	HSJ351K20	AL109939 Human DNA
c 721	21	91.3 110000	2	AL359456_3	Continuation (4 of	c 794	21	91.3 115664	2	AC103024	AC103024 Homo sapi
c 722	21	91.3 110000	2	AL390202_06	Continuation (7 of	c 795	21	91.3 115762	2	AP000663	AP000663 Homo sapi

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797	21	91.3	115806	9	AL591363	AL591363 Human DNA
798	21	91.3	115863	9	HSJ537P22	HSJ537P22 Human DNA
799	21	91.3	115935	9	HS963K23	HS963K23 Human DNA
800	21	91.3	116131	9	AL139324	AL139324 Human DNA
801	21	91.3	116247	9	AC107988	AC107988 Homo sapi
802	21	91.3	116451	9	AL355860	AL355860 Human DNA
803	21	91.3	116524	9	AL138686	AL138686 Human DNA
804	21	91.3	116664	9	HS1191N16	HS1191N16 Human DNA
805	21	91.3	116859	9	AC073410	AC073410 Homo sapi
806	21	91.3	116879	9	AC106854	AC106854 Homo sapi
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811	21	91.3	117297	9	AL672040	AL672040 Human DNA
812	21	91.3	117381	9	AC006392	AC006392 Homo sapi
813	21	91.3	117431	9	HS850H21	AL031680 Human DNA
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816	21	91.3	117602	2	AC087055	AC087055 Homo sapi
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823	21	91.3	118429	9	AL136319	AL136319 Human DNA
824	21	91.3	118430	2	AC103593	AC103593 Homo sapi
825	21	91.3	118572	9	AL133408	AL133408 Human DNA
826	21	91.3	118603	2	AL360017	AL360017 Homo sapi
827	21	91.3	118603	9	AC091819	AC091819 Homo sapi
828	21	91.3	118642	9	AC126283	AC126283 Homo sapi
829	21	91.3	118985	9	AC094102	AC094102 Homo sapi
830	21	91.3	119118	9	HSRY7CC1	AL049760 Human DNA
831	21	91.3	119222	9	AC067742	AC067742 Homo sapi
832	21	91.3	119241	9	HSJ776F14	AL109658 Human DNA
833	21	91.3	119452	9	AC096552	AC096552 Homo sapi
834	21	91.3	119491	9	AC098860	AC098860 Homo sapi
835	21	91.3	119569	9	AC020929	AC020929 Homo sapi
836	21	91.3	119634	2	AF165423	AF165423 Homo sapi
837	21	91.3	119721	9	AC093655	AC093655 Homo sapi
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839	21	91.3	119882	9	AC108024	AC108024 Homo sapi
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843	21	91.3	120192	2	AC093220	AC093220 Homo sapi
844	21	91.3	120480	9	AP000806	AP000806 Homo sapi
845	21	91.3	120481	9	AC099738	AC099738 Homo sapi
846	21	91.3	120528	9	AP000812	AP000812 Homo sapi
847	21	91.3	120533	9	AL353717	AL353717 Human DNA
848	21	91.3	120535	9	HSDJ324B8	AL132793 Human DNA
849	21	91.3	120538	9	AC004815	AC004815 Homo sapi
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856	21	91.3	120873	9	AL445986	AL445986 Human DNA
857	21	91.3	121050	9	AC074135	AC074135 Homo sapi
858	21	91.3	121063	9	AC008843	AC008843 Homo sapi
859	21	91.3	121166	9	AC004613	AC004613 Homo sapi
860	21	91.3	121272	2	AC004956	AC004956 Homo sapi
861	21	91.3	121424	9	HS418A9	Z84480 Homo sapien
862	21	91.3	121606	9	AL160401	AL160401 Human DNA
863	21	91.3	121660	9	AC105235	AC105235 Homo sapi
864	21	91.3	121684	2	AL354655	AL354655 Homo sapi
865	21	91.3	121705	9	AC006452	AC006452 Homo sapi
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867	21	91.3	121724	9	AL136139	AL136139 Human DNA
868	21	91.3	121911	2	AC016318	AC016318 Homo sapi
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AL139253	Homo sapi
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AL606518	Homo sapi
AC005252	Homo sapi
AC008640	Homo sapi
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AX476820	Sequence
HSJ1077B9	Human DNA
AC087253	Pan trogl
AL603882	Human DNA
AP000708	Homo sapi
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ALIGNMENTS
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AF123653 Homo sapiens
AF123653.1 GI:4572463
Homo sapiens
Homo sapiens
SOURCE
ORGANISM

RESULT 1
LOCUS AF123653
DEFINITION Homo sapiens FEZ1 (FEZ1) gene, complete cds.
ACCESSION AF123653
VERSION AF123653.1
KEYWORDS
SOURCE
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9108)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
99199287
MEDLINE 10097140
PUBMED
REFERENCE 2 (bases 1 to 9108)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2338 10th street, Philadelphia, PA 19107, USA
LOCATION/Qualifiers
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ENELQKQKNEALLREKVNLLLEQLQALAAALADMGPTTFPDPVALQRELERLR
AEURERQGHQDMSGSGFHERLVWKEKEKVIQYQKQSQSYVAMYQRNQRLEKALQO
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BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
ORIGIN
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Db 4511 CAGCAGGCATGTGGCAGGTGT 4533
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LOCUS AC025853
DEFINITION Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING
IN PROGRESS ***, 3 unordered pieces.
AC025853
AC025853.13 GI:21431202
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173264)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-353K12
Unpublished
REFERENCE 2 (bases 1 to 173264)
```

## AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPeeters,R., Melidrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

## Direct Submission

Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 173264)

## REFERENCE

## AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Melidrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Riese,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

## JOURNAL

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jun 17, 2002 this sequence version replaced gi:21321864.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: <http://www-seq.wi.mit.edu>

Center code: WTR

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L7454

Center clone name: 353\_K\_12

-----  
\* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 39461: contig of 39461 bp in length  
\* 39462 39561: gap of 100 bp

## FEATURES

## source

\* 39562 108347: contig of 68786 bp in length  
\* 108348 108447: gap of 100 bp  
\* 108448 173264: contig of 64817 bp in length.

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/clone\_lib="RP11-11 Human Male BAC"  
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Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGGTGGCAGGTGT 23

Db 26751 CAGCCAGGCATGGTGGCAGGTGT 26773

## RESULT 3

## HS388M5/c

## LOCUS

## DEFINITION

HS388M5 177568 bp DNA linear PRI 12-DEC-1999  
Human DNA sequence from clone RP3-388M5 on chromosome 22 Contains an RPL4 (60S Ribosomal Protein L4) pseudogene, the HMGI7L1 gene for high-mobility group (nonhistone chromosomal) protein 17-like 1, the gene for a novel Sulfotransferase (sulfokinase, EC 2.8.2.1) like protein, the gene for a GS2 like protein, ESTs, STSS, GSSs and four putative CpG islands, complete sequence.

## ACCESSION

## VERSION

297055.1 GI:2916859

## KEYWORDS

HTG; 60S Ribosomal Protein L4; CpG island; GS2; HMGI7L1; RPL4;

## SOURCE

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
On Feb 28, 1998 this sequence version replaced gi:2213438.

## COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/Celegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>  
RP3-388M5 is from the library RPEC-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR: pCYPAC2>  
This sequence is the entire insert of clone RP3-388M5 The start of



this sequence overlaps with sequence AL023654 The end of this  
sequence overlaps with sequence AL023801.

## FEATURES

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33615. .33739
/note="L1B4 repeat: matches 5320. .5450 of consensus"
33740. .33864
/note="L1B5 repeat: matches 5313. .5587 of consensus"
repeat_region 33894. .34201

Query Match 100.0%; Score 23; DB 9; Length 177568;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGGCATGGTGGCAGGTGT 23
|||||
Db 155046 CAGCAGGCATGGTGGCAGGTGT 155024

RESULT 4
AB046623 1821 bp mRNA linear PRI 01-AUG-2000
LOCUS Macaca fascicularis brain cDNA, clone QcCE-10576.
DEFINITION
AB046623
ACCESSION
AB046623.1 GI:9651056
VERSION
AB046623.1
KEYWORDS
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone lib:macaque brain cDNA library QcCE clone:QcCE-10576.
SOURCE
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (sites)
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
libraries
Unpublished
2 (bases 1 to 1821)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (28-JUL-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: pME18S-FL3 (Acc.No. AB009864)
R. Site2: DralII (CAGCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DralII sites of pME18S-FL3. XhoI sites just outside
the DralII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing ( 5' end
primer [CTTCTGCTCTAAAGCTCGG]; 3' end primer [CGACCTGCAGCTCGACACA]
).
FEATURES
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1. .1821
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QcCE-10576"
/sex="male"
/tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QcCE"
/dev_stage="adult"
/codon_start=1
133. .417
/product="hypothetical protein"
/protein_id="BAB031541.1"
/db_xref="GI:9651057"
/translation="MWTSLLPQPGIRLGHANAVLGNRSRGSEAGSIDLAKGRYVRS
GFLFGRQISLGRKQRTFLMWSKCKSLVRVTEAVSSLSLEAFKKRLGRAR"

repeat_region /note="L1B5 repeat: matches 5265. .5313 of consensus"
33615. .33739
/note="L1B4 repeat: matches 5320. .5450 of consensus"
33740. .33864
/note="L1B5 repeat: matches 5313. .5587 of consensus"
repeat_region 33894. .34201

Query Match 100.0%; Score 23; DB 9; Length 177568;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGGCATGGTGGCAGGTGT 23
|||||
Db 155046 CAGCAGGCATGGTGGCAGGTGT 155024

RESULT 4
AB046623 1821 bp mRNA linear PRI 01-AUG-2000
LOCUS Macaca fascicularis brain cDNA, clone QcCE-10576.
DEFINITION
AB046623
ACCESSION
AB046623.1 GI:9651056
VERSION
AB046623.1
KEYWORDS
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone lib:macaque brain cDNA library QcCE clone:QcCE-10576.
SOURCE
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (sites)
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
libraries
Unpublished
2 (bases 1 to 1821)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (28-JUL-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: pME18S-FL3 (Acc.No. AB009864)
R. Site2: DralII (CAGCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DralII sites of pME18S-FL3. XhoI sites just outside
the DralII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing ( 5' end
primer [CTTCTGCTCTAAAGCTCGG]; 3' end primer [CGACCTGCAGCTCGACACA]
).
FEATURES
source
1. .1821
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QcCE-10576"
/sex="male"
/tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QcCE"
/dev_stage="adult"
/codon_start=1
133. .417
/product="hypothetical protein"
/protein_id="BAB031541.1"
/db_xref="GI:9651057"
/translation="MWTSLLPQPGIRLGHANAVLGNRSRGSEAGSIDLAKGRYVRS
GFLFGRQISLGRKQRTFLMWSKCKSLVRVTEAVSSLSLEAFKKRLGRAR"

repeat_region /note="L1B5 repeat: matches 5265. .5313 of consensus"
33615. .33739
/note="L1B4 repeat: matches 5320. .5450 of consensus"
33740. .33864
/note="L1B5 repeat: matches 5313. .5587 of consensus"
repeat_region 33894. .34201

Query Match 100.0%; Score 22; DB 9; Length 1821;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 538 AGCCAGGCATGGTGGCAGGTGT 559

RESULT 5
AB052149 2787 bp mRNA linear PRI 11-OCT-2001
LOCUS Macaca fascicularis brain cDNA, clone:QcCE-20783.
DEFINITION
AB052149
ACCESSION
AB052149.1 GI:11611578
VERSION
AB052149.1
KEYWORDS
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone lib:macaque brain cDNA library QcCE clone:QcCE-20783.
SOURCE
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1
Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M.,
Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
chromosomes
Gene 275 (1), 31-37 (2001)
2 (bases 1 to 2787)
Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (05-DEC-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)
Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DralII (CAGCATGTG)
R. Site2: DralII (CAGCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DralII sites of pME18S-FL3. XhoI sites just outside
the DralII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAGCTCGG];
3' end primer [CGACCTGCAGCTCGACACA] ).
FEATURES
source
1. .2787
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QcCE-20783"
/sex="male"
/tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QcCE"
/dev_stage="adult"
380. .1495
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/product="hypothetical protein"
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/db_xref="GI:11611579"
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SSPNTLNENGARHKTLVADINISLDSEGLSDDFLDPDLDINVDLETDP
ETUSLEFLNGNELEWGDPTPVATKNMGPSADLFGDGTGTEGGAANGRLWRTVIIG
EQEHRIDLHMRPYMKVYTHGGYGGELNAILVFAACFLPDSSLPDYHYIMENFLVY

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ISSLELLVAEDYMYVLNGATPPRRMPGIGWLKKCYOMIDRRRLKNLKLIIIVHPSWF
IRTVLATSREPISKFTNKQYVHSLDLEQLIPMEHVQIPDCVQVYEEERLKRRES
ARPOPEFMRSEKPKFVAPVENSAPVTQETSMS"

BASE COUNT      657 a      832 c      772 g      526 t
ORIGIN

Query Match      95.7%; Score 22; DB 9; Length 2787;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2  AGCCAGGCATGGTGGCAGGTGT 23
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Db   2675 AGCCAGGCATGGTGGCAGGTGT 2696

RESULT 6
AL451072/c
LOCUS
DEFINITION Human DNA sequence from clone RPI-236H13 on chromosome 6, complete
sequence.
ACCESSION AL451072
VERSION AL451072.14 GI:12666306
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Donnelly,S.
Direct Submission
Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 5, 2001 this sequence version replaced gi:12657210.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em', EMBL; Sw', SWISSPROT; Tr', TREMBL; Wp', WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RPI-236H13 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pcIPAC2
IMPORTANT: This sequence is not the entire insert of clone
RPI-236H13 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RPI-297M16 is at 4814 in this sequence.
The true right end of clone RPI1-613F7 is at 100 in this sequence.
Location/Qualifiers
FEATURES
source
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/db_xref="taxon:9606"
/chromosome="6"
/clone="RPI-236H13"
/clone_lib="RPCI-1"

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/note="L1M4 repeat: matches 25. .164 of consensus"
repeat_region 143. .494

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878. .1208
/note="L1MB2 repeat: matches 5800. .6142 of consensus"
1209. .1522
/note="AluSp repeat: matches 1. .309 of consensus"
1523. .1999
/note="L1MB2 repeat: matches 5374. .5800 of consensus"
2000. .2299
/note="AluX repeat: matches 1. .300 of consensus"
2300. .2538
/note="L1MB2 repeat: matches 5127. .5374 of consensus"
2555. .2659
/note="U6 repeat: matches 1. .107 of consensus"
2751. .2934
/note="MER5A repeat: matches 1. .189 of consensus"
3050. .3149
/note="L2 repeat: matches 2466. .2560 of consensus"
3150. .3454
/note="AluX repeat: matches 1. .303 of consensus"
3455. .3624
/note="L2 repeat: matches 2560. .2749 of consensus"
3646. .3701
/note="28 copies 2 mer aa 69% conserved"
4127. .4418
/note="AluJo repeat: matches 3. .290 of consensus"
4445. .4472
/note="14 copies 2 mer tg 100% conserved"
4473. .4757
/note="AluX repeat: matches 1. .286 of consensus"
BASE COUNT 1383 a 997 c 949 g 1584 t
ORIGIN

Query Match      95.7%; Score 22; DB 9; Length 4913;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CAGCCAGGCATGGTGGCAGGTG 22
      |||||
Db   3320 CAGCCAGGCATGGTGGCAGGTG 3299

RESULT 7
AP000535
LOCUS
DEFINITION Homo sapiens genomic DNA, chromosome 22q11.2, Cat Eye Syndrome
region, clone:c58F10.
ACCESSION AP000535 BA000006
VERSION AP000535.1 GI:5931513
KEYWORDS
SOURCE
ORGANISM Homo sapiens
DNA, clone_lib:Keio Cat Eye Syndrome Cosmid library clone:c58F10.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Shimizu,N.
1 (bases 1 to 39151)
Homo sapiens chromosome 22 clone cosmid c58F10 on 22q11.2
Published Only in Database (1999)
Shimizu,N.
Direct Submission
Submitted (22-SEP-1999) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-Ku, Tokyo
160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
This is a complete sequence of the insert of c58F10 clone. The
proximal adjacent clone is c23H5 (Acc.#AP000534) with 4726-bp
overlapping. The distal adjacent clone is c64C8 (Acc.#AP000536)
with 5211-bp overlapping.
Location/Qualifiers
FEATURES
source
1. .39151
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/map="22q11.2"
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/rpt_family="AluSc"
complement(3282..3702)
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complement(6665..6835)
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complement(6944..7147)
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complement(17097..17424)
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17950..18046
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18072..18093
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18433..19005
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19030..19050
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19141..19334
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complement(19343..19783)
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complement(21304..21520)
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28545..28881
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complement(28984..34339)
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34856..35227
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35235..35511
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35512..35561
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35636..35720
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36404..36465
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repeat_region      complement(36575..36754)
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38263..38299
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38300..38311
/evidence=not_experimental
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ORIGIN
Query Match      95.7%; Score 22; DB 9; Length 39151;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 AGCCAGGCGATGTCGCGAGGTGT 23
Db      34654 AGCCAGGCGATGTCGCGAGGTGT 34675

RESULT 8
AP000536
LOCUS      AP000536 Homo sapiens genomic DNA, chromosome 22q11.2, Cat Eye Syndrome
DEFINITION      Homo sapiens EB transformed lymphoblast cell line:CH91-157
DNA, clone lib:Keio Cat Eye Syndrome Cosmid library clone:c64C8.
ACCESSION      AP000536 BA000006
VERSION      AP000536.1 GI:5931514
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 39668)
AUTHORS      Shimizu,N.
TITLE      Homo sapiens chromosome 22 clone cosmid c64C8 on 22q11.2
JOURNAL      Published Only in Database (1999)
REFERENCE      2 (bases 1 to 39668)
AUTHORS      Shimizu,N.
TITLE      Direct Submission
JOURNAL      Submitted (22-SEP-1999) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail:nshimizu@mb.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
COMMENT      This is a complete sequence of the insert of c64C8 clone. The
proximal adjacent clone is c58f10 (Acc.#AP000535) with 5211-bp
overlapping. The distal adjacent clone is c54B2 (Acc.#AP000537)
with 6784-bp overlapping.
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/db_xref="taxon:9606"
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complement(1..399)
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916..1287
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1295..1571
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1572..1621
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1696..1780
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complement(1807..1837)
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complement(1860..1962)
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2464..2525
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2526..2547
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complement(2635..2814)
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3535..3558
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4046..4322
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4323..4359
/evidence=not_experimental
/rpt_family="(CA)n"
4360..4371
/evidence=not_experimental
/rpt_family="AluSx"
5134..5428
/evidence=not_experimental
/rpt_family="AluY"
complement(5913..6218)
/evidence=not_experimental
/rpt_family="L2"
complement(6381..6686)
/evidence=not_experimental
/rpt_family="AluYb8"
complement(7022..7325)
/evidence=not_experimental
/rpt_family="AluSg"
7640..7666
/evidence=not_experimental
/rpt_family="AT_Rich"
8259..8355
/evidence=not_experimental
/rpt_family="L2"
complement(8374..8531)
/evidence=not_experimental
/rpt_family="AluJo/FRAM"
complement(8532..8834)
/evidence=not_experimental
/rpt_family="AluSg1"
8913..9010
/evidence=not_experimental

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repeat_region /rpt_family="MER58A"
9048. .9322 /evidence=not_experimental
repeat_region /rpt_family="L2"
9603. .9709 /evidence=not_experimental
repeat_region /rpt_family="LTR5"
9905. .9930 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
9931. .10445 /evidence=not_experimental
repeat_region /rpt_family="MER3"
10446. .10480 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
10494. .10780 /evidence=not_experimental
repeat_region /rpt_family="AluSp"
complement(10798. .10989)
/evidence=not_experimental
/rpt_family="L1MD2"
10990. .11018 /evidence=not_experimental
repeat_region /rpt_family="TA)n"
complement(11019. .11088)
/evidence=not_experimental
/rpt_family="L1MD2"
complement(11125. .11558)
/evidence=not_experimental
/rpt_family="L1MD2"
11712. .11965 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
11971. .12385 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
12386. .12600 /evidence=not_experimental
repeat_region /rpt_family="MER20"
12601. .12788 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
12789. .13094 /evidence=not_experimental
repeat_region /rpt_family="AluSg"
13095. .13172 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
13181. .13671 /evidence=not_experimental
repeat_region /rpt_family="MER1A"
13748. .14321 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
14355. .14724 /evidence=not_experimental
repeat_region /rpt_family="L1MEC"
14903. .14938 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
16330. .16368 /evidence=not_experimental
repeat_region /rpt_family="CA)n"
16450. .16728 /evidence=not_experimental
repeat_region /rpt_family="AluY"
16742. .16859 /evidence=not_experimental
repeat_region /rpt_family="MIR"
17135. .17157 /evidence=not_experimental
/rpt_family="AT_rich"
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repeat_region 17392. .17703
/evidence=not_experimental
/rpt_family="AluSx"
18223. .19013 /evidence=not_experimental
repeat_region /rpt_family="L1PA2"
19467. .19487 /evidence=not_experimental
repeat_region /rpt_family="AT_rich"
19596. .19657 /evidence=not_experimental
repeat_region /rpt_family="(CATATTA)n"
complement(20389. .20420)
/evidence=not_experimental
/rpt_family="L2"
20458. .20754 /evidence=not_experimental
repeat_region
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Query Match 95.7%; Score 22; DB 9; Length 39668;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCAGGCATGTCGCGAGTGT 23

Db 714 AGCAGGCATGTCGCGAGTGT 735

## RESULT 9

AC010647 AC010647 40102 bp DNA linear PRI 12-DEC-2001  
LOCUS Homo sapiens chromosome 19 clone LLNLR-279F8, complete sequence.

DEFINITION AC010647

VERSION AC010647.5 GI:17530703

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40102)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 40102)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 40102)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

COMMENT On Dec 12, 2001 this sequence version replaced gi:8576044.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

Quality: Phrap Quality >=40 99.5% of Sequence;

Estimated Total Number of Errors is 0.2.

NOTE: This insert is not the entire sequence of the clone (entire  
sequence is 45kb). It is clipped at the overlap with AC020895. The  
number of bases overlapped is 5950.

FEATURES Location/Qualifiers

source

1. .40102

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="19"

/clone="LLNLR-279F8"

BASE COUNT 9903 a 9289 c 9373 g 11537 t

ORIGIN

Query Match 95.7%; Score 22; DB 9; Length 40102;  
Best Local Similarity 100.0%; Pred. No. 0.0046;



		/notes="BLASTN similarity to Z65958 (nt; .269); match: 0.98; score: 1.0e-90; database searched: nt; H.sapiens CpG DNA, clone 69d1, reverse read cpq69d1.rctia."
misc_feature		/notes="BLASTN similarity to Z65957 (13..213); match: 0.97; score: 8.4e-71; database searched: nt; H.sapiens CpG DNA, clone 69d1, forward read cpq69d1.ctia." 9351..9498
misc_feature		/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: good, score: 66.000"
repeat_region		10096..10160 /rpt_family="(GA)n"
repeat_region		10360..10445 /rpt_family="(CA)n"
repeat_region		10443..10574 /rpt_family="(CA)n"
repeat_region		10796..11097 /rpt_family="AluSq"
repeat_region		10796..11095 /rpt_family="Alu"
repeat_region		10796..11095 /rpt_family="Alu"
repeat_region		complement(11189..11464) /rpt_family="AluJo"
repeat_region		complement(11213..11464) /rpt_family="Alu"
repeat_region		complement(11213..11464) /rpt_family="Alu"
repeat_region		11803..11903 /rpt_family="FLAM_C"
repeat_region		11803..11899 /rpt_family="Alu"
repeat_region		11803..11899 /rpt_family="Alu"
repeat_region		11949..11995 /rpt_family="(CA)n"
misc_feature		12173..12491 /notes="DDS similarity to AA587610 nm95all.s1 NCI CGAP Co9 Homo sapiens cDNA clone IMAGE:1075964; (462..144); 100% identity."
repeat_region		12467..12547 /rpt_family="(GA)n"
misc_feature		12542..12694 /notes="DPS similarity to AA587610 nm95all.s1 NCI CGAP Co9 Homo sapiens cDNA clone IMAGE:1075964; (143..1); 99% identity."
repeat_region		12650..12691 /rpt_family="POLY_A"
misc_feature		complement(14148..14217) /notes="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: good, score: 62.000"
repeat_region		14398..14698 /rpt_family="AluY"
repeat_region		14403..14697 /rpt_family="Alu"
repeat_region		14403..14697 /rpt_family="Alu"
misc_feature		15157..15522 /notes="BLASTN similarity to: AA922094 (4..369); match: 0.99, score: 6.6e-144; database searched: month.na; on41809.s1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:1543624 3~(15178..15466) AA927168 (1..289); match: 0.98, score: 3.3e-110; database
		95.7%; Score 22; DB 9; Length 41159;
Query Match		Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches	22; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2	ACCCAGGCATGGTGGCAGGTGT 23       
Db	20977	AGCCAGGCATGGTGGCAGGTGT 20998       

```

RESULT 11
HSN128A12          41576 bp      DNA       linear    PRI 12-DEC-1999
LOCUS              Human DNA sequence from clone LL22NC03-128A12 on chromosome 22
DEFINITION         Contains STSs, GSSs and a CpG Island, complete sequence.
VERSION            275407
KEYWORDS           HTG; CpG Island.
SOURCE             Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 41576)
AUTHORS            Hunt,A.
TITLE              Direct Submission
JOURNAL            Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
                  CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT            requests: clonesrequest@sanger.ac.uk
                  On Dec 13, 1999 this sequence version replaced gi:1418824.
                  During sequence assembly data is compared from overlapping clones
                  where differences are found these are annotated as variations
                  together with a note of the overlapping clone name. Note that the
                  variation annotation may not be found in the sequence submission
                  corresponding to the overlapping clone, as we submit sequences with
                  only a small overlap as described above.
                  This sequence has been finished according to sequence map criteria
                  as follows. An attempt is made to resolve all sequencing problems,
                  such as compressions and repeats, but not necessarily within known
                  annotated human repeat sequence elements (e.g. Alu). Where the
                  sequence is ambiguous, there is an annotation using the 'unsure'
                  feature key.
                  The following abbreviations are used to associate primary accession
                  numbers given in the feature table with their source databases:
                  En.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information
                  on the WORMPEP database can be found at
                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                  was generated from part of bacterial clone contigs of human
                  chromosome 22, constructed by the Sanger Centre Chromosome 22
                  Mapping Group. Further information can be found at
                  http://www.sanger.ac.uk/HGP/Chr22
                  LL22NC03-128A12 is from the human chromosome 22-specific cosmid
                  library LL22NC03, constructed at the Biomedical Sciences Division,
                  Lawrence Livermore National Laboratory, Livermore, CA 94550 under
                  the auspices of the National Laboratory Gene Library Project
                  sponsored by the US Department of Energy. The source of the flow
                  sorted chromosomes was a human/hamster hybrid containing
                  chromosomes Y, 22 and 9. VECTOR: lawrist16
                  This sequence is the entire insert of clone LL22NC03-128A12.
FEATURES
source             Location/Qualifiers
                   1..41576
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /chromosome="22"
                    /clone="LL22NC03-128A12"
                    /clone_lib="LL22NC03"
repeat_region     972..1031
                 /note="4 copies 15 mer 98 conserved"
misc_feature      2836..4733
                 /note="CpG island"
                 /evidence=not_experimental
repeat_region     4555..4656
                 /notes="17 copies 6 mer ggcggg 66 conserved"
repeat_region     4559..4656
                 /note="49 copies 2 mer gg 61 conserved"
repeat_region     4923..5228
                 /notes="AluX repeat: matches 1..306 of consensus"
repeat_region     5685..5866
                 /notes="THE1B repeat: matches 1..154 of consensus"
repeat_region     5867..6172
                 /note="AluY repeat: matches 1..306 of consensus"
repeat_region     6173..6373
                 /notes="THE1B repeat: matches 154..364 of consensus"
repeat_region     6484..6713

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repeat\_region /note="MER72 repeat: matches 1. .218 of consensus"  
6737. .7214  
repeat\_region /note="MER72 repeat: matches 136. .668 of consensus"  
7361. .7885  
repeat\_region /note="LTR45 repeat: matches 1. .525 of consensus"  
8926. .8973  
repeat\_region /note="8 copies 6 mer tgata 81 conserved"  
9371. .9757  
repeat\_region /note="L1MD repeat: matches -17. .368 of consensus"  
9758. .11291  
repeat\_region /note="L1MB6 repeat: matches 4553. .6175 of consensus"  
11281. .11751  
repeat\_region /note="L1MD1 repeat: matches 1922. .4386 of consensus"  
11752. .12057  
repeat\_region /note="AluSg repeat: matches 1. .308 of consensus"  
12058. .12203  
repeat\_region /note="L1MD1 repeat: matches 4386. .4529 of consensus"  
12204. .12631  
repeat\_region /note="WSTB repeat: matches 1. .426 of consensus"  
12632. .12665  
repeat\_region /note="L1MD1 repeat: matches 4529. .4561 of consensus"  
12666. .12961  
repeat\_region /note="AluSg repeat: matches 1. .296 of consensus"  
12962. .14295  
repeat\_region /note="L1MD1 repeat: matches 4561. .5893 of consensus"  
14296. .14578  
repeat\_region /note="AluSg repeat: matches 1. .283 of consensus"  
14687. .14973  
repeat\_region /note="L1MD1 repeat: matches 5920. .6216 of consensus"  
14986. .15313  
repeat\_region /note="AluJo repeat: matches 1. .312 of consensus"  
15601. .15637  
repeat\_region /note="L1MD1 repeat: matches 511. .547 of consensus"  
15665. .15848  
repeat\_region /note="L2 repeat: matches 1824. .1986 of consensus"  
15849. .16071  
repeat\_region /note="L1P1 repeat: matches 5926. .6155 of consensus"  
16072. .16405  
repeat\_region /note="L2 repeat: matches 1411. .1824 of consensus"  
16522. .16827  
repeat\_region /note="AluSg repeat: matches 1. .306 of consensus"  
17599. .17757  
repeat\_region /note="SVA repeat: matches 1. .152 of consensus"  
17986. .18184  
repeat\_region /note="AluSg/x repeat: matches 123. .298 of consensus"  
18434. .18795  
repeat\_region /note="L1M4 repeat: matches 2291. .2620 of consensus"  
18796. .19023  
repeat\_region /note="AluSg/x repeat: matches 67. .293 of consensus"  
19024. .19663  
repeat\_region /note="L1M4 repeat: matches 1831. .2291 of consensus"  
19667. .19977  
repeat\_region /note="AluSg repeat: matches 1. .312 of consensus"  
19978. .20108  
repeat\_region /note="AluJo/FLAM repeat: matches 2. .133 of consensus"  
20109. .20421  
repeat\_region /note="L1M4 repeat: matches 1547. .1831 of consensus"  
20672. .21063  
repeat\_region /note="L1 repeat: matches 4963. .5391 of consensus"  
21121. .21439  
repeat\_region /note="AluSg repeat: matches 1. .311 of consensus"  
21666. .22198  
repeat\_region /note="HAL1 repeat: matches 1024. .1566 of consensus"  
complement(21836. .22251)  
misc\_feature /note="match: GSS: Em:AQ029230; match: STS: Em:G52064"  
complement(22209. .22781)  
misc\_feature /note="match: GSS: Em:AQ233552"  
complement(22300. .22783)  
misc\_feature /note="match: STS: Em:B14416; match: GSS: Em:B14416"  
complement(22321. .22783)  
misc\_feature /note="match: GSS: Em:B13995; match: STS: Em:B13995"  
22401. .22516  
repeat\_region /note="HAL1 repeat: matches 662. .776 of consensus"

misc\_feature complement(22566. .22776)  
/note="match: GSS: Em:AQ108444"  
22714. .22925  
repeat\_region /note="MER92B repeat: matches 216. .418 of consensus"  
22926. .23229  
repeat\_region /note="AluSg repeat: matches 1. .305 of consensus"  
23230. .23437  
repeat\_region /note="MER92B repeat: matches 418. .628 of consensus"  
24404. .24700  
repeat\_region /note="AluSg repeat: matches 12. .300 of consensus"  
24735. .24826  
repeat\_region /note="MLT1A1 repeat: matches 316. .547 of consensus"  
25273. .25582  
repeat\_region /note="AluSg repeat: matches 1. .306 of consensus"  
25609. .26309  
repeat\_region /note="MER21B repeat: matches 14. .794 of consensus"  
26305. .26395  
repeat\_region /note="MER21B repeat: matches 704. .787 of consensus"  
27337. .27637  
repeat\_region /note="AluSg repeat: matches 1. .310 of consensus"  
28507. .28812  
repeat\_region /note="AluJo repeat: matches 1. .293 of consensus"  
28890. .28954  
repeat\_region /note="MIR repeat: matches 83. .148 of consensus"  
29596. .29838  
repeat\_region /note="L2 repeat: matches 1814. .2071 of consensus"  
complement(29957. .30503)  
misc\_feature /note="match: STS: Em:AL021681; match: STS: Em:HS990A23T"  
29977. .30271  
repeat\_region /note="AluSg repeat: matches 1. .296 of consensus"  
31074. .31376  
repeat\_region /note="AluSg repeat: matches 1. .310 of consensus"  
31589. .31847  
repeat\_region /note="MIR repeat: matches 4. .261 of consensus"  
32326. .33013  
repeat\_region /note="match: GSS: Em:AQ057087"  
33138. .33351  
repeat\_region /note="MIR repeat: matches 15. .242 of consensus"  
33456. .33907  
misc\_feature /note="match: GSS: Em:AQ143587"  
34031. .34336  
repeat\_region /note="AluSg repeat: matches 1. .312 of consensus"  
34362. .34654  
repeat\_region /note="AluSg repeat: matches 1. .298 of consensus"  
34659. .34922  
repeat\_region /note="L2 repeat: matches 2359. .2639 of consensus"  
34944. .35120  
repeat\_region /note="MIR repeat: matches 40. .230 of consensus"  
35349. .35410  
repeat\_region /note="31 copies 2 mer ca 88 conserved"  
35363. .35410  
repeat\_region /note="8 copies 6 mer cacaca 100 conserved"  
35431. .35526  
repeat\_region /note="MIR repeat: matches 47. .146 of consensus"  
35565. .35901  
repeat\_region /note="MLT1A1 repeat: matches 1. .362 of consensus"

Query Match 95.7%; Score 22; DB 9; Length 41576;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGGTGGCAGGTGT 23  
|||||

Db 11887 AGCCAGGCATGGTGGCAGGTGT 11908  
|||||

RESULT 12

AL669893 AL669893 44767 bp DNA linear PRI 31-JAN-2002  
LOCUS Human DNA sequence from clone RP11-122F10 on chromosome 9, complete  
DEFINITION sequence.  
ACCESSION AL669893 AC026643  
VERSION AL669893.4 GI:18477441



KEYWORDS: HTG.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 44767)  
JOURNAL Skuce.C.

COMMENT  
Direct Submission  
Submitted (31-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
On Feb 1, 2002 this sequence version replaced gi:18477022. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9>  
RP11-122F10 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBACe3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-122F10 It may be shorter because we sequence overlapping sections only once, except for a short overlap.  
The true left end of clone RP11-122F10 is at 42768 in this sequence. The true right end of clone RP11-217B7 is at 2000 in this sequence.

FEATURES  
source  
Location/Qualifiers  
1..44767  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="9"  
/clone="RP11-122F10"  
/clone\_lib="RPCI-11.1"  
BASE COUNT 13104 a 8997 c 8942 g 13724 t  
ORIGIN

Query Match 95.7%; Score 22; DB 9; Length 44767;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23  
|||||  
Db 6357 AGCCAGGCATGGTGGCAGGTGT 6378  
|||||

RESULT 13  
AL583845/C  
LOCUS Human DNA sequence from clone RP11-211A7 on chromosome 1, complete  
DEFINITION  
AL583845  
VERSION AL583845.16 GI:18643768  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 54154)  
JOURNAL Wallis.J.

COMMENT  
Direct Submission  
Submitted (08-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
On Feb 10, 2002 this sequence version replaced gi:18476654. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>  
RP11-211A7 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBACe3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-211A7 It may be shorter because we sequence overlapping sections only once, except for a short overlap.  
The true left end of clone RP11-513D4 is at 52155 in this sequence. The true right end of clone RP11-56111 is at 2000 in this sequence.

FEATURES  
source  
Location/Qualifiers  
1..54154  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/clone="RP11-211A7"  
/clone\_lib="RPCI-11.1"  
BASE COUNT 17287 a 10487 c 11029 g 15351 t  
ORIGIN

Query Match 95.7%; Score 22; DB 9; Length 54154;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23  
|||||  
Db 47921 AGCCAGGCATGGTGGCAGGTGT 47900  
|||||

RESULT 14  
AC027427  
LOCUS Homo sapiens chromosome 1 clone RP11-211A7 map 1, LOW-PASS SEQUENCE  
DEFINITION  
AC027427  
VERSION AC027427.3 GI:17048288  
KEYWORDS HTG; HTGS PHASE0.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 56652)

AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 1, clone RP11-211A7  
Unpublished  
2 (bases 1 to 56652)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, P.,  
Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,  
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,  
Gallagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-pierre, N., Grant, J., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., LaRocque, K., Lanazares, R., Landers, T., Lehoczy, J.,  
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,  
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,  
Meldrum, J., Menes, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neil, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT

Direct Submission  
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 22, 2001 this sequence version replaced gi:13443233.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L7689  
Center clone name: 211\_A7  
-----

NOTE: This record contains 72 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

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2435 3148: contig of 714 bp in length  
3149 3248: gap of 100 bp  
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3931 4030: gap of 100 bp  
4031 4745: contig of 715 bp in length  
4746 4845: gap of 100 bp  
4846 5529: contig of 684 bp in length  
5530 5629: gap of 100 bp  
5630 6323: contig of 694 bp in length  
6324 6423: gap of 100 bp  
6424 7118: contig of 695 bp in length  
7119 7218: gap of 100 bp  
7219 7899: contig of 681 bp in length  
7900 7999: gap of 100 bp  
8000 8652: contig of 653 bp in length

8653 8752: gap of 100 bp  
8753 9447: contig of 695 bp in length  
9448 9547: gap of 100 bp  
9548 10205: contig of 658 bp in length  
10206 10305: gap of 100 bp  
10306 11002: contig of 697 bp in length  
11003 11102: gap of 100 bp  
11103 11798: contig of 696 bp in length  
11799 11898: gap of 100 bp  
11899 12566: contig of 668 bp in length  
12567 12666: gap of 100 bp  
12667 13340: contig of 674 bp in length  
13341 13440: gap of 100 bp  
13441 14129: contig of 689 bp in length  
14130 14239: gap of 100 bp  
14239 14893: contig of 664 bp in length  
14894 14993: gap of 100 bp  
14994 15682: contig of 689 bp in length  
15683 15782: gap of 100 bp  
15783 16482: contig of 700 bp in length  
16483 16582: gap of 100 bp  
16583 17273: contig of 691 bp in length  
17274 17373: gap of 100 bp  
17374 18075: contig of 702 bp in length  
18076 18175: gap of 100 bp  
18176 18861: contig of 686 bp in length  
18862 18961: gap of 100 bp  
18962 19639: contig of 678 bp in length  
19640 19739: gap of 100 bp  
19740 20424: contig of 685 bp in length  
20425 20524: gap of 100 bp  
20525 21176: contig of 652 bp in length  
21177 21276: gap of 100 bp  
21277 21958: contig of 682 bp in length  
21959 22058: gap of 100 bp  
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22860 23533: contig of 674 bp in length  
23534 23633: gap of 100 bp  
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24341 24440: gap of 100 bp  
24441 25127: contig of 687 bp in length  
25128 25227: gap of 100 bp  
25228 25930: contig of 703 bp in length  
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26031 26715: contig of 685 bp in length  
26716 26815: gap of 100 bp  
26816 27509: contig of 694 bp in length  
27510 27609: gap of 100 bp  
27610 28313: contig of 704 bp in length  
28314 28413: gap of 100 bp  
28414 29103: contig of 696 bp in length  
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29210 29881: contig of 672 bp in length  
29882 29981: gap of 100 bp  
29982 30652: contig of 671 bp in length  
30653 30752: gap of 100 bp  
30753 31432: contig of 680 bp in length  
31433 31532: gap of 100 bp  
31533 32233: contig of 701 bp in length  
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33096 33776: contig of 681 bp in length  
33777 33876: gap of 100 bp  
33877 34564: contig of 688 bp in length  
34565 34664: gap of 100 bp  
34665 35363: contig of 699 bp in length  
35364 35463: gap of 100 bp  
35464 36126: contig of 663 bp in length  
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* 38601 38700: gap of 100 bp
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* 39474 40161: contig of 688 bp in length
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* 40262 40943: contig of 682 bp in length
* 40944 41043: gap of 100 bp
* 41044 41702: contig of 659 bp in length
* 41703 41802: gap of 100 bp
* 41803 42450: contig of 648 bp in length
* 42451 42550: gap of 100 bp
* 42551 43244: contig of 694 bp in length
* 43245 43344: gap of 100 bp
* 43345 44030: contig of 686 bp in length
* 44031 44130: gap of 100 bp
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* 44917 45588: contig of 672 bp in length
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* 45689 46396: contig of 708 bp in length
* 46397 46496: gap of 100 bp
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* 49541 49640: gap of 100 bp
* 49641 50321: contig of 681 bp in length
* 50322 50421: gap of 100 bp
* 50422 51103: contig of 682 bp in length
* 51104 51203: gap of 100 bp
* 51204 51872: contig of 669 bp in length
* 51873 51972: gap of 100 bp
* 51973 52660: contig of 688 bp in length
* 52661 52760: gap of 100 bp
* 52761 53474: contig of 714 bp in length
* 53475 53574: gap of 100 bp
* 53575 54281: contig of 707 bp in length

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Query Match 95.7%; Score 22; DB 2; Length 56652;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGATGGTGGCAGGTGT 23

Db 7296 AGCCAGGATGGTGGCAGGTGT 7317

#### RESULT 15

AC107942

LOCUS

DEFINITION

AC107942.1 GI:18308669

VERSION

HTG; HTGS PHASE0.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1. (bases 1 to 62833)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 8, clone RP11-241L13

Unpublished

2. (bases 1 to 62833)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,  
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,  
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
Kamat, A., Karatas, A., Kells, C., Lacombe, K., Lamazares, R.,  
Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,  
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,  
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,  
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Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,  
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

#### TITLE JOURNAL

#### COMMENT

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center Project name: L24036

Center Clone name: 241\_L\_13

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\* NOTE: This record contains 76 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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Query Match 95.7%: Score 22; DB 2; Length 62833;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22  
|||||||  
Db 27542 CAGCCAGGCATGGTGGCAGGTG 27563

Search completed: June 17, 2003, 03:57:01  
Job time : 87.3809 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 4.06039 Seconds  
(without alignments)  
12756.396 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_4451\_4473  
Perfect score: 23  
Sequence: 1 cagccaggcatggtgscaggtgt 23

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_101002.\*  
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3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
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24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	23	100.0	9048	21	AAAG4507 Nucleotide sequenc
2	22	95.7	204	21	AA15023 Human secreted pro
3	22	95.7	389	23	ABV39095 Human prostate exp
4	22	95.7	440	23	ABV11210 Human prostate exp
5	22	95.7	477	23	ABV05712 Human prostate exp
6	22	95.7	478	23	ABV32356 Human prostate exp
7	22	95.7	478	23	ABV41286 Human prostate exp
8	22	95.7	495	23	ABV15013 Human prostate exp
9	22	95.7	506	23	ABV32243 Human prostate exp

521	23	ABV05844	Human prostate exp
557	23	ABV21254	Human prostate exp
557	23	ABV21288	Human prostate exp
557	23	ABV21292	Human prostate exp
557	23	ABV23638	Human prostate exp
557	23	ABV23898	Human prostate exp
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557	23	ABV27075	Human prostate exp
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557	23	ABV27111	Human prostate exp
557	23	ABV29498	Human prostate exp
557	23	ABV29567	Human prostate exp
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166	22	AAK84501	Human immune/haema
170	24	AAI69073	Activated T-cell d
186	22	AAS32543	Human genomic DNA
186	22	AAK81683	Human immune/haema
278	22	AAS27850	DNA encoding novel
278	22	AAK27651	DNA encoding novel
352	22	AAK97571	Human neuroregulin g
378	22	AAK67025	Human immune/haema
381	22	AAK67028	Human immune/haema
381	22	AAK67030	Human immune/haema
392	23	ABV37939	Human prostate exp
401	22	AAK96077	Human neuroregulin g
401	22	AAK96078	Human neuroregulin g
401	22	AAK96079	Human neuroregulin g
401	22	AAK96080	Human neuroregulin g
401	22	AAK97570	Human neuroregulin g
401	22	AAK97572	Human neuroregulin g
401	22	AAK97573	Human neuroregulin g
422	22	ABA07807	Human ovarian and
422	22	AAU07806	Human reproductive
504	22	AAK84322	Human immune/haema
525	23	ABV53372	Human prostate exp
527	24	ABN63795	Human cancer relat
534	23	ABV50306	Human prostate exp
541	22	AAI15314	Human breast cance
558	24	ABN64776	Human cancer relat
558	24	ABN65992	Human cancer relat
561	22	AAI23014	Human breast cance
563	22	AAI24160	Human breast cance
580	22	AAI15207	Human cancer relat
581	24	ABN65793	Human cancer relat
600	22	AAK85272	Human immune/haema
600	22	AAK85273	Human breast cance
663	22	AAI14152	Human immune/haema
715	22	AAK81416	Human immune/haema
715	22	AAK81417	Human immune/haema
748	21	AAI66449	Human secreted pro
763	22	AAI24053	Human breast cance
824	21	AAI59548	Human secreted pro
1057	22	ABAI8567	Human nervous syst
1057	22	ABAI8568	Human nervous syst

83	21	91.3	1154	21	AAH51628	Human g35018 cdna	156	21	91.3	32248	22	ABA20412	Human nervous syst
84	21	91.3	1301	21	AAH51627	Human g35018 cdna	c 157	21	91.3	32248	22	AA137122	Human musculoskele
85	21	91.3	1386	21	AAH51631	Human g35018 cdna	c 158	21	91.3	32248	22	AA137122	Human genomic DNA
86	21	91.3	1578	24	ABA021154	Human signalase I	c 159	21	91.3	32248	22	AA137122	Gene #184 used to
87	21	91.3	1643	22	ABA19995	Human nervous syst	c 160	21	91.3	32248	22	AA137122	Human immune/haema
88	21	91.3	1643	22	ABA19996	Human nervous syst	c 161	21	91.3	32248	22	AA137122	Human immune/haema
89	21	91.3	1699	24	ABL92345	Human secreted pro	c 162	21	91.3	32248	22	AA137122	Human immune/haema
90	21	91.3	1847	21	AAH26311	Human secreted pro	c 163	21	91.3	32248	22	AA137122	Gene #3953 used to
91	21	91.3	1879	22	AAH17119	Human cdna sequenc	c 164	21	91.3	32248	22	AA137122	Lung cancer relate
92	21	91.3	2509	21	AAH16679	Human secreted pro	c 165	21	91.3	32248	22	AA137122	Lung cancer relate
93	21	91.3	2646	22	AAI61012	Human polynucleoti	c 166	21	91.3	32248	22	AA137122	Human immune/haema
94	21	91.3	2946	22	AAH68591	Human immune/haema	c 167	21	91.3	32248	22	AA137122	Human immune/haema
95	21	91.3	3172	24	ABL62888	Breast cancer rela	c 168	21	91.3	32248	22	AA137122	Human immune/haema
96	21	91.3	3172	24	ABL63310	Breast cancer rela	c 169	21	91.3	32248	22	AA137122	Human immune/haema
97	21	91.3	3209	23	AAH86285	DNA encoding novel	c 170	21	91.3	32248	22	AA137122	Genomic DNA sequen
98	21	91.3	3591	23	AAH86915	DNA encoding novel	c 171	21	91.3	32248	22	AA137122	Human immune/haema
99	21	91.3	4733	22	ABA07211	Human pancreatic c	c 172	21	91.3	32248	22	AA137122	Human immune/haema
100	21	91.3	4733	22	AAH89843	Human digestive sy	c 173	21	91.3	32248	22	AA137122	Human serine/threo
101	21	91.3	5054	22	AAH35968	Human musculoskele	c 174	21	91.3	32248	22	AA137122	Human immune/haema
102	21	91.3	6496	22	AAH72255	Human immune/haema	c 175	21	91.3	32248	22	AA137122	Breast cancer rela
103	21	91.3	7157	22	ABA19506	Human nervous syst	c 176	21	91.3	32248	22	AA137122	Oesophagus cancer
104	21	91.3	7330	22	AAH65121	Human immune/haema	c 177	21	91.3	32248	22	AA137122	Human apolipoprote
105	21	91.3	7428	22	ABA07164	Human pancreatic c	c 178	21	91.3	32248	22	AA137122	Human methionine a
106	21	91.3	8268	22	AAH28434	Genomic sequence #	c 179	21	91.3	32248	22	AA137122	Human cdna differe
107	21	91.3	8272	22	AAH28433	Genomic sequence #	c 180	21	91.3	32248	22	AA137122	Human osteoblast d
108	21	91.3	8272	22	AAH28433	Genomic sequence #	c 181	21	91.3	32248	22	AA137122	Human transporter
109	21	91.3	8272	22	AAH28433	Genomic sequence #	c 182	21	91.3	32248	22	AA137122	Human cdna differe
110	21	91.3	8272	22	AAH28433	Genomic sequence #	c 183	21	91.3	32248	22	AA137122	Human cdna differe
111	21	91.3	8272	22	AAH28433	Genomic sequence #	c 184	21	91.3	32248	22	AA137122	Human osteoblast d
112	21	91.3	8272	22	AAH28433	Genomic sequence #	c 185	21	91.3	32248	22	AA137122	Human osteoblast d
113	21	91.3	8272	22	AAH28433	Genomic sequence #	c 186	21	91.3	32248	22	AA137122	Human osteoblast d
114	21	91.3	8272	22	AAH28433	Genomic sequence #	c 187	21	91.3	32248	22	AA137122	Human cdna differe
115	21	91.3	8272	22	AAH28433	Genomic sequence #	c 188	21	91.3	32248	22	AA137122	Human cdna differe
116	21	91.3	8272	22	AAH28433	Genomic sequence #	c 189	21	91.3	32248	22	AA137122	Human chromosome 1
117	21	91.3	8272	22	AAH28433	Genomic sequence #	c 190	21	91.3	32248	22	AA137122	Human chromosome 1
118	21	91.3	8272	22	AAH28433	Genomic sequence #	c 191	21	91.3	32248	22	AA137122	Human schizophrenia
119	21	91.3	8272	22	AAH28433	Genomic sequence #	c 192	21	91.3	32248	22	AA137122	Human schizophre
120	21	91.3	8272	22	AAH28433	Genomic sequence #	c 193	21	91.3	32248	22	AA137122	Human Oestrogen re
121	21	91.3	8272	22	AAH28433	Genomic sequence #	c 194	21	91.3	32248	22	AA137122	Human neuregulin-1
122	21	91.3	8272	22	AAH28433	Genomic sequence #	c 195	21	91.3	32248	22	AA137122	Human immune/haema
123	21	91.3	8272	22	AAH28433	Genomic sequence #	c 196	21	91.3	32248	22	AA137122	Human digestive sy
124	21	91.3	8272	22	AAH28433	Genomic sequence #	c 197	21	91.3	32248	22	AA137122	Human cancer relat
125	21	91.3	8272	22	AAH28433	Genomic sequence #	c 198	21	91.3	32248	22	AA137122	AMEF2. Homo sapien
126	21	91.3	8272	22	AAH28433	Genomic sequence #	c 199	21	91.3	32248	22	AA137122	MEF2. Homo sapien
127	21	91.3	8272	22	AAH28433	Genomic sequence #	c 200	21	91.3	32248	22	AA137122	Human myocyte enha
128	21	91.3	8272	22	AAH28433	Genomic sequence #	c 201	21	91.3	32248	22	AA137122	Human cdna seq ID
129	21	91.3	8272	22	AAH28433	Genomic sequence #	c 202	21	91.3	32248	22	AA137122	Human liver cell s
130	21	91.3	8272	22	AAH28433	Genomic sequence #	c 203	21	91.3	32248	22	AA137122	Human liver cell s
131	21	91.3	8272	22	AAH28433	Genomic sequence #	c 204	21	91.3	32248	22	AA137122	Human ABC1 gene ex
132	21	91.3	8272	22	AAH28433	Genomic sequence #	c 205	21	91.3	32248	22	AA137122	Human immune/haema
133	21	91.3	8272	22	AAH28433	Genomic sequence #	c 206	21	91.3	32248	22	AA137122	Human immune/haema
134	21	91.3	8272	22	AAH28433	Genomic sequence #	c 207	21	91.3	32248	22	AA137122	Human immune/haema
135	21	91.3	8272	22	AAH28433	Genomic sequence #	c 208	21	91.3	32248	22	AA137122	Human immune/haema
136	21	91.3	8272	22	AAH28433	Genomic sequence #	c 209	21	91.3	32248	22	AA137122	Human immune/haema
137	21	91.3	8272	22	AAH28433	Genomic sequence #	c 210	21	91.3	32248	22	AA137122	Human immune/haema
138	21	91.3	8272	22	AAH28433	Genomic sequence #	c 211	21	91.3	32248	22	AA137122	Human immune/haema
139	21	91.3	8272	22	AAH28433	Genomic sequence #	c 212	21	91.3	32248	22	AA137122	Human immune/haema
140	21	91.3	8272	22	AAH28433	Genomic sequence #	c 213	21	91.3	32248	22	AA137122	Human immune/haema
141	21	91.3	8272	22	AAH28433	Genomic sequence #	c 214	21	91.3	32248	22	AA137122	Human transporter
142	21	91.3	8272	22	AAH28433	Genomic sequence #	c 215	21	91.3	32248	22	AA137122	Human ABC1 gene ex
143	21	91.3	8272	22	AAH28433	Genomic sequence #	c 216	21	91.3	32248	22	AA137122	Human ABC1 genomic
144	21	91.3	8272	22	AAH28433	Genomic sequence #	c 217	21	91.3	32248	22	AA137122	Human ABC1 genomic
145	21	91.3	8272	22	AAH28433	Genomic sequence #	c 218	21	91.3	32248	22	AA137122	Human ABC1 genomic
146	21	91.3	8272	22	AAH28433	Genomic sequence #	c 219	21	91.3	32248	22	AA137122	Human ABC1 genomic
147	21	91.3	8272	22	AAH28433	Genomic sequence #	c 220	21	91.3	32248	22	AA137122	Human ABC1 genomic
148	21	91.3	8272	22	AAH28433	Genomic sequence #	c 221	21	91.3	32248	22	AA137122	Human ABC1 genomic
149	21	91.3	8272	22	AAH28433	Genomic sequence #	c 222	21	91.3	32248	22	AA137122	Human ABC1 genomic
150	21	91.3	8272	22	AAH28433	Genomic sequence #	c 223	21	91.3	32248	22	AA137122	Human ABC1 genomic
151	21	91.3	8272	22	AAH28433	Genomic sequence #	c 224	21	91.3	32248	22	AA137122	Human ABC1 genomic
152	21	91.3	8272	22	AAH28433	Genomic sequence #	c 225	21	91.3	32248	22	AA137122	Human ABC1 genomic
153	21	91.3	8272	22	AAH28433	Genomic sequence #	c 226	21	91.3	32248	22	AA137122	Human ABC1 genomic
154	21	91.3	8272	22	AAH28433	Genomic sequence #	c 227	21	91.3	32248	22	AA137122	Human ABC1 genomic
155	21	91.3	8272	22	AAH28433	Genomic sequence #	c 228	21	91.3	32248	22	AA137122	Human ABC1 genomic

c 229	19	82.6	232	22	AA32771	Human genomic DNA	302	19	82.6	1495	20	AA224848	Human secreted pro
c 230	19	82.6	233	21	AA04872	Human secreted pro	303	19	82.6	1656	22	AA180590	Human polynucleoti
c 231	19	82.6	234	21	AA081808	Human immune/haema	c 304	19	82.6	1719	22	AA06358	Human reproductive
c 232	19	82.6	244	21	AA014071	Human secreted pro	305	19	82.6	1739	22	AAH15160	Human cDNA sequenc
c 233	19	82.6	287	24	AA084027	Human ovarian canc	306	19	82.6	1746	22	AAH14103	Human normal pancr
c 234	19	82.6	292	24	AA081803	Human immune/haema	307	19	82.6	1851	22	AAH17054	Human cDNA sequenc
c 235	19	82.6	295	22	AA081804	Human immune/haema	308	19	82.6	1886	21	AA069532	Human secreted pro
c 236	19	82.6	296	22	AA039695	Genomic sequence #	309	19	82.6	2049	22	AAH14874	Human cDNA sequenc
c 237	19	82.6	296	22	AA090038	Human digestive sy	310	19	82.6	2129	24	ABL69992	Pancreas cancer re
c 238	19	82.6	298	22	AA073170	Human immune/haema	311	19	82.6	2129	24	AA028256	Human pancreatic t
c 239	19	82.6	305	22	AB015810	Human nervous syst	312	19	82.6	2155	22	AAK72886	Human immune/haema
c 240	19	82.6	305	22	AB018642	Human nervous syst	313	19	82.6	2155	22	AAK83987	Human immune/haema
c 241	19	82.6	317	24	AB084024	Human ovarian canc	314	19	82.6	2168	22	AAK94515	Human full-length
c 242	19	82.6	322	21	AA005361	Human secreted pro	315	19	82.6	2515	22	AAH17444	Human cDNA sequenc
c 243	19	82.6	324	23	AB053523	Human prostate exp	316	19	82.6	2557	22	AAH18475	Human cDNA sequenc
c 244	19	82.6	336	21	AA028935	Human secreted pro	317	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 245	19	82.6	360	22	AA062217	Human immune/haema	c 318	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 246	19	82.6	362	21	AA013772	Human secreted pro	319	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 247	19	82.6	362	21	AA014578	Human secreted pro	320	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 248	19	82.6	365	24	AB084760	Human ovarian canc	c 320	19	82.6	2620	22	AAH18417	Human cDNA sequenc
c 249	19	82.6	394	22	AA066101	Novel human polynu	321	19	82.6	3139	22	AAK71190	Human immune/haema
c 250	19	82.6	401	22	AA065965	Human polynu	c 322	19	82.6	3142	22	AAH17357	Human cDNA sequenc
c 251	19	82.6	403	21	AA000508	Human secreted pro	323	19	82.6	3144	22	AAH13942	Human cDNA sequenc
c 252	19	82.6	409	24	AB062750	Human cancer relat	324	19	82.6	3148	22	AAH17290	Human cDNA sequenc
c 253	19	82.6	412	24	AB087547	Human cancer relat	c 325	19	82.6	3185	22	AAH57528	Human pancreas cel
c 254	19	82.6	439	23	AB050575	Human ovarian canc	326	19	82.6	3309	23	AA0572615	DNA encoding novel
c 255	19	82.6	443	21	AA016023	Human prostate exp	327	19	82.6	3323	22	AA032820	Human genomic DNA
c 256	19	82.6	455	23	AB014244	Human colon cancer	328	19	82.6	3807	22	AA010456	Human stem cell fa
c 257	19	82.6	478	23	AB035337	Human prostate exp	329	19	82.6	3807	22	AAH411340	Human stem cell f
c 258	19	82.6	478	23	AB044168	Human prostate exp	330	19	82.6	3807	22	AA04120	Human genomic SCF
c 259	19	82.6	485	23	AB046908	Human prostate exp	331	19	82.6	3807	22	AA04221	Human genomic SCF
c 260	19	82.6	496	22	AA04570	Human cDNA clone (	332	19	82.6	3807	22	AAH23898	Human genomic SCF
c 261	19	82.6	496	22	AA062961	Human cancer relat	333	19	82.6	3807	22	AAH23898	Human stem cell fa
c 262	19	82.6	507	22	AA032960	Human cDNA 3'-end	334	19	82.6	3807	22	AA035473	Human stem cell fa
c 263	19	82.6	511	24	AB063173	Human cancer relat	335	19	82.6	4063	12	AA011540	Human Stem Cell Fa
c 264	19	82.6	543	23	AB057782	Human prostate exp	c 336	19	82.6	4412	22	AAH57372	Human heart cell s
c 265	19	82.6	548	22	AA050988	Human cDNA clone (	c 337	19	82.6	4544	22	AB015386	Human nervous syst
c 266	19	82.6	554	22	AA050985	Human cDNA clone (	c 338	19	82.6	4864	22	AB015386	Human bone marrow
c 267	19	82.6	559	22	AA010571	Human cDNA clone (	339	19	82.6	5069	22	AA067404	Human immune/haema
c 268	19	82.6	573	22	AA035984	Human cardiovascular	c 340	19	82.6	5075	22	AB016701	Human nervous syst
c 269	19	82.6	576	24	AB065904	Human cancer relat	c 341	19	82.6	5076	22	AB016699	Human nervous syst
c 270	19	82.6	579	24	AB065230	Human cancer relat	c 342	19	82.6	5101	22	AA081960	Human immune/haema
c 271	19	82.6	583	22	AA093607	cDNA isolated from	c 343	19	82.6	5107	22	AAK81959	Human immune/haema
c 272	19	82.6	586	24	AB064986	Human cancer relat	c 344	19	82.6	5118	22	AAK81958	Human immune/haema
c 273	19	82.6	601	23	AB053883	Human prostate exp	345	19	82.6	5351	22	AA031466	Human DNA for a no
c 274	19	82.6	619	22	AA079318	Human immune/haema	346	19	82.6	5351	24	AB066790	Human polynucleoti
c 275	19	82.6	620	22	AA079317	Human immune/haema	347	19	82.6	5646	22	AA031336	Human reproductive
c 276	19	82.6	622	23	AB051983	Human prostate exp	348	19	82.6	5864	22	AA010458	Human stem cell fa
c 277	19	82.6	625	24	AB057233	Human prostate exp	349	19	82.6	5864	22	AAH41342	Human stem cell fa
c 278	19	82.6	644	22	AA034255	Human cDNA encodin	350	19	82.6	5864	22	AA041342	Human SCF (stem ce
c 279	19	82.6	669	24	AB062557	Human cancer relat	351	19	82.6	5864	22	AA04223	Human SCF (stem ce
c 280	19	82.6	700	22	AA092707	Human inflammatory	352	19	82.6	5864	22	AA023900	Human SCF (stem ce
c 281	19	82.6	708	23	AA017113	Human prostate exp	353	19	82.6	5864	22	AA089102	Human stem cell fa
c 282	19	82.6	713	21	AA010667	Human secreted pro	c 354	19	82.6	5864	24	AA035475	Human stem cell fa
c 283	19	82.6	750	20	AA0217166	Human gene express	c 355	19	82.6	5917	24	ABK84584	Human cDNA differe
c 284	19	82.6	753	24	AB089117	Human prostate exp	356	19	82.6	6235	21	AA029169	Human G-CSF genomi
c 285	19	82.6	754	21	AA022212	Human colon cancer	357	19	82.6	6437	22	AAK82889	Human immune/haema
c 286	19	82.6	764	20	AA015768	Human gene express	358	19	82.6	6461	22	AA031467	Human DNA for a no
c 287	19	82.6	764	20	AA015768	Human gene express	359	19	82.6	6461	24	AB066791	Human polynucleoti
c 288	19	82.6	777	22	AA040994	Human cDNA clone (	c 360	19	82.6	6579	22	AAK70497	Human immune/haema
c 289	19	82.6	796	21	AA013767	Human stem cell fa	361	19	82.6	6670	22	AA02846	Human reproductive
c 290	19	82.6	798	16	AA040886	Human SCF genomic	362	19	82.6	6679	21	AA029170	Partial sequence o
c 291	19	82.6	802	22	AA039814	Genomic sequence #	363	19	82.6	6679	22	AAH17443	Human granulocyte
c 292	19	82.6	802	22	AA090170	Human digestive sy	c 364	19	82.6	6679	22	AAK83499	Human immune/haema
c 293	19	82.6	874	21	AA058898	cDNA sequence of a	c 365	19	82.6	7032	23	ABK42542	Genomic sequence #
c 294	19	82.6	916	22	AA033223	Human polynucleoti	366	19	82.6	7032	22	ABA20748	Human nervous syst
c 295	19	82.6	924	21	AA058888	cDNA sequence of a	367	19	82.6	7105	22	AA037450	Human musculoskele
c 296	19	82.6	1046	22	AA018696	Human cDNA sequenc	368	19	82.6	7328	21	AA020874	Human bradykinin r
c 297	19	82.6	1089	22	AA007902	Human secreted pro	369	19	82.6	7328	21	AA020878	Human bradykinin r
c 298	19	82.6	1136	22	AB014624	Human nervous syst	370	19	82.6	7328	21	AA020887	Human bradykinin r
c 299	19	82.6	1238	22	AA082426	Human immune/haema	371	19	82.6	7328	21	AA034752	Human adenosine re
c 300	19	82.6	1238	22	AA082427	Human immune/haema	372	19	82.6	7328	21	AAA34756	Human adenosine re
c 301	19	82.6	1238	22	AA082428	Human immune/haema	373	19	82.6	7328	21	AAA34765	Human adenosine re
	19	82.6	1238	22	AA082428	Human immune/haema	374	19	82.6	7713	22	AA02845	Human reproductive

375	19	82.6	8271	22	AAK78824	Human immune/haema
376	19	82.6	8387	22	ABAI4892	Human nervous syst
377	19	82.6	8387	22	AAK84548	Human immune/haema
378	19	82.6	8418	22	AAS41906	Genomic sequence #
379	19	82.6	8575	22	ABL06019	Human reproductive
380	19	82.6	8575	23	ABL98584	Human testicular a
381	19	82.6	8622	21	AAS95912	Human KIK-L3 gene.
382	19	82.6	9058	22	AAS41691	Genomic sequence #
383	19	82.6	9180	19	AAV57416	Tumour suppressor
384	19	82.6	9180	24	ABN96964	Gene #3462 used to
385	19	82.6	9337	22	AAK76038	Human immune/haema
386	19	82.6	9337	22	AAK78564	Human immune/haema
387	19	82.6	9469	22	AAK79514	Human immune/haema
388	19	82.6	9780	22	AAK72360	Human immune/haema
389	19	82.6	9969	22	AAK04217	Human reproductive
390	19	82.6	10684	17	AAT33758	Control region iso
391	19	82.6	10872	22	AAK03182	Human reproductive
392	19	82.6	10926	22	AAK65370	Human immune/haema
393	19	82.6	11101	24	ABN83947	Human transporter
394	19	82.6	11101	24	AAK66446	Human immune/haema
395	19	82.6	11150	22	ABA07766	Human ovarian and
396	19	82.6	11150	22	AAK03557	Human reproductive
397	19	82.6	11150	22	AAK68451	Human immune/haema
398	19	82.6	11150	22	AAK72674	Human immune/haema
399	19	82.6	11474	23	ABK42672	Genomic sequence #
400	19	82.6	11881	22	AAS36624	Human cardiovascular
401	19	82.6	11881	22	AAS27691	DNA encoding novel
402	19	82.6	11881	22	AAS27693	DNA encoding novel
403	19	82.6	12045	22	AAK07066	Human reproductive
404	19	82.6	12267	22	AAK85733	Human immune/haema
405	19	82.6	12555	22	ABAI8329	Human nervous syst
406	19	82.6	12638	22	AAK70641	Human immune/haema
407	19	82.6	12904	22	AAK85382	Human immune/haema
408	19	82.6	13209	22	AAK81554	Human digestive sy
409	19	82.6	13273	22	AAK96558	Human digestive sy
410	19	82.6	13287	22	ABAI4431	Human nervous syst
411	19	82.6	13646	24	AAS20126	Human gene for ret
412	19	82.6	13646	24	AAS20128	Human gene for ret
413	19	82.6	13912	22	AAK82686	Human immune/haema
414	19	82.6	14543	24	ABK15798	Human of Hippel-L
415	19	82.6	15929	22	ABAI8496	Human nervous syst
416	19	82.6	15929	22	ABAI9020	Human nervous syst
417	19	82.6	15964	22	ABAI8497	Human nervous syst
418	19	82.6	15964	22	ABAI9021	Human nervous syst
419	19	82.6	17509	24	ABN95599	Gene #2097 used to
420	19	82.6	17672	22	ABAI5809	Human nervous syst
421	19	82.6	17672	22	ABAI8641	Human nervous syst
422	19	82.6	17687	22	AAS42069	Genomic sequence #
423	19	82.6	18534	24	ABK94757	Human cDNA differe
424	19	82.6	18664	22	AAK65421	Human immune/haema
425	19	82.6	18664	22	AAK84438	Human immune/haema
426	19	82.6	18820	22	ABA07938	Human ovarian and
427	19	82.6	18820	22	AAK03764	Human reproductive
428	19	82.6	19199	22	AAK70995	Human immune/haema
429	19	82.6	19472	22	AAS26724	Human genomic DNA
430	19	82.6	19696	22	AAS40722	DNA encoding human
431	19	82.6	19696	22	AAK06639	Human reproductive
432	19	82.6	19815	22	AAS42084	Genomic sequence #
433	19	82.6	19965	22	AAK73166	Human immune/haema
434	19	82.6	19965	24	ABK69932	Human secreted pro
435	19	82.6	20420	22	AAK73165	Human immune/haema
436	19	82.6	20420	24	ABK69933	Human secreted pro
437	19	82.6	20444	22	AAS34643	Human DNA for a no
438	19	82.6	20444	22	AAK06734	Human reproductive
439	19	82.6	20444	22	AAK66859	Human immune/haema
440	19	82.6	20444	22	AAI62640	Human breast or ov
441	19	82.6	20445	24	AAS19906	Reference sequence
442	19	82.6	20835	22	AAK86765	Human immune/haema
443	19	82.6	20892	22	ABAI5709	Human nervous syst
444	19	82.6	21371	22	AAK04330	Human reproductive
445	19	82.6	21371	22	AAK04330	Human reproductive
446	19	82.6	21441	22	AAK06761	Human breast or ov
447	19	82.6	21441	22	AAI62667	Human breast or ov
448	19	82.6	21535	22	AAS29834	Human cytoskeletal
449	19	82.6	21535	22	AAS35081	DNA #31 encoding h
450	19	82.6	21535	22	AAK42133	Genomic sequence #
451	19	82.6	22465	23	ABK86932	Human immune/haema
452	19	82.6	23802	22	AAK75632	Human immune/haema
453	19	82.6	24110	22	AAD16628	Human novel protei
454	19	82.6	25715	22	AAS33462	DNA encoding human
455	19	82.6	25806	22	AAK86766	Human immune/haema
456	19	82.6	26372	22	AAK77103	Human immune/haema
457	19	82.6	27754	24	ABO72998	Human transporter
458	19	82.6	28313	22	AAK36829	Human musculoskele
459	19	82.6	28444	24	ABK86948	Human glutathione
460	19	82.6	28690	24	AAK77118	Human IL4Ralpha ge
461	19	82.6	29228	22	AAK36833	Human musculoskele
462	19	82.6	30110	22	AAK89230	Human digestive sy
463	19	82.6	30620	22	AAK66931	Human immune/haema
464	19	82.6	31730	22	AAK37445	Human musculoskele
465	19	82.6	31853	22	AAI98993	Human excretory re
466	19	82.6	31853	22	AAI63343	Human kidney relat
467	19	82.6	31934	22	AAS30619	DNA encoding novel
468	19	82.6	31934	22	AAS28165	Genomic sequence #
469	19	82.6	32148	22	AAK04218	Human reproductive
470	19	82.6	32169	22	ABAI4358	Human nervous syst
471	19	82.6	32173	22	AAK07767	Human ovarian and
472	19	82.6	32173	22	AAK03558	Human reproductive
473	19	82.6	32177	22	AAK36886	Human musculoskele
474	19	82.6	32177	22	AAK04279	Human reproductive
475	19	82.6	32191	22	AAK37009	Human musculoskele
476	19	82.6	32199	22	AAK90296	Human digestive sy
477	19	82.6	32199	22	AAI5673	Human colorectal c
478	19	82.6	32224	22	AAK89986	Human digestive sy
479	19	82.6	32247	22	ABAI9669	Human nervous syst
480	19	82.6	33747	22	AAK69279	Human immune/haema
481	19	82.6	33747	22	AAK73093	Human immune/haema
482	19	82.6	35651	22	AAS7595	ATM complete genom
483	19	82.6	36797	24	AAD26738	Human synaptosomal
484	19	82.6	36797	24	AAD26738	Human synaptosomal
485	19	82.6	36797	24	AAD26830	Human SNAP29 gene
486	19	82.6	36797	24	AAD26830	Human SNAP29 gene
487	19	82.6	38136	22	AAK82172	Human immune/haema
488	19	82.6	38140	22	AAK82171	Human immune/haema
489	19	82.6	38653	22	AAK72348	Human immune/haema
490	19	82.6	38928	22	AAK68452	Human immune/haema
491	19	82.6	39353	22	AAK65396	Human immune/haema
492	19	82.6	39353	22	AAK67232	Human immune/haema
493	19	82.6	39358	22	AAK65397	Human immune/haema
494	19	82.6	39358	22	AAK67233	Human immune/haema
495	19	82.6	43680	24	ABK62024	Human genomic clon
496	19	82.6	43680	21	AAK21451	Human bradykinin r
497	19	82.6	49744	24	ABK12807	Human tumour suppr
498	19	82.6	50442	22	AAK73083	Human immune/haema
499	19	82.6	50442	22	AAK87551	Human immune/haema
500	19	82.6	54548	21	AAK45596	DNA sequence of th
501	19	82.6	55008	22	AAK80495	Human immune/haema
502	19	82.6	57248	24	AAK83563	Human cDNA differe
503	19	82.6	5837	24	ABK52612	Human Claspino geno
504	19	82.6	65608	24	ABL62910	Breast cancer rela
505	19	82.6	65608	24	ABL64414	Stomach cancer rel
506	19	82.6	65608	24	ABL67668	Oesophagus cancer
507	19	82.6	72928	20	AAI18355	Human ASTHJ 5' ge
508	19	82.6	72928	21	AAA80253	Human ASTHJ 5' ge
509	19	82.6	78925	21	AAK89888	Human FN gene. Ho
510	19	82.6	86080	24	ABQ88164	Human osteoblast d
511	19	82.6	86080	24	ABQ88164	Human osteoblast d
512	19	82.6	86080	24	ABK83561	Human cDNA differe
513	19	82.6	86080	24	ABK83561	Human cDNA differe
514	19	82.6	103747	24	ABQ88139	Human osteoblast d
515	19	82.6	107602	24	AAK99657	DNA of the PAC clo
516	19	82.6	107602	24	AAK99657	DNA of the PAC clo
517	19	82.6	107612	24	ABL54503	Human PAC clone se
518	19	82.6	107612	24	ABL54503	Human PAC clone se
519	19	82.6	110000	22	AAK84800	Nucleotide sequenc
520	19	82.6	114793	22	AAD08215	Human genome from





667	18	78.3	302250	24	ABL67703	Oesophagus cancer	740	17	73.9	266	24	ABL84721	Human ovarian canc
668	17	73.9	47	21	AAZ67562	Human map-related	741	17	73.9	269	22	ABA14427	Human nervous syst
669	17	73.9	51	22	AAI75713	Human silent SNP c	742	17	73.9	270	21	AAZ23148	Human secreted pro
670	17	73.9	51	22	AAI79864	Human nonconservat	743	17	73.9	272	22	AAK85288	Human immune/haema
671	17	73.9	51	22	AAH89316	Human coding sequ	744	17	73.9	274	22	AAK82889	Human immune/haema
672	17	73.9	51	22	AAH89566	Human coding sequ	745	17	73.9	278	22	AAK82889	Human reproductive
673	17	73.9	83	22	AAI36934	Human musculoskele	746	17	73.9	281	21	AAI04186	Human secreted pro
674	17	73.9	83	22	AAK84808	Human immune/haema	747	17	73.9	289	21	AAI31043	Human secreted pro
675	17	73.9	83	22	AAK84809	Human immune/haema	748	17	73.9	300	20	AAK98324	Human cancer cell
676	17	73.9	86	22	AAK76473	Human immune/haema	749	17	73.9	300	21	AAK30183	Human secreted pro
677	17	73.9	87	22	AAK36541	Human cardiovascu	750	17	73.9	300	21	AAA00567	Human colon cancer
678	17	73.9	87	22	AAK85201	Human immune/haema	751	17	73.9	302	21	AAK23855	Human secreted pro
679	17	73.9	99	22	AAK83638	Human immune/haema	752	17	73.9	303	21	AAK00363	Human secreted pro
680	17	73.9	99	22	AAK83639	Human immune/haema	753	17	73.9	314	22	AAK72490	Human immune/haema
681	17	73.9	102	22	AAK87320	Human immune/haema	754	17	73.9	315	22	AAI19757	Human nervous syst
682	17	73.9	102	22	AAK87321	Human immune/haema	755	17	73.9	319	22	AAK79658	Human immune/haema
683	17	73.9	102	22	AAK87322	Human immune/haema	756	17	73.9	323	22	AAK62080	Human immune/haema
684	17	73.9	102	22	AAK83184	Human immune/haema	757	17	73.9	323	24	ABL83854	Human ovarian canc
685	17	73.9	102	22	AAK83187	Human immune/haema	758	17	73.9	324	22	AAK38626	Novel human diagno
686	17	73.9	102	22	AAK83201	Human immune/haema	759	17	73.9	325	22	AAK38626	Human breast canc
687	17	73.9	102	22	AAK83215	Human immune/haema	760	17	73.9	326	24	ABL85203	Human ovarian canc
688	17	73.9	102	22	AAK83216	Human immune/haema	761	17	73.9	327	22	AAK87158	Human immune/haema
689	17	73.9	103	22	AAK84802	Human immune/haema	762	17	73.9	328	22	AAK74195	Human immune/haema
690	17	73.9	106	22	ABA21361	Human nervous syst	763	17	73.9	328	22	AAK74197	Human immune/haema
691	17	73.9	106	22	ABA21364	Human nervous syst	764	17	73.9	328	24	ABN62283	Human cancer relat
692	17	73.9	107	22	AAI05621	Human reproductive	765	17	73.9	328	24	ABL80420	Human ovarian canc
693	17	73.9	107	22	AAK74126	Human immune/haema	766	17	73.9	331	22	AAI82792	Human polynucleoti
694	17	73.9	107	22	AAK74127	Human immune/haema	767	17	73.9	332	22	AAI89846	Human polynucleoti
695	17	73.9	107	22	AAK74128	Human immune/haema	768	17	73.9	334	22	AAI80060	Human polynucleoti
696	17	73.9	107	22	AAK79672	Human immune/haema	769	17	73.9	335	22	AAI36377	Human musculoskele
697	17	73.9	107	22	AAK83761	Human immune/haema	770	17	73.9	336	24	ABL84097	Human ovarian canc
698	17	73.9	107	22	AAK85307	Human immune/haema	771	17	73.9	348	22	ABL86240	Human polynucleoti
699	17	73.9	108	21	AAK26212	Human secreted pro	772	17	73.9	351	22	AAI83957	Human polynucleoti
700	17	73.9	114	22	ABAL6309	Human nervous syst	773	17	73.9	351	22	AAI83957	Human ORFX polynu
701	17	73.9	114	22	ABAL6310	Human nervous syst	774	17	73.9	357	22	AAK20408	DNA encoding human
702	17	73.9	130	22	AAI04573	Human reproductive	775	17	73.9	357	22	AAK00662	Human reproductive
703	17	73.9	130	22	AAI05109	Human reproductive	776	17	73.9	359	24	ABN63013	Human cancer relat
704	17	73.9	130	23	ABL97496	Human testicular a	777	17	73.9	360	22	ABN63679	Human cancer relat
705	17	73.9	130	23	ABL98001	Human testicular a	778	17	73.9	362	22	AAI81586	Human polynucleoti
706	17	73.9	135	21	AAK13477	Human secreted pro	779	17	73.9	366	23	ABV00304	Human prostate exp
707	17	73.9	142	21	AAK20241	Human secreted pro	780	17	73.9	367	22	AAK39981	Genomic sequence #
708	17	73.9	147	22	AAK83526	Human immune/haema	781	17	73.9	367	22	AAK39982	Genomic sequence #
709	17	73.9	147	22	AAK85842	Human immune/haema	782	17	73.9	367	22	AAK90673	Human digestive sy
710	17	73.9	162	22	AAK65059	Human immune/haema	783	17	73.9	367	22	AAK90674	Human digestive sy
711	17	73.9	171	22	AAK65109	Human immune/haema	784	17	73.9	368	23	ABV08383	Human prostate exp
712	17	73.9	172	22	AAK32544	Human genomic DNA	785	17	73.9	369	22	ABV08383	Novel human polynu
713	17	73.9	175	22	AAK31645	Human immune/haema	786	17	73.9	371	22	AAK65052	Human reproductive
714	17	73.9	178	22	AAK78398	Human immune/haema	787	17	73.9	371	22	AAI04928	Human testicular a
715	17	73.9	179	22	AAK66061	Human immune/haema	788	17	73.9	372	14	AAQ60002	Human brain Expres
716	17	73.9	179	22	AAK66062	Human immune/haema	789	17	73.9	372	22	AAI86149	Human polynucleoti
717	17	73.9	179	22	AAK66065	Human immune/haema	790	17	73.9	378	22	AAI86149	Novel human polynu
718	17	73.9	183	21	AAK25411	Human secreted pro	791	17	73.9	379	22	AAK65419	Novel human polynu
719	17	73.9	188	21	AAK15303	Human secreted pro	792	17	73.9	379	22	AAK65419	Novel human polynu
720	17	73.9	188	22	AAK30622	DNA encoding novel	793	17	73.9	379	23	AAK67015	Novel human polynu
721	17	73.9	188	22	AAK28168	Genomic sequence #	794	17	73.9	380	22	AAI84732	Human prostate exp
722	17	73.9	201	21	AAK26227	Human secreted pro	795	17	73.9	380	22	AAI91246	Human polynucleoti
723	17	73.9	209	21	AAK13197	Human secreted pro	796	17	73.9	383	22	AAK85975	Human immune/haema
724	17	73.9	213	22	AAK30318	DNA encoding novel	797	17	73.9	385	22	AAK66116	Novel human polynu
725	17	73.9	213	22	AAK01999	Human reproductive	798	17	73.9	387	23	AAK20595	Human prostate exp
726	17	73.9	214	21	AAK05925	Human secreted pro	799	17	73.9	387	23	AAK20595	Human prostate exp
727	17	73.9	216	22	AAK72299	Human immune/haema	800	17	73.9	387	23	ABV20823	Human prostate exp
728	17	73.9	216	22	AAK72300	Human immune/haema	801	17	73.9	387	23	ABV26670	Human prostate exp
729	17	73.9	221	21	AAK12462	Human secreted pro	802	17	73.9	388	24	ABL84947	Human ovarian canc
730	17	73.9	231	21	AAK29656	Human secreted pro	803	17	73.9	389	22	AAI89027	Human polynucleoti
731	17	73.9	233	22	AAI05834	Human reproductive	804	17	73.9	390	22	AAK38763	Novel human diagno
732	17	73.9	233	22	ABL98398	Human testicular a	805	17	73.9	391	24	ABL37254	Human colon tumour
733	17	73.9	243	22	AAK83640	Human immune/haema	806	17	73.9	392	22	AAI81540	Human polynucleoti
734	17	73.9	246	21	AAI4911	Human secreted pro	807	17	73.9	392	22	AAK58892	Human immune/haema
735	17	73.9	251	21	AAK26789	Human secreted pro	808	17	73.9	393	23	ABV01294	Human prostate exp
736	17	73.9	253	21	AAK21861	Human secreted pro	809	17	73.9	394	22	AAI83715	Human polynucleoti
737	17	73.9	259	22	AAK35889	Human musculoskele	810	17	73.9	395	22	AAI88167	Human polynucleoti
738	17	73.9	260	21	AAK04921	Human secreted pro	811	17	73.9	395	22	AAI88167	Human polynucleoti
739	17	73.9	265	23	ABV50154	Human prostate exp	812	17	73.9	395	24	ABL85373	Human ovarian canc

C 813	17	73.9	396	21	AAH30338	Human colon cancer	C 886	17	73.9	450	22	AAH10230	Human breast cancer
C 814	17	73.9	397	22	AAI193102	Human polynucleoti	887	17	73.9	451	22	ABA16121	Human nervous syst
815	17	73.9	397	23	ABV10463	Human prostate exp	888	17	73.9	451	22	AAK67925	Human immune/haema
C 816	17	73.9	397	24	ABK46028	cDNA encoding colo	889	17	73.9	451	22	AAK81748	Human immune/haema
C 817	17	73.9	399	22	AAI181227	Human polynucleoti	890	17	73.9	451	22	AAK86495	Human immune/haema
C 818	17	73.9	400	22	AAK55649	Human immune/haema	891	17	73.9	451	24	ABN64146	Human cancer relat
C 819	17	73.9	401	21	AAK26724	Human secreted pro	C 892	17	73.9	452	20	ABN66930	EST clone BK304
820	17	73.9	401	22	AAK96247	Human neurogulin g	893	17	73.9	452	24	ABN60246	Human cancer relat
821	17	73.9	401	22	AAK96363	Human neurogulin g	C 894	17	73.9	453	22	AAI87017	Human polynucleoti
822	17	73.9	401	22	AAK97740	Human neurogulin g	C 895	17	73.9	454	23	ABV31547	Human prostate exp
823	17	73.9	401	22	AAK97856	Human neurogulin g	C 896	17	73.9	454	23	ABV40516	Human prostate exp
C 824	17	73.9	401	22	AAI93768	Human polynucleoti	C 897	17	73.9	455	23	ABV04766	Human prostate exp
C 825	17	73.9	401	23	ABV38290	Human prostate exp	C 898	17	73.9	459	24	ABN64956	Human cancer relat
826	17	73.9	403	22	AAK78684	Human immune/haema	C 899	17	73.9	460	23	ABV35045	Human prostate exp
827	17	73.9	404	22	AAI13876	Human breast cancer	C 900	17	73.9	460	23	ABV43892	Human prostate exp
828	17	73.9	404	24	ABL82168	Human ovarian canc	C 901	17	73.9	462	22	ABA13430	Human nervous syst
C 829	17	73.9	405	22	AAK96582	Human neurogulin g	C 902	17	73.9	462	22	AAK88726	Human digestive sy
C 830	17	73.9	405	22	AAK98075	Human neurogulin g	903	17	73.9	462	22	AAK31760	Human liver associ
C 831	17	73.9	405	22	AAI19810	Human breast cancer	904	17	73.9	462	24	ABN90115	Human polynucleoti
832	17	73.9	405	23	ABV17264	Human prostate exp	905	17	73.9	463	22	AAI92921	Human polynucleoti
833	17	73.9	405	24	ABN65098	Human cancer relat	C 906	17	73.9	465	22	AAK66120	Novel human polynu
834	17	73.9	406	22	AAI93108	Human polynucleoti	907	17	73.9	466	23	ABV54356	Human prostate exp
C 835	17	73.9	407	23	ABV10376	Human prostate exp	908	17	73.9	467	23	ABV05433	Human prostate exp
C 836	17	73.9	408	24	ABN2527	Human cancer relat	C 909	17	73.9	471	23	ABV50430	Human prostate exp
C 837	17	73.9	408	24	ABL69276	Prostate cancer re	910	17	73.9	471	24	ABL77318	Human ovarian canc
C 838	17	73.9	411	22	AAI92812	Human polynucleoti	911	17	73.9	474	23	ABV35024	Human prostate exp
839	17	73.9	411	22	AAK58425	Human immune/haema	912	17	73.9	474	23	ABV43872	Human prostate exp
840	17	73.9	411	22	AAK72730	Human immune/haema	C 913	17	73.9	475	22	AAH06073	Human cDNA clone (
841	17	73.9	411	22	AAK72731	Human immune/haema	C 914	17	73.9	475	22	ABV03691	Human prostate exp
842	17	73.9	413	23	ABV27839	Human prostate exp	915	17	73.9	479	21	AAH31036	Human colon cancer
C 843	17	73.9	418	22	AAK84692	Human polynucleoti	C 916	17	73.9	479	23	ABV20073	Human prostate exp
844	17	73.9	419	22	AAK83978	Human immune/haema	917	17	73.9	483	22	ABA07465	Human prostate exp
C 845	17	73.9	419	23	ABV13935	Human prostate exp	918	17	73.9	483	22	AAI00081	Human reproductive
846	17	73.9	419	23	ABV31245	Human prostate exp	919	17	73.9	486	22	AAK98597	Human ovarian canc
847	17	73.9	420	14	AAQ59417	Human brain Expres	920	17	73.9	486	22	AAK98603	Human ovarian canc
C 848	17	73.9	420	22	AAK18266	Human breast cancer	921	17	73.9	488	22	AAH50757	Human tumour assoc
849	17	73.9	421	23	ABV16484	Human prostate exp	C 922	17	73.9	488	22	AAH13146	Human cDNA clone (
C 850	17	73.9	423	23	ABV50907	Human prostate exp	923	17	73.9	490	23	ABV47336	Human prostate exp
C 851	17	73.9	424	20	AAK56588	Human R87078 DNA f	924	17	73.9	492	23	ABV18599	Human prostate exp
852	17	73.9	424	22	AAK77756	Human immune/haema	925	17	73.9	492	23	ABV57477	Human prostate exp
853	17	73.9	424	22	AAK77759	Human immune/haema	926	17	73.9	494	22	AAI14931	Human breast cancer
C 854	17	73.9	424	22	AAK80712	Human immune/haema	927	17	73.9	497	23	ABV47221	Human prostate exp
855	17	73.9	425	22	AAI92310	Human polynucleoti	928	17	73.9	499	24	ABN63949	Human cancer relat
856	17	73.9	425	22	AAK67972	Human immune/haema	929	17	73.9	499	24	ABN65076	Human cancer relat
857	17	73.9	425	22	AAK77758	Human immune/haema	C 930	17	73.9	500	22	AAK60873	Human immune/haema
C 858	17	73.9	426	24	ABL81527	Human ovarian canc	931	17	73.9	501	24	ABN62125	Human cancer relat
859	17	73.9	428	22	AAI07285	Human reproductive	932	17	73.9	504	23	ABV46282	Human prostate exp
860	17	73.9	428	23	ABL98831	Human testicular a	C 933	17	73.9	506	22	AAH10348	Human cDNA clone (
861	17	73.9	429	23	ABV13913	Human prostate exp	C 934	17	73.9	507	22	AAK65942	Human immune/haema
862	17	73.9	433	23	ABV31633	Human prostate exp	C 935	17	73.9	507	22	AAK65943	Human immune/haema
863	17	73.9	433	23	ABV40215	Human prostate exp	936	17	73.9	507	23	ABV59162	Human prostate exp
864	17	73.9	433	23	ABV40601	Human prostate exp	937	17	73.9	508	24	ABN64087	Human cancer relat
865	17	73.9	433	24	ABL82737	Human ovarian canc	938	17	73.9	509	22	AAI87035	Human polynucleoti
C 866	17	73.9	434	22	AAI08822	Human breast cancer	939	17	73.9	509	23	ABV35680	Human prostate exp
867	17	73.9	434	24	ABN60782	Human cancer relat	940	17	73.9	509	23	ABV44485	Human prostate exp
C 868	17	73.9	436	21	AAC30648	Human secreted pro	941	17	73.9	509	24	ABN65466	Human cancer relat
C 869	17	73.9	439	23	ABV33986	Human prostate exp	942	17	73.9	511	23	ABV50613	Human prostate exp
C 870	17	73.9	439	23	ABV42853	Human prostate exp	943	17	73.9	512	22	AAI12079	Human breast cancer
871	17	73.9	440	22	AAI87406	Human polynucleoti	C 944	17	73.9	513	22	AAK78783	Human immune/haema
872	17	73.9	440	23	ABV04744	Human prostate exp	945	17	73.9	514	22	AAK78998	Human immune/haema
C 873	17	73.9	441	22	AAK74903	Human immune/haema	C 946	17	73.9	514	22	AAH09857	Human cDNA clone (
C 874	17	73.9	442	21	AAC14949	Human secreted pro	947	17	73.9	514	24	ABN63007	Human cancer relat
875	17	73.9	442	24	ABL80544	Human ovarian canc	C 948	17	73.9	518	23	ABV12860	Human prostate exp
C 876	17	73.9	443	22	AAI90641	Human polynucleoti	949	17	73.9	524	24	ABN61736	Human cancer relat
C 877	17	73.9	443	22	AAK70807	Human immune/haema	950	17	73.9	526	22	AAK78822	Human immune/haema
C 878	17	73.9	444	23	ABV01207	Human prostate exp	C 951	17	73.9	526	22	AAH12261	Human cDNA clone (
C 879	17	73.9	444	23	ABV17427	Human prostate exp	952	17	73.9	527	24	ABN64882	Human cancer relat
C 880	17	73.9	445	24	ABL86841	Human ovarian canc	C 953	17	73.9	530	22	AAH12591	Human cDNA clone (
881	17	73.9	447	22	ABA16120	Human nervous syst	C 954	17	73.9	531	22	AAH09176	Human cDNA clone (
C 882	17	73.9	447	22	ABA20765	Human nervous syst	955	17	73.9	531	24	ABN60671	Human cancer relat
883	17	73.9	447	22	AAK59455	Human immune/haema	C 956	17	73.9	533	24	ABN63875	Human cancer relat
C 884	17	73.9	448	22	AAH92630	Human inflammatory	C 957	17	73.9	537	23	ABV53454	Human prostate exp
885	17	73.9	449	23	ABV47059	Human prostate exp	C 958	17	73.9	539	22	AAH13209	Human cDNA clone (

c 959 17 73.9 539 22 AAH13377 Human CDNA clone (
 c 960 17 73.9 540 22 AAH11668 Human CDNA clone (
 c 961 17 73.9 540 22 AAH13348 Human CDNA clone (
 c 962 17 73.9 541 22 AAH10011 Human CDNA clone (
 c 963 17 73.9 543 22 AAH11477 Human CDNA clone (
 c 964 17 73.9 548 22 AAH09840 Human CDNA clone (
 c 965 17 73.9 549 22 AAH11757 Human CDNA clone (
 c 966 17 73.9 551 22 AAH08023 Human breast cancer
 c 967 17 73.9 554 22 AAH13592 Human CDNA clone (
 c 968 17 73.9 554 22 ABNG2717 Human cancer relat
 c 969 17 73.9 554 22 ABNG2717 EST clone CW1682.
 c 970 17 73.9 555 20 AAV90098 Human prostate exp
 c 971 17 73.9 557 23 ABV49831 Human prostate exp
 c 972 17 73.9 558 23 ABV52574 Human prostate exp
 c 973 17 73.9 567 22 AAH10209 Human immune/haema
 c 974 17 73.9 569 22 AAK83434 Human immune/haema
 c 975 17 73.9 569 22 AAK82551 Human CDNA 3'-end
 c 976 17 73.9 569 24 ABNG4487 Human cancer relat
 c 977 17 73.9 570 23 ABV59420 Human prostate exp
 c 978 17 73.9 572 23 ABV48382 Human prostate exp
 c 979 17 73.9 572 23 ABV48675 Human prostate exp
 c 980 17 73.9 573 23 ABV20085 Human prostate exp
 c 981 17 73.9 573 23 ABV20321 Human prostate exp
 c 982 17 73.9 573 23 ABV25915 Human prostate exp
 c 983 17 73.9 573 23 ABV26153 Human prostate exp
 c 984 17 73.9 574 23 ABV57915 Human prostate exp
 c 985 17 73.9 574 24 ABNG3280 Human cancer relat
 c 986 17 73.9 575 24 ABNG1271 Human cancer relat
 c 987 17 73.9 577 22 AAH11883 Human CDNA clone (
 c 988 17 73.9 581 22 AAH11274 Human CDNA clone (
 c 989 17 73.9 581 24 ABNG4519 Human immune/haema
 c 990 17 73.9 582 22 AAK75122 Human immune/haema
 c 991 17 73.9 582 23 ABV47242 Human prostate exp
 c 992 17 73.9 583 22 AAK75123 Human immune/haema
 c 993 17 73.9 585 22 AAS45098 cDNA encoding nove
 c 994 17 73.9 589 24 ABNG5211 Human cancer relat
 c 995 17 73.9 591 23 ABV50080 Human prostate exp
 c 996 17 73.9 592 22 ABA12000 Human nervous syst
 c 997 17 73.9 592 22 AAK545286 cDNA encoding nove
 c 998 17 73.9 597 22 AAK58693 Human immune/haema
 c 999 17 73.9 598 22 AAL16037 Human breast cancer
 c1000 17 73.9 598 23 ABV46839 Human prostate exp

## ALIGNMENTS

RESULT 1  
 AAA64507  
 ID AAA64507 standard; DNA; 9048 BP.  
 XX  
 AC AAA64507;  
 XX  
 DT 02-JAN-2001 (first entry)  
 XX  
 DE Nucleotide sequence comprising the human FEZ1 gene.  
 XX  
 KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
 KW tumour proliferation; tubulin; microtubule; protein EPI-gamma;  
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
 KW tumorigenesis; tumour survival; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200050565-A2.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 25-FEB-2000; 2000WO-US04950.  
 XX  
 PR 25-FEB-1999; 99US-0121537.  
 XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human  
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
 PT cancer -

XX Claim 2; Fig 5A; 255pp; English..

CC The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour  
 CC suppressor gene, located at chromosome location 8p22. Decreased or no  
 CC expression of FEZ1 is detected in a variety of cancer cells. Expression  
 CC of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts  
 CC with tubulin, with microtubules, and with protein EPI-gamma.  
 CC Post-translational phosphorylation and dephosphorylation modulates the  
 CC effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are  
 CC useful for inducing cells to proliferate. Compounds which modulate FEZ1  
 CC association with tubulin are useful for alleviating tubulin hyper- or  
 CC hypo- polymerisation disorders, such as those associated with aberrant  
 CC initiation of mitosis, modulation of the initiation and rate of cell  
 CC proliferation and cell growth, modulation of cell shape, cell rigidity,  
 CC cell motility, rate and stage of cellular DNA replication, intracellular  
 CC distribution of organelles, metastatic potential of cell and cellular  
 CC transformation from a non-cancerous to cancerous phenotype. Compounds  
 CC which modulate FEZ1 binding and phosphorylation are also useful for  
 CC alleviating a disorder, such as tumorigenesis, tumour survival, growth  
 CC and metastasis.

XX Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;

Query Match 100.0%; Score 23; DB 21; Length 9048;  
 Best Local Similarity 100.0%; Pred. No. 0.0066;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGTCGCGAGTGT 23  
 |||||  
 Db 4451 CAGCCAGGCATGTCGCGAGTGT 4473

## RESULT 2

AAC15023/C

ID AAC15023 standard; cDNA; 204 BP.

XX AAC15023;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 19098.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX

OS Homo sapiens.

XX EPI033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 19098; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively

CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer

CC cDNA sequences have been obtained, the full 5' UTR is rarely included.

CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be

CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used

CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors.

XX

SQ Sequence 204 BP; 33 A; 50 C; 59 G; 57 T; 5 other;

Query Match 95.7%; Score 22; DB 21; Length 204;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22

Db 124 CAGCCAGGCATGGTGGCAGGTG 103

RESULT 3

ABV39095/C

ID ABV39095 standard; cDNA; 389 BP.

XX

AC ABV39095;

XX

DT 16-SEP-2002 (first entry)

XX

XX Human prostate expression marker cDNA 39086.

XX

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX

OS Homo sapiens.

XX

XX WO200160860-A2.

PN

XX 23-AUG-2001.

XX

XX 20-FEB-2001; 2001WO-US05171.

XX

XX 17-FEB-2000; 2000US-183319P.

PR

XX 16-MAR-2000; 2000US-189862P.

PR

XX 25-MAY-2000; 2000US-207454P.

PR

XX 09-JUN-2000; 2000US-211314P.

PR

XX 18-JUL-2000; 2000US-219007P.

PR

XX 13-DEC-2000; 2000US-255281P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

XX Schlegel R, Endege WO, Monahan JE;

XX

XX WPI; 2001-662795/76.

XX

XX Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -

XX

XX Claim 1; Page 7939; 11750pp; English.

XX

XX The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

PS cancer in a patient;

XX

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX

SQ Sequence 389 BP; 74 A; 99 C; 93 G; 123 T; 0 other;

Query Match 95.7%; Score 22; DB 23; Length 389;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22

Db 221 CAGCCAGGCATGGTGGCAGGTG 200

RESULT 4

ABV11210

ID ABV11210 standard; cDNA; 440 BP.

XX

AC ABV11210;

XX

DT 13-SEP-2002 (first entry)

XX

XX Human prostate expression marker cDNA 11201.

XX

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX

XX Homo sapiens.

XX

XX WO200160860-A2.

PN

XX 23-AUG-2001.

XX

XX 20-FEB-2001; 2001WO-US05171.

XX

XX 17-FEB-2000; 2000US-183319P.

PR

XX 16-MAR-2000; 2000US-189862P.

PR

XX 25-MAY-2000; 2000US-207454P.

PR

XX 09-JUN-2000; 2000US-211314P.

PR

XX 18-JUL-2000; 2000US-219007P.

PR

XX 13-DEC-2000; 2000US-255281P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

XX Schlegel R, Endege WO, Monahan JE;

XX

XX WPI; 2001-662795/76.

XX

XX Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -

XX

XX Claim 1; Page 1818-1819; 11750pp; English.

XX

XX The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX  
SQ Sequence 440 BP; 130 A; 100 C; 90 G; 119 T; 1 other;  
Query Match 95.7%; Score 22; DB 23; Length 440;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCCAGGCATGGTGGCAGGTG 22  
DB 402 CAGCCAGGCATGGTGGCAGGTG 423

RESULT 5  
ABV05712/c  
ID ABV05712 standard; cDNA; 477 BP.  
XX  
AC ABV05712;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 5703.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 954; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX  
SQ Sequence 477 BP; 93 A; 119 C; 111 G; 153 T; 1 other;  
Query Match 95.7%; Score 22; DB 23; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCCAGGCATGGTGGCAGGTG 22  
DB 193 CAGCCAGGCATGGTGGCAGGTG 172

RESULT 6  
ABV32356  
ID ABV32356 standard; cDNA; 478 BP.  
XX  
AC ABV32356;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 32347.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 6909; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX  
SQ Sequence 478 BP; 141 A; 112 C; 102 G; 122 T; 1 other;  
Query Match 95.7%; Score 22; DB 23; Length 478;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22  
 ID ABV41286  
 Db 440 CAGCCAGGCATGGTGGCAGGTG 461

RESULT 7  
 ABV41286  
 ID ABV41286 standard; cDNA; 478 BP.  
 XX  
 AC ABV41286;  
 XX  
 DT 16-SEP-2002 (first entry)  
 DE Human prostate expression marker cDNA 41277.  
 XX  
 OS Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 XX pharmacogenomic marker; gene; ss.  
 XX Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 8302; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 SQ Sequence 478 BP; 141 A; 112 C; 102 G; 122 T; 1 other;  
 Query Match 95.7%; Score 22; DB 23; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22  
 ID ABV41286  
 Db 440 CAGCCAGGCATGGTGGCAGGTG 461

RESULT 8  
 ABV15013/c  
 ID ABV15013 standard; cDNA; 495 BP.  
 XX  
 AC ABV15013;  
 XX  
 DT 13-SEP-2002 (first entry)  
 DE Human prostate expression marker cDNA 15004.  
 XX  
 OS Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 XX pharmacogenomic marker; gene; ss.  
 XX Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 2518; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 SQ Sequence 495 BP; 97 A; 117 C; 109 G; 172 T; 0 other;  
 Query Match 95.7%; Score 22; DB 23; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22  
 Db 177 CAGCCAGGCATGGTGGCAGGTG 156

RESULT 9  
 ABV32243  
 ID ABV32243 standard; cDNA; 506 BP.  
 XX  
 AC ABV32243;  
 XX

```
DT 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 32234.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 6890; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 506 BP; 158 A; 119 C; 112 G; 117 T; 0 other;
SQ
Query Match 95.7%; Score 22; DB 23; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGGTGGCAGGTG 22
|||||
DB 442 CAGCCAGGCATGGTGGCAGGTG 463

RESULT 10
ABV05844/c
ID ABV05844 standard; cDNA; 521 BP.
XX
XX ABV05844;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 5835.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 6890; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 521 BP; 104 A; 118 C; 108 G; 158 T; 33 other;
SQ
Query Match 95.7%; Score 22; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCAGGCATGGTGGCAGGTG 22
|||||
DB 222 CAGCCAGGCATGGTGGCAGGTG 201

RESULT 11
ABV21254
ID ABV21254 standard; cDNA; 557 BP.
XX
XX ABV21254;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 21245.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
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XX 20-FEB-2001; 2001WO-US05171.
PF
XX
XX 17-FEB-2000; 2000US-183319P.
PR
XX 16-MAR-2000; 2000US-189862P.
PR
XX 25-MAY-2000; 2000US-207454P.
PR
XX 09-JUN-2000; 2000US-211314P.
PR
XX 18-JUL-2000; 2000US-219007P.
PR
XX 13-DEC-2000; 2000US-255281P.
PR
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
PI
XX
XX WPI; 2001-662795/76.
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3525; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;
SQ
Query Match 95.7%; Score 22; DB 23; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAGCCAGGCATGTTGGCAGGTG 22
Db 410 CAGCCAGGCATGTTGGCAGGTG 431
|||||
RESULT 12
ABV21288
ID ABV21288 standard; cDNA; 557 BP.
XX
XX AC ABV21288;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 21279.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX
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PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
PI
XX
XX WPI; 2001-662795/76.
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3531; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;
SQ
Query Match 95.7%; Score 22; DB 23; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAGCCAGGCATGTTGGCAGGTG 22
Db 410 CAGCCAGGCATGTTGGCAGGTG 431
|||||
RESULT 13
ABV21292
ID ABV21292 standard; cDNA; 557 BP.
XX
XX AC ABV21292;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 21283.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX
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PI Schlegel R, Endege WO, Monahan JE;  
 XX WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 3532; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX  
 SQ Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;  
 Query Match 95.7%; Score 22; DB 23; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAGCCAGGCATGGTGGCAGGTG 22  
 Db 410 CAGCCAGGCATGGTGGCAGGTG 431  
 RESULT 14  
 ABV23638  
 ID ABV23638 standard; cDNA; 557 BP.  
 XX  
 AC ABV23638;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 23629.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 3532; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX  
 SQ Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;  
 Query Match 95.7%; Score 22; DB 23; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAGCCAGGCATGGTGGCAGGTG 22  
 Db 410 CAGCCAGGCATGGTGGCAGGTG 431  
 RESULT 15  
 ABV23698  
 ID ABV23698 standard; cDNA; 557 BP.  
 XX  
 AC ABV23698;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 23689.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 4345; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 4332; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
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 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX  
 SQ Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;  
 Query Match 95.7%; Score 22; DB 23; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAGCCAGGCATGGTGGCAGGTG 22  
 Db 410 CAGCCAGGCATGGTGGCAGGTG 431  
 RESULT 15  
 ABV23698  
 ID ABV23698 standard; cDNA; 557 BP.  
 XX  
 AC ABV23698;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 23689.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 4345; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:  
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CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 557 BP; 157 A; 125 C; 129 G; 140 T; 6 other;  
  
Query Match 95.7%; Score 22; DB 23; Length 557;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CAGCCAGGCATGGTGGCAGGTG 22  
|||||  
Db 410 CAGCCAGGCATGGTGGCAGGTG 431

Search completed: June 16, 2003, 20:03:08  
Job time : 26.0604 secs



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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 0.900335 Seconds  
(without alignments)  
7834.381 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_4451\_4473  
Perfect score: 23  
Sequence: 1 cagccaggcatggtgcaggtgt 23

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 1533381 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued patents\_NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	91.3	59065	4	US-09-813-817-3
2	21	91.3	59065	4	US-09-978-197-3
3	21	91.3	70000	4	US-09-851-896-3
C 4	21	91.3	81001	4	US-09-750-580-1
C 5	21	91.3	84495	4	US-09-797-906-3
C 6	20	87.0	2950	5	PCT-US93-08386-7
C 7	20	87.0	2968	5	PCT-US93-08386-1
8	19	82.6	443	4	US-09-385-982-28
9	19	82.6	3807	4	US-08-482-918-43
10	19	82.6	3807	4	US-08-224-681-43
11	19	82.6	3807	4	US-08-336-728A-43
12	19	82.6	5864	4	US-08-482-918-47
13	19	82.6	5864	4	US-08-224-681-47
14	19	82.6	5864	4	US-08-336-728A-47
C 15	19	82.6	5917	4	US-09-780-175-17
16	19	82.6	6235	4	US-09-305-384-5
17	19	82.6	6679	4	US-09-305-384-1
18	19	82.6	10684	3	US-08-618-100B-3
19	19	82.6	12571	4	US-09-810-347-3
20	19	82.6	62804	4	US-09-800-960-3
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22	19	82.6	112132	4	US-09-741-150-3
23	18	78.3	2598	4	US-09-026-033-18
24	18	78.3	3441	4	US-09-026-033-17
25	18	78.3	6987	4	US-09-026-033-3
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28	18	78.3	8342	5	PCT-US94-04496-63
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30	18	78.3	8392	3	US-08-465-713-6
31	18	78.3	8392	5	PCT-US93-05857-6
C 32	18	78.3	36741	4	US-09-301-665-3
C 33	18	78.3	38584	4	US-09-734-673-3
C 34	18	78.3	162450	4	US-09-345-882-1
35	18	78.3	246240	2	US-08-724-394A-20
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38	17	73.9	646	4	US-09-385-982-314
C 39	17	73.9	811	4	US-09-404-879A-55
40	17	73.9	1001	4	US-09-641-638-312
41	17	73.9	2125	4	US-09-305-639-6
C 42	17	73.9	2394	4	US-09-414-010-3
43	17	73.9	2529	3	US-08-461-607-1
44	17	73.9	2529	4	US-09-363-600-1
45	17	73.9	2813	4	US-09-689-255C-3
46	17	73.9	3663	4	US-09-499-884-11
47	17	73.9	4358	3	US-08-461-607-3
48	17	73.9	4358	4	US-09-363-600-3
49	17	73.9	4773	3	US-08-884-324-9
50	17	73.9	4853	4	US-08-881-450A-22
51	17	73.9	5037	4	US-09-705-299-13
52	17	73.9	5363	3	US-08-461-607-4
53	17	73.9	5363	3	US-08-461-607-6
54	17	73.9	5363	3	US-08-461-607-8
55	17	73.9	5363	4	US-09-363-600-4
56	17	73.9	5363	4	US-09-363-600-6
57	17	73.9	5363	4	US-09-363-600-8
58	17	73.9	6038	4	US-09-305-639-4
59	17	73.9	7622	4	US-09-305-639-1
C 60	17	73.9	7720	3	US-09-318-448-5
C 61	17	73.9	8835	3	US-08-884-324-10
62	17	73.9	11464	3	US-08-884-324-13
63	17	73.9	11613	1	US-08-484-044-10
64	17	73.9	11811	4	US-09-078-294-7
C 65	17	73.9	14581	4	US-08-520-373D-4
C 66	17	73.9	14636	4	US-09-173-914-6
67	17	73.9	14796	4	US-08-975-080-35
C 68	17	73.9	14796	4	US-08-975-080-35
C 69	17	73.9	14796	4	US-09-630-706-10
C 70	17	73.9	14796	4	US-09-630-706-10
71	17	73.9	14796	4	US-09-496-694B-3
C 72	17	73.9	14796	4	US-09-496-694B-3
73	17	73.9	15297	4	US-09-817-180-3
C 74	17	73.9	15297	4	US-09-817-180-3
C 75	17	73.9	15328	2	US-08-888-497-33
C 76	17	73.9	15328	4	US-09-362-230-33
C 77	17	73.9	15328	5	PCT-US94-07926-33
78	17	73.9	15977	4	US-09-608-285A-59
C 79	17	73.9	18596	4	US-09-318-448-11
C 80	17	73.9	19011	1	US-08-310-356-36
C 81	17	73.9	19557	5	PCT-US92-06300-1
C 82	17	73.9	22481	4	US-08-367-841A-43
C 83	17	73.9	22481	5	PCT-US95-07201-43
C 84	17	73.9	22484	3	US-09-875-223-2
C 85	17	73.9	22484	3	US-08-884-324-14
C 86	17	73.9	28994	3	US-08-884-324-14
C 87	17	73.9	31571	1	US-08-323-448B-1
C 88	17	73.9	36159	4	US-09-749-588-3
C 89	17	73.9	43950	4	US-09-735-934A-3
90	17	73.9	45546	4	US-09-146-053-6
C 91	17	73.9	45716	4	US-08-965-048-5
C 92	17	73.9	45989	4	US-08-965-048-6
C 93	17	73.9	53526	3	US-08-658-136-2
C 94	17	73.9	53577	3	US-08-658-136-1
95	17	73.9	65042	4	US-09-784-316-3
96	17	73.9	72604	4	US-09-268-992-7
97	17	73.9	72604	4	US-09-557-474-7
C 98	17	73.9	87350	3	US-08-781-891-79
C 99	17	73.9	87543	4	US-09-791-211-3
C 100	17	73.9	98844	4	US-09-791-211-10

101	17	73.9	99500	4	US-09-798-096-10	Sequence 10, Appl	174	16	69.6	40352	3	US-08-846-111D-15	Sequence 15, Appl
C 102	17	73.9	99500	4	US-09-798-096-10	Sequence 10, Appl	175	16	69.6	40352	4	US-09-443-077-15	Sequence 15, Appl
C 103	17	73.9	112132	4	US-09-741-150-3	Sequence 3, Appl	176	16	69.6	43950	4	US-09-735-934A-3	Sequence 3, Appl
C 104	16	69.6	20	4	US-09-780-175-26	Sequence 26, Appl	177	16	69.6	45716	4	US-08-965-048-5	Sequence 5, Appl
C 105	16	69.6	434	2	US-08-332-766A-10	Sequence 10, Appl	178	16	69.6	45989	4	US-08-965-048-6	Sequence 6, Appl
C 106	16	69.6	620	4	US-09-385-982-245	Sequence 245, App	179	16	69.6	50000	4	US-09-146-053-3	Sequence 3, Appl
C 107	16	69.6	1001	4	US-09-641-638-113	Sequence 113, App	180	16	69.6	56516	2	US-08-996-306-1	Sequence 1, Appl
C 108	16	69.6	1001	4	US-09-641-638-131	Sequence 131, App	181	16	69.6	56516	4	US-09-338-907-1	Sequence 1, Appl
C 109	16	69.6	1811	1	US-08-848-252-1	Sequence 1, Appl	182	16	69.6	56516	4	US-09-218-207-1	Sequence 1, Appl
C 110	16	69.6	3366	4	US-09-345-650-2	Sequence 2, Appl	183	16	69.6	56520	4	US-09-338-907-179	Sequence 179, App
C 111	16	69.6	3586	4	US-08-847-296B-3	Sequence 3, Appl	184	16	69.6	56520	4	US-09-218-207-179	Sequence 179, App
C 112	16	69.6	3877	2	US-08-599-895-1	Sequence 1, Appl	185	16	69.6	70000	4	US-09-851-896-3	Sequence 3, Appl
C 113	16	69.6	3877	3	US-09-211-230-1	Sequence 1, Appl	186	16	69.6	72604	4	US-09-268-992-7	Sequence 7, Appl
C 114	16	69.6	3877	3	US-09-322-676-1	Sequence 1, Appl	187	16	69.6	72604	4	US-09-857-474-7	Sequence 7, Appl
C 115	16	69.6	3877	4	US-09-466-036A-1	Sequence 1, Appl	188	16	69.6	84435	4	US-09-797-906-3	Sequence 3, Appl
C 116	16	69.6	4342	4	US-09-338-907-107	Sequence 107, App	189	16	69.6	152331	3	US-09-128-155-16	Sequence 16, Appl
C 117	16	69.6	4342	4	US-09-218-207-107	Sequence 107, App	190	16	69.6	168575	4	US-09-426-290-1	Sequence 1, Appl
C 118	16	69.6	4582	4	US-09-338-907-118	Sequence 118, App	191	16	69.6	168575	4	US-09-676-610B-24	Sequence 24, Appl
C 119	16	69.6	4582	4	US-09-218-207-118	Sequence 118, App	192	16	69.6	176373	3	US-09-128-155-17	Sequence 17, Appl
C 120	16	69.6	4686	4	US-09-338-907-117	Sequence 117, App	193	15	65.2	34	1	US-08-644-664B-20	Sequence 20, Appl
C 121	16	69.6	4686	4	US-09-218-207-117	Sequence 117, App	194	15	65.2	34	2	US-08-761-277A-20	Sequence 20, Appl
C 122	16	69.6	4875	4	US-09-338-907-114	Sequence 114, App	195	15	65.2	239	2	US-08-687-080-93	Sequence 93, Appl
C 123	16	69.6	4875	4	US-09-218-207-114	Sequence 114, App	196	15	65.2	330	4	US-09-078-294-24	Sequence 24, Appl
C 124	16	69.6	4958	4	US-09-338-907-116	Sequence 116, App	197	15	65.2	364	4	US-09-222-575-167	Sequence 167, App
C 125	16	69.6	4958	4	US-09-218-207-116	Sequence 116, App	198	15	65.2	470	2	US-08-967-101-77	Sequence 77, Appl
C 126	16	69.6	4986	4	US-09-338-907-121	Sequence 121, App	199	15	65.2	470	2	US-08-592-541-77	Sequence 77, Appl
C 127	16	69.6	4986	4	US-09-218-207-121	Sequence 121, App	200	15	65.2	470	3	US-09-124-698-77	Sequence 77, Appl
C 128	16	69.6	5020	4	US-09-338-907-120	Sequence 120, App	201	15	65.2	470	4	US-09-127-480-77	Sequence 77, Appl
C 129	16	69.6	5020	4	US-09-218-207-120	Sequence 120, App	202	15	65.2	470	4	US-08-496-841C-77	Sequence 77, Appl
C 130	16	69.6	5044	4	US-09-338-907-115	Sequence 115, App	203	15	65.2	470	4	US-09-124-523-77	Sequence 77, Appl
C 131	16	69.6	5044	4	US-09-218-207-115	Sequence 115, App	204	15	65.2	483	2	US-08-475-844-14	Sequence 14, Appl
C 132	16	69.6	5057	4	US-09-338-907-123	Sequence 123, App	205	15	65.2	483	5	PCT-US95-08429-14	Sequence 14, Appl
C 133	16	69.6	5057	4	US-09-218-207-123	Sequence 123, App	206	15	65.2	500	2	US-08-967-101-57	Sequence 57, Appl
C 134	16	69.6	5100	4	US-09-338-907-122	Sequence 122, App	207	15	65.2	500	2	US-08-967-101-90	Sequence 90, Appl
C 135	16	69.6	5100	4	US-09-218-207-122	Sequence 122, App	208	15	65.2	500	2	US-08-592-541-57	Sequence 57, Appl
C 136	16	69.6	5148	4	US-09-338-907-112	Sequence 112, App	209	15	65.2	500	3	US-08-592-541-90	Sequence 90, Appl
C 137	16	69.6	5148	4	US-09-218-207-112	Sequence 112, App	210	15	65.2	500	3	US-09-124-698-57	Sequence 57, Appl
C 138	16	69.6	5227	2	US-08-996-306-3	Sequence 3, Appl	211	15	65.2	500	3	US-09-124-698-90	Sequence 90, Appl
C 139	16	69.6	5234	4	US-09-338-907-113	Sequence 113, App	212	15	65.2	500	4	US-09-127-480-57	Sequence 57, Appl
C 140	16	69.6	5234	4	US-09-218-207-113	Sequence 113, App	213	15	65.2	500	4	US-09-127-480-90	Sequence 90, Appl
C 141	16	69.6	5245	4	US-09-338-907-3	Sequence 3, Appl	214	15	65.2	500	4	US-08-496-841C-57	Sequence 57, Appl
C 142	16	69.6	5245	4	US-09-218-207-3	Sequence 3, Appl	215	15	65.2	500	4	US-08-496-841C-90	Sequence 90, Appl
C 143	16	69.6	5250	4	US-09-338-907-69	Sequence 69, Appl	216	15	65.2	500	4	US-09-124-523-57	Sequence 57, Appl
C 144	16	69.6	5250	4	US-09-218-207-69	Sequence 69, Appl	217	15	65.2	500	4	US-09-124-523-90	Sequence 90, Appl
C 145	16	69.6	5290	4	US-09-338-907-119	Sequence 119, App	218	15	65.2	565	4	US-09-328-111-267	Sequence 267, App
C 146	16	69.6	5290	4	US-09-218-207-119	Sequence 119, App	219	15	65.2	615	4	US-09-385-982-528	Sequence 528, App
C 147	16	69.6	5326	4	US-09-338-907-124	Sequence 124, App	220	15	65.2	668	4	US-09-347-114A-93	Sequence 93, Appl
C 148	16	69.6	5326	4	US-09-218-207-124	Sequence 124, App	221	15	65.2	1000	4	US-09-018-584A-30	Sequence 30, Appl
C 149	16	69.6	6232	4	US-08-456-200B-11	Sequence 11, Appl	222	15	65.2	1000	4	US-09-018-584A-31	Sequence 31, Appl
C 150	16	69.6	6330	4	US-09-880-427-2	Sequence 2, Appl	223	15	65.2	1320	1	US-08-599-252-84	Sequence 84, Appl
C 151	16	69.6	6330	4	US-09-306-538B-2	Sequence 2, Appl	224	15	65.2	1320	1	US-08-436-074-57	Sequence 57, Appl
C 152	16	69.6	6769	1	US-08-480-784-20	Sequence 20, Appl	225	15	65.2	1320	5	PCT-US96-06352-84	Sequence 84, Appl
C 153	16	69.6	6769	1	US-08-483-553-20	Sequence 20, Appl	226	15	65.2	1320	5	PCT-US96-06583-84	Sequence 84, Appl
C 154	16	69.6	6769	1	US-08-487-002-20	Sequence 20, Appl	227	15	65.2	1630	4	US-09-175-928-17	Sequence 17, Appl
C 155	16	69.6	6769	1	US-08-483-554B-20	Sequence 20, Appl	228	15	65.2	1763	4	US-09-449-437A-3	Sequence 3, Appl
C 156	16	69.6	6769	1	US-08-488-011B-20	Sequence 20, Appl	229	15	65.2	2133	3	US-08-808-032-1	Sequence 1, Appl
C 157	16	69.6	6769	4	US-08-850-727-20	Sequence 20, Appl	230	15	65.2	2309	4	US-09-449-437A-5	Sequence 5, Appl
C 158	16	69.6	6769	5	PCT-US95-10202-20	Sequence 20, Appl	231	15	65.2	2309	4	US-09-195-106-1	Sequence 1, Appl
C 159	16	69.6	6769	5	PCT-US95-10203-20	Sequence 20, Appl	232	15	65.2	2713	2	US-08-916-901-6	Sequence 6, Appl
C 160	16	69.6	6769	5	PCT-US95-10220-20	Sequence 20, Appl	233	15	65.2	2713	2	US-09-154-602-6	Sequence 6, Appl
C 161	16	69.6	8353	3	US-08-611-587-1	Sequence 1, Appl	234	15	65.2	2854	2	US-08-724-394A-17	Sequence 17, Appl
C 162	16	69.6	10079	2	US-08-476-866-20	Sequence 20, Appl	235	15	65.2	3336	4	US-09-026-033-1	Sequence 1, Appl
C 163	16	69.6	14581	4	US-08-520-373D-4	Sequence 4, Appl	236	15	65.2	3336	4	US-08-026-033-2	Sequence 2, Appl
C 164	16	69.6	15602	4	US-09-844-634-17	Sequence 17, Appl	237	15	65.2	3373	1	US-08-273-411-2	Sequence 2, Appl
C 165	16	69.6	17327	1	US-07-906-871-15	Sequence 15, Appl	238	15	65.2	3507	1	US-08-832-883-67	Sequence 67, Appl
C 166	16	69.6	22481	4	US-08-367-841A-43	Sequence 43, Appl	239	15	65.2	3507	2	US-08-832-877-67	Sequence 67, Appl
C 167	16	69.6	22481	5	PCT-US95-07201-43	Sequence 43, Appl	240	15	65.2	3621	2	US-09-019-201A-1	Sequence 1, Appl
C 168	16	69.6	22484	4	US-09-875-223-2	Sequence 2, Appl	241	15	65.2	4157	2	US-08-162-146-2	Sequence 2, Appl
C 169	16	69.6	28001	4	US-09-819-993-3	Sequence 3, Appl	242	15	65.2	4157	2	US-09-314-127-2	Sequence 2, Appl
C 170	16	69.6	28629	4	US-09-729-995-3	Sequence 3, Appl	243	15	65.2	4326	2	US-08-852-807-12	Sequence 12, Appl
C 171	16	69.6	32042	4	US-09-245-281-44	Sequence 44, Appl	244	15	65.2	8174	1	US-07-914-281-5	Sequence 5, Appl
C 172	16	69.6	36651	4	US-09-738-894A-3	Sequence 3, Appl	245	15	65.2	8174	1	US-08-393-246-5	Sequence 5, Appl
C 173	16	69.6	38844	4	US-09-734-675-3	Sequence 3, Appl	246	15	65.2	8174	1	US-08-525-058A-5	Sequence 5, Appl

c 247	15	65.2	8174	2	US-08-696-731-5	Sequence 5, Appli	320	14	60.9	2561	4	US-09-270-542-101	Sequence 101, App
c 248	15	65.2	8174	4	US-09-042-531-5	Sequence 5, Appli	321	14	60.9	2561	4	US-09-270-542-119	Sequence 119, App
c 249	15	65.2	8174	5	PCT-US91-00899-3	Sequence 3, Appli	322	14	60.9	2886	2	US-08-687-080-55	Sequence 55, Appl
c 250	15	65.2	8453	4	US-09-167-681-45	Sequence 45, Appl	323	14	60.9	3035	1	US-08-726-725-2	Sequence 2, Appli
c 251	15	65.2	8835	3	US-08-884-324-10	Sequence 10, Appl	324	14	60.9	3061	2	US-08-692-787-47	Sequence 47, Appl
c 252	15	65.2	9734	4	US-09-347-114A-80	Sequence 80, Appl	325	14	60.9	3061	4	US-09-097-199-47	Sequence 47, Appl
c 253	15	65.2	12394	4	US-09-488-856A-10	Sequence 10, Appl	326	14	60.9	3715	4	US-09-085-199B-44	Sequence 44, Appl
c 254	15	65.2	12597	4	US-09-705-299-12	Sequence 12, Appl	327	14	60.9	3715	2	US-08-381-691-16	Sequence 16, Appl
c 255	15	65.2	13674	2	US-08-852-807-1	Sequence 1, Appli	328	14	60.9	4015	4	US-08-810-009-4	Sequence 4, Appli
c 256	15	65.2	15652	4	US-09-422-936-60	Sequence 60, Appl	329	14	60.9	4042	4	US-08-406-030A-17	Sequence 17, Appl
c 257	15	65.2	16389	4	US-09-741-154-3	Sequence 3, Appli	330	14	60.9	4084	3	US-08-866-340-1	Sequence 1, Appli
c 258	15	65.2	17041	1	US-08-076-011-1	Sequence 1, Appli	331	14	60.9	4338	4	US-09-360-237-4	Sequence 4, Appli
c 259	15	65.2	20137	4	US-09-262-773-206	Sequence 206, App	332	14	60.9	4460	4	US-09-103-875-4	Sequence 4, Appli
c 260	15	65.2	20138	4	US-09-262-773-9	Sequence 9, Appli	333	14	60.9	4576	1	US-08-832-883-49	Sequence 49, Appl
c 261	15	65.2	20674	4	US-09-641-638-651	Sequence 651, App	334	14	60.9	4576	2	US-08-832-877-49	Sequence 49, Appl
c 262	15	65.2	23071	4	US-09-262-773-210	Sequence 210, App	335	14	60.9	4586	1	US-08-832-883-53	Sequence 53, Appl
c 263	15	65.2	29598	4	US-08-341-587-6	Sequence 6, Appli	336	14	60.9	4586	2	US-08-832-877-53	Sequence 53, Appl
c 264	15	65.2	35100	1	US-08-306-651B-19	Sequence 19, Appl	337	14	60.9	4773	3	US-08-884-324-9	Sequence 9, Appli
c 265	15	65.2	35100	5	PCT-US93-06251-19	Sequence 19, Appl	338	14	60.9	5109	4	US-08-930-055A-2	Sequence 2, Appli
c 266	15	65.2	36651	4	US-09-738-894A-3	Sequence 3, Appli	339	14	60.9	6678	3	US-08-816-617A-1	Sequence 1, Appli
c 267	15	65.2	36741	4	US-09-301-665-3	Sequence 3, Appli	340	14	60.9	8396	4	US-09-328-174A-1	Sequence 1, Appli
c 268	15	65.2	38564	4	US-09-734-673-3	Sequence 3, Appli	341	14	60.9	8409	4	US-09-167-681-37	Sequence 37, Appl
c 269	15	65.2	40000	4	US-09-780-049-18	Sequence 18, Appl	342	14	60.9	11454	3	US-08-884-324-13	Sequence 13, Appl
c 270	15	65.2	44453	4	US-09-146-053-5	Sequence 5, Appli	343	14	60.9	12537	4	US-09-705-299-12	Sequence 12, Appl
c 271	15	65.2	56516	2	US-08-996-306-1	Sequence 1, Appli	344	14	60.9	13104	4	US-08-256-799-4	Sequence 4, Appli
c 272	15	65.2	56516	4	US-09-338-907-1	Sequence 1, Appli	345	14	60.9	13104	4	US-08-462-437-4	Sequence 4, Appli
c 273	15	65.2	56516	4	US-09-218-207-1	Sequence 1, Appli	346	14	60.9	16063	4	US-09-801-052-3	Sequence 3, Appli
c 274	15	65.2	56520	4	US-09-338-907-179	Sequence 179, App	347	14	60.9	17327	1	US-07-906-871-15	Sequence 15, Appl
c 275	15	65.2	56520	4	US-09-218-207-179	Sequence 179, App	348	14	60.9	17410	1	US-07-841-646-3	Sequence 3, Appli
c 276	15	65.2	59065	4	US-09-813-817-3	Sequence 3, Appli	349	14	60.9	17410	1	US-08-147-023-3	Sequence 3, Appli
c 277	15	65.2	59065	4	US-09-978-197-3	Sequence 3, Appli	350	14	60.9	17410	2	US-08-447-570-3	Sequence 3, Appli
c 278	15	65.2	80246	4	US-09-078-294-4	Sequence 4, Appli	351	14	60.9	17410	2	US-08-449-700-3	Sequence 3, Appli
c 279	15	65.2	80595	4	US-09-078-294-3	Sequence 3, Appli	352	14	60.9	17410	2	US-08-449-699A-3	Sequence 3, Appli
c 280	15	65.2	81001	4	US-09-750-580-1	Sequence 1, Appli	353	14	60.9	17415	3	US-08-486-343A-1	Sequence 1, Appli
c 281	15	65.2	87350	3	US-08-781-891-79	Sequence 79, Appl	354	14	60.9	17415	5	PCT-US95-07343-1	Sequence 1, Appli
c 282	15	65.2	87350	4	US-09-791-211-10	Sequence 10, Appl	355	14	60.9	17425	4	US-09-511-625B-5	Sequence 5, Appli
c 283	15	65.2	98844	4	US-09-754-350-3	Sequence 3, Appli	357	14	60.9	29629	4	US-09-729-995-3	Sequence 3, Appli
c 284	15	65.2	111282	4	US-09-754-350-3	Sequence 3, Appli	358	14	60.9	48974	4	US-08-920-422-17	Sequence 17, Appl
c 285	15	65.2	111282	4	US-09-128-155-16	Sequence 16, Appl	359	14	60.9	53526	3	US-08-658-136-2	Sequence 2, Appli
c 286	15	65.2	152331	3	US-09-345-882-1	Sequence 1, Appli	360	14	60.9	53577	4	US-08-658-136A-3	Sequence 3, Appli
c 287	15	65.2	162450	4	US-09-446-290-1	Sequence 1, Appli	361	14	60.9	55827	4	US-09-813-133A-3	Sequence 3, Appli
c 288	15	65.2	168575	4	US-09-128-155-17	Sequence 17, Appl	362	14	60.9	80246	4	US-09-078-294-4	Sequence 4, Appli
c 289	15	65.2	176373	3	US-08-724-394A-20	Sequence 20, Appl	363	14	60.9	80595	4	US-09-078-294-3	Sequence 3, Appli
c 290	15	65.2	246240	2	US-08-724-394A-21	Sequence 21, Appl	364	13	56.5	20	1	US-08-384-490-8	Sequence 8, Appli
c 291	15	65.2	246240	2	US-08-724-394A-22	Sequence 22, Appl	365	13	56.5	20	1	US-08-459-383-8	Sequence 8, Appli
c 292	15	65.2	246240	2	US-08-849-764C-8	Sequence 8, Appli	366	13	56.5	38	1	US-08-424-424B-5	Sequence 5, Appli
c 293	14	60.9	39	4	US-08-282-087-8	Sequence 8, Appli	367	13	56.5	48	1	US-08-468-709B-7	Sequence 7, Appli
c 294	14	60.9	39	4	US-08-463-261B-5	Sequence 5, Appli	368	13	56.5	48	2	US-08-241-664B-7	Sequence 7, Appli
c 295	14	60.9	265	2	US-08-849-701-1	Sequence 1, Appli	369	13	56.5	190	4	US-09-723-473-1	Sequence 1, Appli
c 296	14	60.9	295	4	US-09-172-108-21	Sequence 21, Appl	370	13	56.5	190	4	US-09-517-933-1	Sequence 1, Appli
c 297	14	60.9	312	4	US-09-172-108-7	Sequence 7, Appli	371	13	56.5	190	4	US-09-723-424A-1	Sequence 1, Appli
c 298	14	60.9	312	4	US-09-172-108-7	Sequence 7, Appli	372	13	56.5	190	4	US-09-723-520-1	Sequence 1, Appli
c 299	14	60.9	317	4	US-08-732-139A-10	Sequence 10, Appl	373	13	56.5	282	1	US-08-121-063-6	Sequence 6, Appli
c 300	14	60.9	350	4	US-09-018-584A-14	Sequence 14, Appl	374	13	56.5	282	1	US-08-121-063-3	Sequence 3, Appli
c 301	14	60.9	602	4	US-09-385-982-254	Sequence 254, App	375	13	56.5	363	4	US-09-657-453A-26	Sequence 26, Appl
c 302	14	60.9	626	4	US-08-998-416-121	Sequence 121, App	376	13	56.5	372	4	US-09-018-584A-13	Sequence 13, Appl
c 303	14	60.9	652	4	US-08-998-416-1121	Sequence 1121, App	377	13	56.5	388	1	US-08-121-063-1	Sequence 1, Appli
c 304	14	60.9	720	4	US-08-998-416-901	Sequence 901, App	378	13	56.5	439	1	US-08-121-063-5	Sequence 5, Appli
c 305	14	60.9	819	4	US-09-605-785-571	Sequence 571, App	379	13	56.5	468	3	US-08-665-259-33	Sequence 33, Appl
c 306	14	60.9	850	4	US-09-288-143-26	Sequence 26, Appl	380	13	56.5	468	3	US-08-762-500-33	Sequence 33, Appl
c 307	14	60.9	990	4	US-09-641-638-277	Sequence 277, App	381	13	56.5	505	1	US-08-121-063-4	Sequence 4, Appli
c 308	14	60.9	1000	4	US-09-018-584A-34	Sequence 34, Appl	382	13	56.5	515	1	US-08-375-170-21	Sequence 21, Appl
c 309	14	60.9	1002	4	US-09-641-638-587	Sequence 587, App	383	13	56.5	515	1	US-08-367-968-21	Sequence 21, Appl
c 310	14	60.9	1110	2	US-08-719-758-1	Sequence 1, Appli	384	13	56.5	515	1	US-08-665-484-21	Sequence 21, Appl
c 311	14	60.9	1110	4	US-09-119-827-1	Sequence 1, Appli	385	13	56.5	561	4	US-09-404-879A-50	Sequence 50, Appl
c 312	14	60.9	1110	4	US-09-511-625B-43	Sequence 43, Appl	386	13	56.5	569	4	US-09-449-285A-18	Sequence 18, Appl
c 313	14	60.9	1145	4	US-09-078-294-17	Sequence 17, Appl	387	13	56.5	582	4	US-09-385-982-98	Sequence 98, Appl
c 314	14	60.9	1243	4	US-09-103-875-16	Sequence 16, Appl	388	13	56.5	601	4	US-09-814-951A-12	Sequence 12, Appl
c 315	14	60.9	1820	4	US-09-732-199A-3	Sequence 3, Appli	389	13	56.5	700	4	US-08-998-416-1131	Sequence 1131, Ap
c 316	14	60.9	1838	4	US-09-227-357-32	Sequence 32, Appl	390	13	56.5	727	1	US-08-367-968-27	Sequence 27, Appl
c 317	14	60.9	2336	1	US-08-247-946A-1	Sequence 1, Appli	391	13	56.5	926	1	US-08-665-484-27	Sequence 27, Appl
c 318	14	60.9	2336	5	PCT-US95-06420-1	Sequence 1, Appli	392	13	56.5	926	4	US-08-938-669A-4	Sequence 4, Appli

393	13	56.5	937	4	US-09-484-970B-136	Sequence 136, App	466	13	56.5	17949	4	US-09-087-465-3	Sequence 3, Appli
394	13	56.5	996	1	US-07-975-526-2	Sequence 2, Appli	467	13	56.5	19011	1	US-08-310-356-36	Sequence 36, Appl
395	13	56.5	996	4	US-07-974-409C-424	Sequence 424, App	468	13	56.5	19557	5	PCT-US92-06300-1	Sequence 1, Appli
396	13	56.5	996	5	PCT-US93-15353-38	Sequence 38, Appl	469	13	56.5	24417	2	US-08-846-762-1	Sequence 1, Appli
397	13	56.5	996	5	PCT-US95-15353-40	Sequence 40, Appl	470	13	56.5	28720	4	US-09-341-587-7	Sequence 7, Appli
398	13	56.5	1000	4	US-09-018-584A-33	Sequence 33, Appl	471	13	56.5	35060	3	US-08-814-095-7	Sequence 7, Appli
399	13	56.5	1001	4	US-09-641-638-458	Sequence 458, App	472	13	56.5	40000	4	US-09-780-049-18	Sequence 18, Appl
400	13	56.5	1096	4	US-09-000-127-2	Sequence 2, Appli	473	13	56.5	44453	4	US-09-146-053-5	Sequence 5, Appli
401	13	56.5	1101	4	US-09-134-001C-2665	Sequence 2665, Ap	474	13	56.5	48974	4	US-08-920-422-17	Sequence 17, Appl
402	13	56.5	1224	1	US-08-127-278-3	Sequence 3, Appli	475	13	56.5	50000	4	US-09-146-053-3	Sequence 3, Appli
403	13	56.5	1224	1	US-08-555-860-3	Sequence 3, Appli	476	13	56.5	50000	4	US-09-146-053-4	Sequence 4, Appli
404	13	56.5	1279	1	US-08-146-010A-4	Sequence 4, Appli	477	13	56.5	169998	4	US-09-676-610B-24	Sequence 24, Appl
405	13	56.5	1279	1	US-08-674-168-9	Sequence 9, Appli	478	13	56.5	18	2	US-08-117-952-375	Sequence 375, App
406	13	56.5	1328	1	US-08-592-126-94	Sequence 94, Appl	479	12	52.2	19	3	US-09-135-021-58	Sequence 58, Appl
407	13	56.5	1357	4	US-09-668-680-3	Sequence 3, Appli	480	12	52.2	19	4	US-09-135-020-60	Sequence 60, Appl
408	13	56.5	1445	4	US-09-814-951A-1	Sequence 1, Appli	481	12	52.2	19	4	US-09-135-010A-60	Sequence 60, Appl
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410	13	56.5	1761	4	US-08-481-190-1	Sequence 1, Appli	483	12	52.2	19	4	US-09-597-735-60	Sequence 60, Appl
411	13	56.5	1761	5	PCT-US93-00869-1	Sequence 1, Appli	484	12	52.2	19	4	US-09-444-295-60	Sequence 60, Appl
412	13	56.5	1772	1	US-08-362-706A-1	Sequence 1, Appli	485	12	52.2	19	4	US-09-597-732-60	Sequence 60, Appl
413	13	56.5	1772	4	US-09-549-808-1	Sequence 1, Appli	486	12	52.2	20	4	US-09-210-748A-4	Sequence 4, Appli
414	13	56.5	1974	3	US-08-762-500-78	Sequence 78, Appl	487	12	52.2	21	4	US-09-177-650-33	Sequence 33, Appl
415	13	56.5	2055	3	US-08-872-855-3	Sequence 3, Appli	488	12	52.2	32	4	US-08-482-073-18	Sequence 18, Appl
416	13	56.5	2071	4	US-09-816-088-1	Sequence 1, Appli	489	12	52.2	33	2	US-08-411-607A-9	Sequence 9, Appli
417	13	56.5	2096	5	PCT-US94-08119-9	Sequence 9, Appli	490	12	52.2	39	4	US-09-428-589-3	Sequence 3, Appli
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419	13	56.5	2096	5	PCT-US94-12913A-9	Sequence 9, Appli	492	12	52.2	41	2	US-08-822-830B-9	Sequence 9, Appli
420	13	56.5	2099	1	US-08-094-533B-9	Sequence 9, Appli	493	12	52.2	41	2	US-08-950-660-9	Sequence 9, Appli
421	13	56.5	2099	1	US-08-276-860A-9	Sequence 9, Appli	494	12	52.2	41	4	US-09-026-033-22	Sequence 22, Appl
422	13	56.5	2099	1	US-08-444-393-9	Sequence 9, Appli	495	12	52.2	243	4	US-08-905-223-63	Sequence 63, Appl
423	13	56.5	2099	1	US-08-799-913-9	Sequence 9, Appli	496	12	52.2	276	2	US-08-481-658B-62	Sequence 62, Appl
424	13	56.5	2099	2	US-08-711-893-9	Sequence 9, Appli	497	12	52.2	276	2	US-08-477-504A-62	Sequence 62, Appl
425	13	56.5	2099	2	US-09-150-200-9	Sequence 9, Appli	498	12	52.2	276	2	US-08-486-756A-62	Sequence 62, Appl
426	13	56.5	2099	3	US-09-150-201-9	Sequence 9, Appli	499	12	52.2	276	2	US-08-485-862B-62	Sequence 62, Appl
427	13	56.5	2099	4	US-09-452-370-9	Sequence 9, Appli	500	12	52.2	276	3	US-08-787-739-62	Sequence 62, Appl
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430	13	56.5	2254	3	US-09-239-843A-27	Sequence 27, Appl	503	12	52.2	276	4	US-08-485-049D-62	Sequence 62, Appl
431	13	56.5	2254	3	US-09-088-337B-27	Sequence 27, Appl	504	12	52.2	276	4	US-09-178-115-62	Sequence 62, Appl
432	13	56.5	2254	5	PCT-US93-11153-27	Sequence 27, Appl	505	12	52.2	276	4	US-09-177-776-62	Sequence 62, Appl
433	13	56.5	2507	4	US-09-605-785-332	Sequence 332, App	506	12	52.2	344	3	US-08-925-230-3	Sequence 3, Appli
434	13	56.5	2507	4	US-09-439-313-332	Sequence 332, App	507	12	52.2	344	3	US-08-925-230-4	Sequence 4, Appli
435	13	56.5	2507	4	US-09-352-616A-332	Sequence 332, App	508	12	52.2	388	2	US-08-967-101-68	Sequence 68, Appl
436	13	56.5	2507	4	US-09-232-149A-332	Sequence 332, App	509	12	52.2	388	2	US-08-592-541-68	Sequence 68, Appl
437	13	56.5	2507	4	US-08-931-608A-1	Sequence 1, Appli	510	12	52.2	388	3	US-09-124-698-68	Sequence 68, Appl
438	13	56.5	2520	4	US-08-872-855-1	Sequence 2, Appli	511	12	52.2	388	4	US-09-127-480-68	Sequence 68, Appl
439	13	56.5	2800	3	US-07-821-716-1	Sequence 1, Appli	512	12	52.2	388	4	US-08-496-841C-68	Sequence 68, Appl
440	13	56.5	3011	1	US-09-199-637A-173	Sequence 173, App	513	12	52.2	388	4	US-09-325-932A-11	Sequence 11, Appl
441	13	56.5	3119	4	US-09-931-608A-1	Sequence 1, Appli	514	12	52.2	484	4	US-09-325-932A-11	Sequence 11, Appl
442	13	56.5	3487	4	US-09-412-210-2	Sequence 2, Appli	515	12	52.2	489	2	US-08-967-101-27	Sequence 27, Appl
443	13	56.5	3518	4	US-09-705-299-11	Sequence 11, Appl	516	12	52.2	489	2	US-08-592-541-27	Sequence 27, Appl
444	13	56.5	3609	4	US-08-306-691B-13	Sequence 13, Appl	517	12	52.2	489	3	US-09-124-698-27	Sequence 27, Appl
445	13	56.5	3622	1	PCT-US93-06251-24	Sequence 24, App	518	12	52.2	489	4	US-09-127-480-27	Sequence 27, Appl
446	13	56.5	3622	5	US-08-370-319C-12	Sequence 12, Appl	519	12	52.2	489	4	US-08-496-841C-27	Sequence 27, Appl
447	13	56.5	4129	2	US-09-224-834-12	Sequence 12, Appl	520	12	52.2	489	4	US-09-124-523-27	Sequence 27, Appl
448	13	56.5	4129	4	US-08-340-428B-1	Sequence 1, Appli	521	12	52.2	500	4	US-09-370-838-128	Sequence 128, App
449	13	56.5	5191	1	PCT-US93-07306-1	Sequence 1, Appli	522	12	52.2	516	2	US-08-967-101-55	Sequence 55, Appl
450	13	56.5	5191	3	US-08-757-223-7	Sequence 7, Appli	523	12	52.2	516	2	US-08-924-698-55	Sequence 55, Appl
451	13	56.5	5375	3	US-08-665-259-19	Sequence 19, App	524	12	52.2	516	3	US-09-127-480-55	Sequence 55, Appl
452	13	56.5	6803	3	US-08-762-500-19	Sequence 19, Appl	525	12	52.2	516	4	US-09-127-480-55	Sequence 55, Appl
453	13	56.5	7301	4	US-09-816-088-3	Sequence 3, Appli	526	12	52.2	516	4	US-08-496-841C-55	Sequence 55, Appl
454	13	56.5	7396	4	US-09-328-174A-1	Sequence 1, Appli	527	12	52.2	516	4	US-09-124-523-55	Sequence 55, Appl
455	13	56.5	8409	4	US-09-167-681-37	Sequence 37, Appl	528	12	52.2	525	1	US-08-468-709B-3	Sequence 3, Appli
456	13	56.5	9701	4	US-09-449-218D-18	Sequence 18, Appl	529	12	52.2	525	2	US-08-241-664B-3	Sequence 3, Appli
457	13	56.5	9704	4	US-09-814-951A-3	Sequence 3, Appli	530	12	52.2	525	5	PCT-US93-03938-3	Sequence 3, Appli
458	13	56.5	11531	1	US-08-068-945A-1	Sequence 1, Appli	531	12	52.2	526	1	US-08-686-878A-35	Sequence 35, Appl
459	13	56.5	11531	1	US-08-442-806-1	Sequence 1, Appli	532	12	52.2	526	4	US-09-175-928-35	Sequence 35, Appl
460	13	56.5	11601	2	US-08-232-617A-3	Sequence 3, Appli	533	12	52.2	526	4	US-08-991-789A-15	Sequence 15, Appl
461	13	56.5	11601	2	US-08-232-617A-3	Sequence 3, Appli	534	12	52.2	526	4	US-09-062-451-15	Sequence 15, Appl
462	13	56.5	11673	4	US-09-334-220-3	Sequence 3, Appli	535	12	52.2	526	4	US-09-598-326-15	Sequence 15, Appl
463	13	56.5	11673	4	US-09-078-294-7	Sequence 7, Appli	536	12	52.2	576	4	US-09-385-982-440	Sequence 440, App
464	13	56.5	11811	4	US-09-453-702B-71	Sequence 71, Appl	537	12	52.2	576	2	US-08-334-545-1	Sequence 1, Appli
465	13	56.5	15472	4			538	12	52.2	577	4	US-09-328-111-302	Sequence 302, App



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540	12	52.2	611	4	US-09-328-111-517	Sequence 517, App	C 613	12	52.2	1319	3	US-08-458-731-17	Sequence 17, Appl
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C 542	12	52.2	635	1	US-08-455-633A-35	Sequence 35, Appl	C 615	12	52.2	1360	4	US-09-820-001-1	Sequence 1, Appl
C 543	12	52.2	635	1	US-08-416-336-5	Sequence 5, Appl	C 616	12	52.2	1363	1	US-08-776-088-21	Sequence 21, Appl
C 544	12	52.2	635	2	US-08-456-460C-35	Sequence 35, Appl	C 617	12	52.2	1363	5	PCT-US95-09145A-21	Sequence 21, Appl
C 545	12	52.2	635	5	PCT-US94-08354-35	Sequence 35, Appl	C 618	12	52.2	1371	3	US-08-884-324-11	Sequence 11, Appl
546	12	52.2	649	4	US-09-040-984-59	Sequence 59, Appl	C 619	12	52.2	1383	3	US-09-400-742-7	Sequence 7, Appl
547	12	52.2	649	4	US-09-123-912-59	Sequence 59, Appl	C 620	12	52.2	1383	3	US-08-618-651A-7	Sequence 6, Appl
548	12	52.2	649	4	US-09-643-597-59	Sequence 59, Appl	C 621	12	52.2	1383	4	US-09-215-252-6	Sequence 6, Appl
549	12	52.2	654	4	US-09-288-143-37	Sequence 37, Appl	C 622	12	52.2	1400	1	US-07-930-686-9	Sequence 9, Appl
C 550	12	52.2	668	4	US-09-129-030-31	Sequence 31, Appl	C 623	12	52.2	1400	2	US-08-460-998-9	Sequence 9, Appl
551	12	52.2	697	4	US-09-450-072-14	Sequence 14, Appl	C 624	12	52.2	1400	2	US-08-481-658B-43	Sequence 43, Appl
552	12	52.2	697	4	US-09-351-348-14	Sequence 14, Appl	C 625	12	52.2	1400	2	US-08-477-504A-43	Sequence 43, Appl
C 553	12	52.2	734	4	US-08-896-164-79	Sequence 79, Appl	C 626	12	52.2	1400	2	US-08-486-756A-43	Sequence 43, Appl
C 554	12	52.2	737	4	US-08-469-260A-22	Sequence 22, Appl	C 627	12	52.2	1400	2	US-08-485-862B-43	Sequence 43, Appl
C 555	12	52.2	780	4	US-09-385-982-32	Sequence 32, Appl	C 628	12	52.2	1400	3	US-08-787-739-43	Sequence 43, Appl
C 556	12	52.2	789	4	US-09-280-116-114	Sequence 114, App	C 629	12	52.2	1400	3	US-08-487-077A-43	Sequence 43, Appl
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C 558	12	52.2	823	2	US-08-967-101-11	Sequence 11, Appl	C 631	12	52.2	1400	3	US-08-485-049D-43	Sequence 43, Appl
C 559	12	52.2	823	2	US-08-967-101-159	Sequence 159, App	C 632	12	52.2	1400	4	US-09-178-115-43	Sequence 43, Appl
C 560	12	52.2	823	2	US-08-592-541-11	Sequence 11, Appl	C 633	12	52.2	1400	4	US-09-177-776-43	Sequence 43, Appl
C 561	12	52.2	823	2	US-08-592-541-159	Sequence 159, App	C 634	12	52.2	1419	4	US-08-943-731-214	Sequence 214, App
C 562	12	52.2	823	3	US-08-888-077A-9	Sequence 9, Appl	C 635	12	52.2	1427	6	5194375-3	Patent No. 5194375
C 563	12	52.2	823	3	US-09-124-698-11	Sequence 11, Appl	C 636	12	52.2	1442	2	US-08-454-557C-120	Sequence 120, App
C 564	12	52.2	823	3	US-09-124-698-159	Sequence 159, App	C 637	12	52.2	1442	2	US-08-340-426D-120	Sequence 120, App
C 565	12	52.2	823	3	US-09-127-480-11	Sequence 11, Appl	C 638	12	52.2	1442	2	US-08-450-673C-120	Sequence 120, App
C 566	12	52.2	823	4	US-09-127-480-159	Sequence 159, App	C 639	12	52.2	1479	1	US-08-476-008-68	Sequence 68, Appl
C 567	12	52.2	823	4	US-08-496-841C-11	Sequence 11, Appl	C 640	12	52.2	1479	1	US-08-306-063-68	Sequence 68, Appl
C 568	12	52.2	823	4	US-08-496-841C-159	Sequence 159, App	C 641	12	52.2	1479	1	US-08-833-485-68	Sequence 68, Appl
C 569	12	52.2	823	4	US-09-124-523-11	Sequence 11, Appl	C 642	12	52.2	1479	4	US-09-137-440-68	Sequence 68, Appl
C 570	12	52.2	823	4	US-09-124-523-159	Sequence 159, App	C 643	12	52.2	1482	2	US-08-886-640-5	Sequence 5, Appl
571	12	52.2	834	2	US-08-967-101-113	Sequence 113, App	C 644	12	52.2	1482	4	US-08-884-235-13	Sequence 13, Appl
572	12	52.2	834	2	US-08-592-541-113	Sequence 113, App	C 645	12	52.2	1482	2	US-08-875-972-3	Sequence 3, Appl
573	12	52.2	834	3	US-09-124-698-113	Sequence 113, App	C 646	12	52.2	1489	2	US-08-886-640-4	Sequence 4, Appl
574	12	52.2	834	4	US-09-127-480-113	Sequence 113, App	C 647	12	52.2	1489	2	US-08-884-235-12	Sequence 12, Appl
575	12	52.2	834	4	US-08-496-841C-113	Sequence 113, App	C 648	12	52.2	1493	2	US-08-820-170A-9	Sequence 9, Appl
576	12	52.2	834	4	US-09-124-523-113	Sequence 113, App	C 649	12	52.2	1493	3	US-09-055-699-9	Sequence 9, Appl
C 577	12	52.2	837	1	US-08-832-883-56	Sequence 56, Appl	C 650	12	52.2	1493	4	US-09-273-565-9	Sequence 9, Appl
C 578	12	52.2	837	2	US-08-832-883-56	Sequence 56, Appl	C 651	12	52.2	1493	4	US-09-565-538-9	Sequence 9, Appl
579	12	52.2	849	3	US-08-733-230-5	Sequence 5, Appl	C 652	12	52.2	1493	4	US-09-661-468-9	Sequence 9, Appl
C 580	12	52.2	849	4	US-08-953-326-5	Sequence 5, Appl	C 653	12	52.2	1501	2	US-08-886-640-6	Sequence 6, Appl
C 581	12	52.2	889	1	US-08-832-883-52	Sequence 52, Appl	C 654	12	52.2	1501	4	US-08-884-235-14	Sequence 14, Appl
C 582	12	52.2	889	2	US-08-832-877-52	Sequence 52, Appl	C 655	12	52.2	1553	4	US-09-364-230-31	Sequence 31, Appl
583	12	52.2	923	4	US-09-336-643A-15	Sequence 15, App	C 656	12	52.2	1596	1	US-08-531-601-2	Sequence 2, Appl
584	12	52.2	951	4	US-09-605-785-570	Sequence 570, App	C 657	12	52.2	1596	2	US-08-859-032-2	Sequence 2, Appl
C 585	12	52.2	1000	2	US-08-747-121-20	Sequence 20, App	C 658	12	52.2	1600	3	US-08-602-791-1	Sequence 1, Appl
586	12	52.2	1001	4	US-09-641-638-175	Sequence 175, App	C 659	12	52.2	1614	4	US-09-522-217-7	Sequence 7, Appl
587	12	52.2	1001	4	US-09-641-638-400	Sequence 400, App	C 660	12	52.2	1620	3	US-08-925-230-2	Sequence 2, Appl
C 588	12	52.2	1001	4	US-09-641-638-514	Sequence 514, App	C 661	12	52.2	1631	1	US-08-583-318-4	Sequence 4, Appl
C 589	12	52.2	1039	4	US-09-011-197-2	Sequence 2, Appl	C 662	12	52.2	1659	2	US-08-886-640-1	Sequence 1, Appl
C 590	12	52.2	1045	2	US-09-014-969-6	Sequence 6, Appl	C 663	12	52.2	1659	2	US-08-886-640-2	Sequence 2, Appl
C 591	12	52.2	1062	2	US-08-466-103A-13	Sequence 13, Appl	C 664	12	52.2	1659	2	US-08-884-235-1	Sequence 1, Appl
C 592	12	52.2	1079	1	US-08-454-196-16	Sequence 16, Appl	C 665	12	52.2	1659	4	US-08-884-235-2	Sequence 2, Appl
C 593	12	52.2	1079	3	US-09-064-033-16	Sequence 16, Appl	C 666	12	52.2	1674	6	5194375-1	Patent No. 5194375
594	12	52.2	1080	1	US-08-225-757B-1	Sequence 1, Appl	C 667	12	52.2	1701	1	US-07-863-169A-2	Sequence 2, Appl
C 595	12	52.2	1080	2	US-08-722-050-1	Sequence 1, Appl	C 668	12	52.2	1701	2	US-08-429-964-2	Sequence 2, Appl
C 596	12	52.2	1129	4	US-09-383-586-10	Sequence 10, Appl	C 669	12	52.2	1701	3	US-07-935-087-2	Sequence 2, Appl
C 597	12	52.2	1259	2	US-08-672-814D-12	Sequence 12, Appl	C 670	12	52.2	1701	5	PCT-US93-08062-2	Sequence 2, Appl
C 598	12	52.2	1259	4	US-09-333-696-12	Sequence 12, Appl	C 671	12	52.2	1735	4	US-09-440-936-3	Sequence 3, Appl
599	12	52.2	1277	1	US-08-176-427B-1	Sequence 1, Appl	C 672	12	52.2	1743	3	US-09-221-235-9	Sequence 9, Appl
C 600	12	52.2	1277	2	US-08-356-060A-1	Sequence 1, Appl	C 673	12	52.2	1743	3	US-09-221-928-9	Sequence 9, Appl
601	12	52.2	1277	4	US-08-460-900C-1	Sequence 1, Appl	C 674	12	52.2	1743	3	US-09-221-527-9	Sequence 9, Appl
602	12	52.2	1277	4	US-08-674-509B-1	Sequence 1, Appl	C 675	12	52.2	1743	3	US-09-221-236-9	Sequence 9, Appl
603	12	52.2	1277	4	US-08-954-698-1	Sequence 1, Appl	C 676	12	52.2	1743	3	US-09-221-416-9	Sequence 9, Appl
604	12	52.2	1277	4	US-08-957-874-1	Sequence 1, Appl	C 677	12	52.2	1743	4	US-08-221-245-9	Sequence 9, Appl
C 605	12	52.2	1277	4	US-09-325-256-5	Sequence 5, Appl	C 678	12	52.2	1743	4	US-09-163-115-9	Sequence 9, Appl
C 606	12	52.2	1290	4	US-09-289-349-9	Sequence 9, Appl	C 679	12	52.2	1743	4	US-09-221-528-9	Sequence 9, Appl
607	12	52.2	1295	4	US-09-254-465A-8	Sequence 8, Appl	C 680	12	52.2	1743	4	US-09-593-553-9	Sequence 9, Appl
608	12	52.2	1306	3	US-08-948-705-7	Sequence 7, Appl	C 681	12	52.2	1743	4	US-09-221-237-9	Sequence 9, Appl
C 609	12	52.2	1319	2	US-08-484-993B-17	Sequence 17, Appl	C 682	12	52.2	1746	4	US-09-422-936-58	Sequence 58, Appl
C 610	12	52.2	1319	2	US-08-484-158B-17	Sequence 17, Appl	C 683	12	52.2	1749	4	US-09-450-072-56	Sequence 56, Appl
C 611	12	52.2	1319	2	US-08-484-596A-17	Sequence 17, Appl	C 684	12	52.2	1749	4	US-09-450-072-57	Sequence 57, Appl

685	12	52.2	1749	4	US-09-450-072-58	Sequence 58, Appl	C 758	12	52.2	2765	4	US-08-706-344C-27	Sequence 27, Appl
686	12	52.2	1749	4	US-09-351-348-56	Sequence 56, Appl	C 759	12	52.2	2765	4	US-08-706-344C-29	Sequence 29, Appl
687	12	52.2	1749	4	US-09-351-348-57	Sequence 57, Appl	C 760	12	52.2	2765	4	US-08-706-344C-31	Sequence 31, Appl
688	12	52.2	1749	4	US-09-351-348-58	Sequence 58, Appl	C 761	12	52.2	2772	3	US-09-280-420-1	Sequence 1, Appl
689	12	52.2	1750	3	US-08-670-964-3	Sequence 3, Appl	C 762	12	52.2	2788	4	US-09-221-017B-644	Sequence 644, App
690	12	52.2	1762	3	US-08-670-964-1	Sequence 1, Appl	C 763	12	52.2	2791	2	US-08-967-101-1	Sequence 1, Appl
691	12	52.2	1816	2	US-08-951-148-2	Sequence 2, Appl	C 764	12	52.2	2791	2	US-08-967-101-133	Sequence 133, App
692	12	52.2	1816	2	US-08-165-234-2	Sequence 2, Appl	C 765	12	52.2	2791	2	US-08-592-541-1	Sequence 1, Appl
693	12	52.2	1816	3	US-09-274-570-2	Sequence 2, Appl	C 766	12	52.2	2791	2	US-08-592-541-133	Sequence 133, App
694	12	52.2	1821	4	US-09-522-217-96	Sequence 96, Appl	C 767	12	52.2	2791	3	US-09-124-698-1	Sequence 1, Appl
695	12	52.2	1855	4	US-08-810-009-1	Sequence 1, Appl	C 768	12	52.2	2791	3	US-09-124-698-133	Sequence 133, App
696	12	52.2	1896	1	US-08-605-541B-11	Sequence 11, Appl	C 769	12	52.2	2791	4	US-09-127-480-1	Sequence 1, Appl
697	12	52.2	1914	2	US-08-670-479-24	Sequence 24, Appl	C 770	12	52.2	2791	4	US-09-127-480-133	Sequence 133, App
698	12	52.2	1937	1	US-08-370-193A-10	Sequence 10, Appl	C 771	12	52.2	2791	4	US-08-496-841C-1	Sequence 1, Appl
699	12	52.2	1967	4	US-09-398-395A-23	Sequence 23, Appl	C 772	12	52.2	2791	4	US-09-124-523-1	Sequence 1, Appl
700	12	52.2	1968	4	US-08-937-540-3	Sequence 3, Appl	C 773	12	52.2	2791	4	US-09-124-523-133	Sequence 133, App
701	12	52.2	1997	2	US-08-667-809B-3	Sequence 3, Appl	C 774	12	52.2	2792	4	US-08-496-841C-133	Sequence 133, App
702	12	52.2	1999	4	US-09-167-109-4	Sequence 4, Appl	C 775	12	52.2	2808	3	US-08-870-126-7	Sequence 7, Appl
703	12	52.2	2002	2	US-08-747-121-1	Sequence 1, Appl	C 776	12	52.2	2808	4	US-09-445-247-7	Sequence 4, Appl
704	12	52.2	2002	4	US-08-819-923-1	Sequence 1, Appl	C 777	12	52.2	2821	4	US-09-484-970B-44	Sequence 44, Appl
705	12	52.2	2004	2	US-08-631-814B-1	Sequence 1, Appl	C 778	12	52.2	2857	4	US-08-981-392-4	Sequence 4, Appl
706	12	52.2	2004	3	US-09-188-930-230	Sequence 230, App	C 779	12	52.2	2883	4	US-09-422-936-44	Sequence 44, Appl
707	12	52.2	2099	4	US-08-938-669A-5	Sequence 5, Appl	C 780	12	52.2	2895	4	US-09-422-936-52	Sequence 52, Appl
708	12	52.2	2127	1	US-08-832-883-54	Sequence 54, Appl	C 781	12	52.2	2896	2	US-08-709-923-1	Sequence 1, Appl
709	12	52.2	2127	2	US-08-832-877-54	Sequence 54, Appl	C 782	12	52.2	2900	3	US-09-038-832-1	Sequence 1, Appl
710	12	52.2	2132	4	US-08-552-322-1	Sequence 1, Appl	C 783	12	52.2	2933	4	US-09-262-773-209	Sequence 209, App
711	12	52.2	2162	3	US-08-948-705-5	Sequence 5, Appl	C 784	12	52.2	2935	4	US-09-480-921B-27	Sequence 27, Appl
712	12	52.2	2192	1	US-08-035-392-1	Sequence 1, Appl	C 785	12	52.2	3018	2	US-08-860-150-6	Sequence 6, Appl
713	12	52.2	2192	1	US-08-504-511A-1	Sequence 1, Appl	C 786	12	52.2	3018	3	US-09-338-132-6	Sequence 2, Appl
714	12	52.2	2205	3	US-08-035-392-3	Sequence 3, Appl	C 787	12	52.2	3031	1	US-08-785-241-2	Sequence 2, Appl
715	12	52.2	2205	1	US-08-504-511A-3	Sequence 3, Appl	C 788	12	52.2	3064	4	US-09-600-776-5	Sequence 5, Appl
716	12	52.2	2236	3	US-08-948-705-4	Sequence 4, Appl	C 789	12	52.2	3086	3	US-08-888-077A-3	Sequence 3, Appl
717	12	52.2	2260	2	US-08-788-750-1	Sequence 1, Appl	C 790	12	52.2	3087	2	US-08-967-101-5	Sequence 5, Appl
718	12	52.2	2274	3	US-09-440-936-1	Sequence 1, Appl	C 791	12	52.2	3087	2	US-08-592-541-5	Sequence 5, Appl
719	12	52.2	2289	3	US-08-948-705-8	Sequence 8, Appl	C 792	12	52.2	3087	3	US-09-124-698-5	Sequence 5, Appl
720	12	52.2	2311	3	US-08-712-709-6	Sequence 6, Appl	C 793	12	52.2	3087	4	US-09-127-480-5	Sequence 5, Appl
721	12	52.2	2311	3	US-09-111-444-6	Sequence 6, Appl	C 794	12	52.2	3087	4	US-08-496-841C-5	Sequence 5, Appl
722	12	52.2	2311	4	US-09-541-228-6	Sequence 6, Appl	C 795	12	52.2	3087	4	US-09-124-523-5	Sequence 5, Appl
723	12	52.2	2361	4	US-09-011-197-1	Sequence 1, Appl	C 796	12	52.2	3115	4	US-09-221-017B-849	Sequence 849, App
724	12	52.2	2370	4	US-09-031-295-1	Sequence 1, Appl	C 797	12	52.2	3158	2	US-08-464-517-36	Sequence 36, Appl
725	12	52.2	2377	4	US-09-479-195-1	Sequence 1, Appl	C 798	12	52.2	3158	2	US-08-246-361A-36	Sequence 36, Appl
726	12	52.2	2387	4	US-09-634-957-1	Sequence 1, Appl	C 799	12	52.2	3158	3	US-08-463-772-36	Sequence 36, Appl
727	12	52.2	2387	4	US-09-723-153-1	Sequence 1, Appl	C 800	12	52.2	3214	1	US-08-484-105-17	Sequence 17, Appl
728	12	52.2	2387	4	US-08-723-429-1	Sequence 1, Appl	C 801	12	52.2	3214	1	US-08-484-106-17	Sequence 17, Appl
729	12	52.2	2403	1	US-08-454-720A-41	Sequence 41, Appl	C 802	12	52.2	3216	2	US-08-828-007-1	Sequence 1, Appl
730	12	52.2	2454	3	US-09-221-235-7	Sequence 7, Appl	C 803	12	52.2	3223	1	US-07-980-528-1	Sequence 1, Appl
731	12	52.2	2454	3	US-09-221-928-7	Sequence 7, Appl	C 804	12	52.2	3224	4	US-08-965-729A-2	Sequence 2, Appl
732	12	52.2	2454	3	US-09-221-527-7	Sequence 7, Appl	C 805	12	52.2	3288	1	US-08-208-008C-3	Sequence 3, Appl
733	12	52.2	2454	3	US-09-221-236-7	Sequence 7, Appl	C 806	12	52.2	3321	4	US-08-855-146-1	Sequence 1, Appl
734	12	52.2	2454	3	US-09-221-416-7	Sequence 7, Appl	C 807	12	52.2	3321	4	US-08-855-146-3	Sequence 3, Appl
735	12	52.2	2454	4	US-09-221-245-7	Sequence 7, Appl	C 808	12	52.2	3386	4	US-09-041-886-1	Sequence 1, Appl
736	12	52.2	2454	4	US-08-163-115-7	Sequence 7, Appl	C 809	12	52.2	3748	2	US-08-958-240-1	Sequence 1, Appl
737	12	52.2	2454	4	US-09-221-528-7	Sequence 7, Appl	C 810	12	52.2	3789	1	US-08-454-455-5	Sequence 5, Appl
738	12	52.2	2454	4	US-09-593-553-7	Sequence 7, Appl	C 811	12	52.2	3825	1	US-08-737-597-1	Sequence 1, Appl
739	12	52.2	2454	4	US-09-221-237-7	Sequence 7, Appl	C 812	12	52.2	3825	3	US-08-823-110-2	Sequence 2, Appl
740	12	52.2	2484	4	US-09-276-531-46	Sequence 46, Appl	C 813	12	52.2	3833	3	US-08-604-298-2	Sequence 2, Appl
741	12	52.2	2522	3	US-09-062-416-13	Sequence 13, Appl	C 814	12	52.2	3833	2	US-08-853-659A-26	Sequence 26, Appl
742	12	52.2	2535	3	US-08-422-936-46	Sequence 46, Appl	C 815	12	52.2	4072	4	US-09-272-496-7	Sequence 7, Appl
743	12	52.2	2556	3	US-08-699-103B-9	Sequence 9, Appl	C 816	12	52.2	4104	1	US-07-998-003A-94	Sequence 94, Appl
744	12	52.2	2556	4	US-09-229-059-9	Sequence 9, Appl	C 817	12	52.2	4104	1	US-08-453-274B-94	Sequence 94, Appl
745	12	52.2	2559	2	US-09-070-060-2	Sequence 2, Appl	C 818	12	52.2	4104	1	US-08-453-695A-94	Sequence 94, Appl
746	12	52.2	2559	3	US-09-357-746-2	Sequence 2, Appl	C 819	12	52.2	4104	1	US-08-268-161A-94	Sequence 94, Appl
747	12	52.2	2665	3	US-09-040-005-1	Sequence 1, Appl	C 820	12	52.2	4104	2	US-08-453-702A-94	Sequence 94, Appl
748	12	52.2	2692	4	US-08-981-392-11	Sequence 11, Appl	C 821	12	52.2	4104	2	US-08-453-702A-94	Sequence 94, Appl
749	12	52.2	2724	3	US-08-823-110-5	Sequence 5, Appl	C 822	12	52.2	4104	4	US-09-099-639-94	Sequence 94, Appl
750	12	52.2	2724	3	US-08-604-298-5	Sequence 5, Appl	C 823	12	52.2	4104	5	PCT-US93-12588-94	Sequence 94, Appl
751	12	52.2	2731	3	US-08-699-103B-11	Sequence 11, Appl	C 824	12	52.2	4104	4	PCT-US95-08071-94	Sequence 94, Appl
752	12	52.2	2731	3	US-09-229-059-11	Sequence 11, Appl	C 825	12	52.2	4296	4	US-09-060-410-3	Sequence 3, Appl
753	12	52.2	2764	3	US-08-923-454A-9	Sequence 9, Appl	C 826	12	52.2	4326	2	US-08-852-807-12	Sequence 12, Appl
754	12	52.2	2764	3	US-08-832-867-2	Sequence 2, Appl	C 827	12	52.2	4508	5	PCT-US93-06251-34	Sequence 34, Appl
755	12	52.2	2765	3	US-08-888-077A-1	Sequence 1, Appl	C 828	12	52.2	4533	3	US-08-726-214-5	Sequence 5, Appl
756	12	52.2	2765	4	US-08-706-344C-1	Sequence 1, Appl	C 829	12	52.2	4606	4	US-09-221-017B-282	Sequence 282, App
757	12	52.2	2765	4	US-08-706-344C-3	Sequence 3, Appl	C 830	12	52.2	4635	2	US-08-404-531B-27	Sequence 27, Appl

C 831	12	52.2	4635	3	US-08-476-900A-27	Sequence 27, Appl	C 904	12	52.2	14747	4	US-09-608-285A-42	Sequence 42, Appl
C 832	12	52.2	4635	3	US-08-488-546A-27	Sequence 27, Appl	C 905	12	52.2	15977	4	US-09-608-285A-59	Sequence 59, Appl
C 833	12	52.2	4650	1	US-07-998-003A-102	Sequence 102, App	C 906	12	52.2	16595	4	US-09-146-053-7	Sequence 7, Appl
C 834	12	52.2	4650	1	US-08-453-274B-102	Sequence 102, App	C 907	12	52.2	17710	4	US-08-976-259-70	Sequence 70, Appl
C 835	12	52.2	4650	1	US-08-433-659A-102	Sequence 102, App	C 908	12	52.2	18073	4	US-09-078-294-12	Sequence 12, Appl
C 836	12	52.2	4650	1	US-08-288-161A-102	Sequence 102, App	C 909	12	52.2	19736	4	US-09-740-035-3	Sequence 3, Appl
C 837	12	52.2	4650	2	US-08-453-702A-102	Sequence 102, App	C 910	12	52.2	19736	4	US-09-740-035-3	Sequence 3, Appl
C 838	12	52.2	4650	2	US-09-099-639-102	Sequence 102, App	C 911	12	52.2	20303	1	US-08-370-975B-6	Sequence 6, Appl
C 839	12	52.2	4650	5	PCT-US93-12588-102	Sequence 102, App	C 912	12	52.2	21119	4	US-09-453-702B-111	Sequence 111, App
C 840	12	52.2	4650	5	PCT-US93-08071-102	Sequence 102, App	C 913	12	52.2	22067	4	US-09-820-001-3	Sequence 3, Appl
C 841	12	52.2	4859	4	US-09-453-702B-154	Sequence 154, App	C 914	12	52.2	22846	2	US-08-469-461-3	Sequence 3, Appl
C 842	12	52.2	5110	2	US-08-404-531B-5	Sequence 4, Appl	C 915	12	52.2	22846	3	US-07-890-609-3	Sequence 3, Appl
C 843	12	52.2	5110	2	US-08-404-531B-5	Sequence 4, Appl	C 916	12	52.2	24701	2	US-08-853-659A-2	Sequence 2, Appl
C 844	12	52.2	5110	3	US-08-476-900A-5	Sequence 4, Appl	C 917	12	52.2	24701	2	US-08-853-659A-3	Sequence 3, Appl
C 845	12	52.2	5110	3	US-08-476-900A-5	Sequence 4, Appl	C 918	12	52.2	24701	2	US-08-853-659A-60	Sequence 60, Appl
C 846	12	52.2	5110	3	US-08-488-546A-4	Sequence 4, Appl	C 919	12	52.2	24701	2	US-08-853-659A-61	Sequence 61, Appl
C 847	12	52.2	5110	3	US-08-488-546A-5	Sequence 5, Appl	C 920	12	52.2	26764	1	US-08-370-975B-1	Sequence 1, Appl
C 848	12	52.2	5232	3	US-08-232-971-3	Sequence 3, Appl	C 921	12	52.2	28473	4	US-08-961-527-83	Sequence 83, Appl
C 849	12	52.2	5232	3	US-08-800-929A-3	Sequence 3, Appl	C 922	12	52.2	32042	4	US-09-245-281-44	Sequence 44, Appl
C 850	12	52.2	5232	4	US-09-617-053A-3	Sequence 3, Appl	C 923	12	52.2	32446	4	US-09-103-330-35	Sequence 35, Appl
C 851	12	52.2	5359	2	US-09-070-060-1	Sequence 1, Appl	C 924	12	52.2	35100	1	US-08-306-691B-19	Sequence 19, Appl
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C 853	12	52.2	5375	3	US-08-757-223-7	Sequence 7, Appl	C 926	12	52.2	43795	3	US-08-742-185-101	Sequence 101, App
C 854	12	52.2	5615	4	US-09-302-769-47	Sequence 47, Appl	C 927	12	52.2	45546	4	US-09-146-053-6	Sequence 6, Appl
C 855	12	52.2	6246	4	US-08-943-731-640	Sequence 640, App	C 928	12	52.2	48908	4	US-09-453-702B-137	Sequence 137, App
C 856	12	52.2	6312	1	US-08-531-601-3	Sequence 3, Appl	C 929	12	52.2	55827	4	US-09-813-133A-3	Sequence 3, Appl
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C 898	12	52.2	10898	4	US-09-177-776-5	Sequence 5, Appl	C 971	11	47.8	42	4	US-09-067-615-38	Sequence 38, Appl
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## ALIGNMENTS

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; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3
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Best Local Similarity 100.0%; Pred. No. 0.0072;
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Db 53714 AGCCAGGCATGGTGGCAGGTG 53734
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; Patent No. 6403353
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; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/09/978,197
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
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US-09-978-197-3
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Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: R1S-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
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US-09-851-896-3
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; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2 CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
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PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: US 60/141,032  
PRIOR FILING DATE: 1999-06-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent.pm  
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LENGTH: 81001  
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ORGANISM: Homo sapiens  
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US-09-750-580-1

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; Patent No. 6329188  
; GENERAL INFORMATION:  
; APPLICANT: Zianche YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
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; CURRENT APPLICATION NUMBER: US/09/797,906  
; CURRENT FILING DATE: 2001-03-05  
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; OTHER INFORMATION: n = A,T,C or G  
US-09-797-906-3

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RESULT 6  
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; GENERAL INFORMATION:  
; APPLICANT: Bernardo Nadal-Ginard  
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; TITLE OF INVENTION: TRANSCRIPTION  
; TITLE OF INVENTION: ENHANCING FACTOR 2  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
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; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08386  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/939,898  
; FILING DATE: 04 SEP 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: John W. Freeman  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: .00108/088001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2950

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; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-08386-7

Query Match 87.0%; Score 20; DB 5; Length 2950;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCGATGGTGGCAGG 20  
Db 202 CAGCCAGGCGATGGTGGCAGG 183

RESULT 7  
PCT-US93-08386-1/c  
; Sequence 1, Application PC/TUS9308386  
; GENERAL INFORMATION:  
; APPLICANT: Bernardo Nadal-Ginard  
; TITLE OF INVENTION: MYOCYTE-SPECIFIC  
; TITLE OF INVENTION: TRANSCRIPTION  
; TITLE OF INVENTION: ENHANCING FACTOR 2  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08386  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/939,898  
; FILING DATE: 04 SEP 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: John W. Freeman  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: .00108/088001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2968  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-08386-1

Query Match 87.0%; Score 20; DB 5; Length 2968;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCGATGGTGGCAGG 20  
Db 202 CAGCCAGGCGATGGTGGCAGG 183

RESULT 8  
US-09-385-982-28  
; Sequence 28, Application US/09385982  
; Patent No. 6262334  
; GENERAL INFORMATION:  
; APPLICANT: ENDEGE, WILSON O., ET AL.

;; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
;; FILE OF INVENTION: PRODUCTS: II  
;; FILE REFERENCE: CCNDA-260XX  
;; CURRENT APPLICATION NUMBER: US/09/385,982  
;; CURRENT FILING DATE: 1999-08-30  
;; EARLIER APPLICATION NUMBER: 09/328,111  
;; EARLIER FILING DATE: 1999-06-08  
;; EARLIER APPLICATION NUMBER: 60/117,393  
;; EARLIER FILING DATE: 1999-01-27  
;; EARLIER APPLICATION NUMBER: 60/098,639  
;; EARLIER FILING DATE: 1998-08-31  
;; NUMBER OF SEQ ID NOS: 544  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 28  
;; LENGTH: 443  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(443)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-28

Query Match 82.6%; Score 19; DB 4; Length 443;  
Best Local Similarity 100.0%; Pred. No. 0.099;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGGTGGCAGG 20  
|||||  
Db 242 AGCCAGGCATGGTGGCAGG 260

RESULT 9  
US-08-482-918-43  
; Sequence 43, Application US/08482918  
; Patent No. 6207417  
; GENERAL INFORMATION:  
; APPLICANT: Zsebo, Krisztina M.  
; APPLICANT: Bosselman, Robert A.  
; APPLICANT: Suggs, Sidney V.  
; APPLICANT: Martin, Francis H.  
; TITLE OF INVENTION: Stem Cell Factor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,918  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 01017/33005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3607 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

;; MOLECULE TYPE: protein  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152  
;; LOCATION: ..3307, 3513..3595)  
;; FEATURE:  
;; NAME/KEY: mat\_peptide  
;; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152  
;; LOCATION: ..3307, 3513..3595)  
US-08-482-918-43

Query Match 82.6%; Score 19; DB 4; Length 3807;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCCAGGCATGGTGGCAGG 20  
|||||  
Db 2412 AGCCAGGCATGGTGGCAGG 2430

RESULT 10  
US-09-224-681-43  
; Sequence 43, Application US/09224681  
; Patent No. 6207454  
; GENERAL INFORMATION:  
; APPLICANT: Zsebo, Krisztina M.  
; APPLICANT: Bosselman, Robert A.  
; APPLICANT: Suggs, Sidney V.  
; APPLICANT: Martin, Francis H.  
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene  
; Transfer with Stem Cell Factor (SCF) Polypeptide  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/224,681  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/005,893  
; FILING DATE: 12-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/449,653  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/982,255  
; FILING DATE: 25-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/589,701  
; FILING DATE: 01-OCT-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/573,616  
; FILING DATE: 24-AUG-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/537,198  
; FILING DATE: 11-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/422,383  
; FILING DATE: 16-OCT-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.

```

; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3513..3595)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3513..3595)
; US-09-224-681-43
;
; Query Match 82.6%; Score 19; DB 4; Length 3807;
; Best Local Similarity 100.0%; Pred. No. 0.089;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 AGCCAGGCATGGTGGCAGG 20
; |||||
; DB 2412 AGCCAGGCATGGTGGCAGG 2430
;
; RESULT 11
; US-08-336-728A-43
; Sequence 43, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
;
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3512..3597)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
; LOCATION: ..3307, 3512..3597)
; US-08-336-728A-43
;
; Query Match 82.6%; Score 19; DB 4; Length 3807;
; Best Local Similarity 100.0%; Pred. No. 0.089;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 AGCCAGGCATGGTGGCAGG 20
; |||||
; DB 2412 AGCCAGGCATGGTGGCAGG 2430
;
; RESULT 12
; US-08-482-918-47
; Sequence 47, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5964 base pairs
;
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
; LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,
; LOCATION: 5677..5713)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932
; LOCATION: 4088, 4314..4397, 4778..4887, 5208..5275, 5677
; LOCATION: 5713)
; US-08-482-918-47
;
; Query Match 82.6%; Score 19; DB 4; Length 5864;
; Best Local Similarity 100.0%; Pred. No. 0.087;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 AGCAGCGCATGGTGGCAGG 20
; Db 3191 AGCAGCGCATGGTGGCAGG 3209
;
; RESULT 13
; US-09-224-681-47
; Sequence 47, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
; LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,
; LOCATION: 5677..5713)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932
; LOCATION: 4088, 4314..4397, 4778..4887, 5208..5275, 5677
; LOCATION: 5713)
; US-08-482-918-47
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; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
; LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,
; LOCATION: 5677..5713)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932
; LOCATION: 4088, 4314..4397, 4778..4887, 5208..5275, 5677
; LOCATION: 5713)
; US-09-224-681-47
;
; Query Match 82.6%; Score 19; DB 4; Length 5864;
; Best Local Similarity 100.0%; Pred. No. 0.087;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 AGCAGCGCATGGTGGCAGG 20
; Db 3191 AGCAGCGCATGGTGGCAGG 3209
;
; RESULT 14
; US-08-336-728A-47
; Sequence 47, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,
; LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,
; LOCATION: 5677..5713)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932
; LOCATION: ..4088, 4314..4397, 4778..4887, 5208..5275, 5677
; LOCATION: ..5713)
; US-08-336-728A-47

Query Match      82.6%; Score 19; DB 4; Length 5864;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AGCCAGGCATGGTGCAGG 20
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Db      3191 AGCCAGGCATGGTGCAGG 3209

RESULT 15
US-09-780-175-17/c
; Sequence 17, Application US/09780175
; Patent No. 6440738
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
; FILE REFERENCE: RTS-0164
; CURRENT APPLICATION NUMBER: US/09/780,175
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 17
; LENGTH: 5917
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1634)...(1990)
; NAME/KEY: CDS
; LOCATION: (2676)...(2750)
; NAME/KEY: CDS
; LOCATION: (3344)...(3382)
; NAME/KEY: CDS
; LOCATION: (3969)...(3992)
; NAME/KEY: CDS
; LOCATION: (4185)...(4403)
; NAME/KEY: CDS
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; LOCATION: (4670)...(4735)
US-09-780-175-17

Query Match      82.6%; Score 19; DB 4; Length 5917;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AGCCAGGCATGGTGCAGG 20
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Db      2098 AGCCAGGCATGGTGCAGG 2080

Search completed: June 17, 2003, 06:28:31
Job time : 30.9003 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 2.4315 Seconds  
(without alignments)  
13697.491 Million cell updates/sec

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Perfect score: 23  
Sequence: 1 cagccagcagtggtgcaggtgt 23

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 1029858 seqs, 724030393 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA: \*

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- 3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	22	95.7	601	10	US-09-777-921A-69
C 3	22	95.7	69327	10	US-09-777-921A-3
C 4	21	91.3	278	9	US-09-764-868-1310
C 5	21	91.3	278	9	US-09-764-868-1311
C 6	21	91.3	300	9	US-09-796-692-8688
C 7	21	91.3	300	9	US-10-040-862-8688
C 8	21	91.3	383	12	US-10-033-528-1863
C 9	21	91.3	401	9	US-09-946-807-876
C 10	21	91.3	401	9	US-09-946-807-877
C 11	21	91.3	401	9	US-09-946-807-878
C 12	21	91.3	401	9	US-09-946-807-879
C 13	21	91.3	401	10	US-09-795-668-876
C 14	21	91.3	401	10	US-09-795-668-877
C 15	21	91.3	401	10	US-09-795-668-878
C 16	21	91.3	401	10	US-09-795-668-879
C 17	21	91.3	401	10	US-09-795-668-876
C 18	21	91.3	401	10	US-09-795-668-877
C 19	21	91.3	401	10	US-09-795-668-878

93	19	82.6	340	10	US-09-998-598-1649	Sequence 1649, Ap	166	19	82.6	31994	10	US-09-764-860-599	Sequence 599, App
C 94	19	82.6	365	10	US-09-867-701-7738	Sequence 7738, Ap	167	19	82.6	32148	9	US-09-764-891-6906	Sequence 6906, Ap
C 95	19	82.6	404	9	US-09-918-995-15969	Sequence 15969, A	C 168	19	82.6	32173	9	US-09-764-891-6246	Sequence 6246, Ap
C 96	19	82.6	412	10	US-09-867-701-10525	Sequence 10525, A	C 169	19	82.6	32177	9	US-09-764-891-6967	Sequence 6967, Ap
C 97	19	82.6	425	9	US-10-060-036-3493	Sequence 3493, Ap	C 170	19	82.6	32177	10	US-09-764-877-3351	Sequence 3251, Ap
C 98	19	82.6	443	9	US-09-871-161-3374	Sequence 28, Appl	C 171	19	82.6	32191	10	US-09-764-877-3374	Sequence 3374, Ap
C 99	19	82.6	465	9	US-09-918-995-13117	Sequence 13117, A	C 172	19	82.6	32199	9	US-10-072-349-210	Sequence 210, App
C 100	19	82.6	466	9	US-09-918-995-13117	Sequence 13117, A	C 173	19	82.6	32199	10	US-09-764-855-210	Sequence 210, App
C 101	19	82.6	486	9	US-09-918-995-13117	Sequence 2048, Ap	C 174	19	82.6	40090	10	US-09-820-004-3	Sequence 3, Appl
C 102	19	82.6	490	9	US-10-060-036-3697	Sequence 3697, Ap	C 175	19	82.6	42571	9	US-10-224-413-3	Sequence 3, Appl
C 103	19	82.6	533	9	US-10-060-036-3697	Sequence 4066, Ap	C 176	19	82.6	48841	9	US-09-844-653-32	Sequence 32, Appl
C 104	19	82.6	573	9	US-10-091-504-1484	Sequence 1484, Ap	C 177	19	82.6	49744	10	US-09-927-091-4	Sequence 4, Appl
C 105	19	82.6	573	10	US-09-764-869-1484	Sequence 1484, Ap	C 178	19	82.6	56737	10	US-09-782-378A-17	Sequence 17, Appl
C 106	19	82.6	804	9	US-09-764-872-711	Sequence 711, App	C 179	19	82.6	58837	10	US-09-982-091A-5	Sequence 5, Appl
C 107	19	82.6	874	10	US-09-864-711-12	Sequence 12, Appl	C 180	19	82.6	62804	12	US-10-096-960-3	Sequence 3, Appl
C 108	19	82.6	924	10	US-09-864-711-12	Sequence 2, Appl	C 181	19	82.6	62804	9	US-09-859-888-3	Sequence 3, Appl
C 109	19	82.6	1719	9	US-09-764-891-9046	Sequence 9046, Ap	C 182	19	82.6	65608	9	US-09-954-531-180	Sequence 180, App
C 110	19	82.6	1886	9	US-10-050-704-31	Sequence 31, Appl	C 183	19	82.6	65608	10	US-09-962-436-292	Sequence 292, App
C 111	19	82.6	2129	10	US-09-872-153-15	Sequence 15, Appl	C 184	19	82.6	65608	10	US-09-962-832-119	Sequence 119, App
C 112	19	82.6	2129	10	US-09-969-347-200	Sequence 200, App	C 185	19	82.6	75270	9	US-09-790-852-1	Sequence 1, Appl
C 113	19	82.6	2174	9	US-10-138-846-10088	Sequence 10088, A	C 186	19	82.6	96649	9	US-09-956-712-10	Sequence 10, Appl
C 114	19	82.6	2218	9	US-10-138-846-13152	Sequence 13152, A	C 187	19	82.6	167343	10	US-09-962-436-281	Sequence 281, App
C 115	19	82.6	2969	9	US-09-954-531-179	Sequence 179, App	C 188	19	82.6	167343	10	US-09-964-824A-273	Sequence 273, App
C 116	19	82.6	3807	10	US-09-005-243-43	Sequence 43, Appl	C 189	19	82.6	170834	10	US-09-835-232-7	Sequence 7, Appl
C 117	19	82.6	3807	10	US-09-224-683-47	Sequence 43, Appl	C 190	19	82.6	174493	9	US-10-238-709-3	Sequence 3, Appl
C 118	19	82.6	5351	9	US-10-125-540-545	Sequence 545, App	C 191	19	82.6	174493	10	US-09-804-471A-3	Sequence 3, Appl
C 119	19	82.6	5351	10	US-09-764-870-545	Sequence 545, App	C 192	19	82.6	197997	10	US-09-822-246-3	Sequence 3, Appl
C 120	19	82.6	5646	9	US-09-764-891-5824	Sequence 5824, Ap	C 193	19	82.6	465237	10	US-09-933-267A-1	Sequence 1, Appl
C 121	19	82.6	5864	10	US-09-005-243-47	Sequence 47, Appl	C 194	19	82.6	684973	10	US-09-263-959-1	Sequence 1, Appl
C 122	19	82.6	5864	10	US-09-224-683-47	Sequence 47, Appl	C 195	18	78.3	168	10	US-09-783-590-4800	Sequence 4800, Ap
C 123	19	82.6	6235	9	US-09-845-020A-5	Sequence 5, Appl	C 196	18	78.3	298	9	US-09-764-872-777	Sequence 777, App
C 124	19	82.6	6461	9	US-10-125-540-546	Sequence 546, App	C 197	18	78.3	329	10	US-09-764-877-420	Sequence 420, App
C 125	19	82.6	6461	10	US-09-764-870-546	Sequence 546, App	C 198	18	78.3	343	9	US-09-803-719-2108	Sequence 2108, Ap
C 126	19	82.6	6670	9	US-09-764-891-5534	Sequence 5534, Ap	C 199	18	78.3	423	9	US-09-918-995-35756	Sequence 35756, A
C 127	19	82.6	6679	9	US-09-845-020A-1	Sequence 1, Appl	C 200	18	78.3	423	9	US-09-918-995-15589	Sequence 15589, A
C 128	19	82.6	7032	9	US-10-092-154-1429	Sequence 1429, Ap	C 201	18	78.3	455	9	US-09-918-995-9664	Sequence 9664, Ap
C 129	19	82.6	7032	10	US-09-764-847-1429	Sequence 1429, Ap	C 202	18	78.3	481	10	US-09-964-824A-218	Sequence 218, App
C 130	19	82.6	7105	10	US-09-764-877-3815	Sequence 3815, Ap	C 203	18	78.3	589	9	US-10-092-154-1093	Sequence 1093, Ap
C 131	19	82.6	7713	9	US-09-764-891-5533	Sequence 5533, Ap	C 204	18	78.3	589	9	US-10-092-154-1094	Sequence 1094, Ap
C 132	19	82.6	8575	9	US-09-764-891-8707	Sequence 8707, Ap	C 205	18	78.3	589	10	US-09-764-847-1093	Sequence 1093, Ap
C 133	19	82.6	9180	10	US-09-880-107-3461	Sequence 3461, Ap	C 206	18	78.3	589	10	US-09-764-847-1094	Sequence 1094, Ap
C 134	19	82.6	9969	9	US-09-764-891-6905	Sequence 6905, Ap	C 207	18	78.3	614	9	US-10-040-739-1399	Sequence 1399, Ap
C 135	19	82.6	10872	9	US-09-764-891-5870	Sequence 5870, Ap	C 208	18	78.3	830	9	US-10-198-846-3855	Sequence 3855, Ap
C 136	19	82.6	11150	9	US-09-764-891-6245	Sequence 6245, Ap	C 209	18	78.3	830	10	US-09-764-853-213	Sequence 213, App
C 137	19	82.6	11474	9	US-10-092-154-1559	Sequence 1559, Ap	C 210	18	78.3	1730	9	US-10-118-783-18	Sequence 18, Appl
C 138	19	82.6	11474	10	US-09-764-847-1559	Sequence 1559, Ap	C 211	18	78.3	2598	9	US-10-118-783-17	Sequence 17, Appl
C 139	19	82.6	11881	9	US-09-764-868-1351	Sequence 1351, Ap	C 212	18	78.3	3441	9	US-09-822-846-296	Sequence 296, App
C 140	19	82.6	11881	9	US-09-764-868-1353	Sequence 1353, Ap	C 213	18	78.3	3858	9	US-09-764-891-5824	Sequence 5824, Ap
C 141	19	82.6	11881	9	US-10-091-504-2124	Sequence 2124, Ap	C 214	18	78.3	5646	9	US-10-118-783-3	Sequence 3, Appl
C 142	19	82.6	11881	9	US-09-764-869-2124	Sequence 2124, Ap	C 215	18	78.3	6987	9	US-10-118-783-23	Sequence 23, Appl
C 143	19	82.6	12045	9	US-09-764-891-9754	Sequence 9754, Ap	C 216	18	78.3	6987	9	US-10-102-627-100	Sequence 100, App
C 144	19	82.6	17509	10	US-09-880-107-2097	Sequence 2097, Ap	C 217	18	78.3	9968	9	US-09-860-670-265	Sequence 265, App
C 145	19	82.6	18820	10	US-09-764-891-6452	Sequence 6452, Ap	C 218	18	78.3	11617	9	US-09-764-891-9890	Sequence 9890, Ap
C 146	19	82.6	19472	10	US-09-764-864-1698	Sequence 1698, Ap	C 219	18	78.3	11618	9	US-09-764-864-1726	Sequence 1726, Ap
C 147	19	82.6	19696	9	US-10-091-572-874	Sequence 874, App	C 220	18	78.3	11977	10	US-09-880-107-3783	Sequence 3783, Ap
C 148	19	82.6	19696	9	US-09-764-891-9327	Sequence 9327, Ap	C 221	18	78.3	15016	9	US-10-091-504-2355	Sequence 2355, Ap
C 149	19	82.6	20444	9	US-09-764-891-9422	Sequence 9422, Ap	C 222	18	78.3	15714	10	US-09-764-869-2355	Sequence 2355, Ap
C 150	19	82.6	21371	9	US-09-764-891-7018	Sequence 7018, Ap	C 223	18	78.3	15714	10	US-10-079-854-217	Sequence 217, App
C 151	19	82.6	21371	9	US-09-764-891-7018	Sequence 7018, Ap	C 224	18	78.3	16854	10	US-09-764-878-217	Sequence 217, App
C 152	19	82.6	21441	9	US-09-764-891-9449	Sequence 9449, Ap	C 225	18	78.3	16854	10	US-10-142-356-3	Sequence 3, Appl
C 153	19	82.6	21535	9	US-10-103-313-609	Sequence 609, App	C 226	18	78.3	19740	9	US-09-764-877-2146	Sequence 2146, Ap
C 154	19	82.6	22161	9	US-10-092-154-1020	Sequence 1020, Ap	C 227	18	78.3	22609	10	US-10-074-095-1108	Sequence 1108, Ap
C 155	19	82.6	22161	10	US-09-764-847-1020	Sequence 1020, Ap	C 228	18	78.3	32170	9	US-09-764-860-1108	Sequence 1108, Ap
C 156	19	82.6	24110	9	US-10-074-045-55	Sequence 55, Appl	C 229	18	78.3	32170	10	US-09-764-891-6161	Sequence 6161, Ap
C 157	19	82.6	27359	10	US-09-822-863-3	Sequence 3, Appl	C 230	18	78.3	32172	9	US-09-764-877-3933	Sequence 3933, Ap
C 158	19	82.6	28313	10	US-09-764-877-3194	Sequence 3194, Ap	C 231	18	78.3	32193	10	US-09-764-877-3933	Sequence 3933, Ap
C 159	19	82.6	28690	10	US-10-010-802-1	Sequence 1, Appl	C 232	18	78.3	32220	10	US-09-782-378A-12	Sequence 12, Appl
C 160	19	82.6	29228	9	US-09-764-877-3198	Sequence 3198, Ap	C 233	18	78.3	36741	9	US-10-007-078-10	Sequence 10, Appl
C 161	19	82.6	30350	9	US-10-118-328-3	Sequence 3, Appl	C 234	18	78.3	42500	9	US-10-222-334-7	Sequence 7, Appl
C 162	19	82.6	31730	10	US-09-764-877-3810	Sequence 3810, Ap	C 235	18	78.3	60153	9	US-10-041-856-1	Sequence 1, Appl
C 163	19	82.6	31994	9	US-09-764-904-71	Sequence 71, Appl	C 236	18	78.3	66479	9	US-09-781-558-3	Sequence 3, Appl
C 164	19	82.6	31994	9	US-10-091-548-71	Sequence 71, Appl	C 237	18	78.3	74586	10	US-09-770-689A-3	Sequence 3, Appl
C 165	19	82.6	31994	9	US-10-074-095-599	Sequence 599, App	C 238	18	78.3	98865	10	US-10-227-195A-1	Sequence 1, Appl

c 239	18	78.3	113604	9	US-10-227-195A-2	Sequence 2, Appli	c 312	17	73.9	455	9	US-10-198-846-1579	Sequence 1579, Ap
c 240	18	78.3	183337	9	US-10-020-141-5	Sequence 5, Appli	313	17	73.9	458	9	US-09-796-692-4095	Sequence 4095, Ap
c 241	18	78.3	186957	9	US-10-185-770-3	Sequence 3, Appli	c 314	17	73.9	458	9	US-09-918-995-13127	Sequence 13127, A
c 242	18	78.3	192885	10	US-09-880-107-3814	Sequence 3814, Ap	315	17	73.9	458	9	US-10-040-862-4095	Sequence 4095, Ap
c 243	18	78.3	235033	9	US-10-301-844-1	Sequence 1, Appli	316	17	73.9	459	9	US-09-918-995-25888	Sequence 25888, A
c 244	18	78.3	237326	9	US-10-301-844-2	Sequence 2, Appli	317	17	73.9	461	9	US-09-918-995-28860	Sequence 28860, A
c 245	18	78.3	302250	10	US-09-962-832-154	Sequence 154, App	318	17	73.9	462	9	US-10-073-961-90	Sequence 90, Appl
c 246	18	78.3	397558	10	US-09-813-320-3	Sequence 3, Appli	319	17	73.9	462	10	US-09-764-887-90	Sequence 10286, A
c 247	17	73.9	83	10	US-09-764-877-3299	Sequence 3299, Ap	320	17	73.9	463	9	US-09-918-995-10286	Sequence 296, App
c 248	17	73.9	87	10	US-10-091-504-2041	Sequence 2041, Ap	321	17	73.9	471	10	US-09-867-701-296	Sequence 15068, A
c 249	17	73.9	87	10	US-09-764-869-2041	Sequence 809, Ap	c 322	17	73.9	472	9	US-09-918-995-15068	Sequence 626, App
c 250	17	73.9	107	9	US-09-764-891-8309	Sequence 8309, Ap	323	17	73.9	474	9	US-10-198-846-1926	Sequence 132, App
c 251	17	73.9	130	9	US-09-764-891-7261	Sequence 7261, Ap	c 324	17	73.9	476	9	US-09-918-995-36512	Sequence 36512, A
c 252	17	73.9	130	9	US-09-764-891-7797	Sequence 7797, Ap	325	17	73.9	478	9	US-09-728-444-820	Sequence 820, App
c 253	17	73.9	155	7	US-08-781-986A-1509	Sequence 1509, Ap	c 326	17	73.9	480	9	US-09-918-995-19739	Sequence 19739, A
c 254	17	73.9	188	9	US-09-764-904-74	Sequence 74, Appl	327	17	73.9	482	9	US-09-918-995-11118	Sequence 11118, A
c 255	17	73.9	188	9	US-10-091-548-74	Sequence 74, Appl	328	17	73.9	483	9	US-09-764-891-82	Sequence 82, Appl
c 256	17	73.9	188	9	US-10-074-095-602	Sequence 602, App	c 329	17	73.9	483	9	US-10-060-036-820	Sequence 820, App
c 257	17	73.9	218	10	US-09-764-860-602	Sequence 602, App	c 330	17	73.9	487	9	US-09-783-590-10242	Sequence 10242, A
c 258	17	73.9	218	9	US-09-764-891-2000	Sequence 2000, Ap	331	17	73.9	491	10	US-09-918-995-14808	Sequence 408, A
c 259	17	73.9	222	9	US-09-918-995-29702	Sequence 29702, A	c 332	17	73.9	494	9	US-09-783-590-405	Sequence 405, App
c 260	17	73.9	233	9	US-09-764-891-8522	Sequence 8522, Ap	c 333	17	73.9	504	10	US-09-796-692-5235	Sequence 5235, Ap
c 261	17	73.9	259	10	US-09-764-877-2254	Sequence 2254, Ap	334	17	73.9	508	9	US-10-040-862-5235	Sequence 5235, Ap
c 262	17	73.9	266	10	US-09-867-701-7659	Sequence 7659, Ap	c 335	17	73.9	508	9	US-09-918-995-15924	Sequence 15924, A
c 263	17	73.9	278	9	US-09-764-891-6874	Sequence 6874, Ap	c 336	17	73.9	550	9	US-09-796-692-9560	Sequence 9560, Ap
c 264	17	73.9	291	9	US-09-918-995-7570	Sequence 7570, Ap	337	17	73.9	569	9	US-10-040-862-9560	Sequence 9560, Ap
c 265	17	73.9	299	12	US-10-068-067-12	Sequence 12, Appl	c 338	17	73.9	584	9	US-10-040-862-9560	Sequence 9560, Ap
c 266	17	73.9	323	10	US-09-867-701-6832	Sequence 6832, Ap	339	17	73.9	584	9	US-10-271-887-22	Sequence 22, Appl
c 267	17	73.9	324	9	US-09-803-719-1684	Sequence 1684, Ap	c 340	17	73.9	604	9	US-09-871-161-314	Sequence 314, App
c 268	17	73.9	326	10	US-09-867-701-8181	Sequence 8181, Ap	c 341	17	73.9	646	9	US-09-776-724A-65	Sequence 65, Appl
c 269	17	73.9	328	10	US-09-867-701-3398	Sequence 3398, Ap	c 342	17	73.9	689	9	US-09-764-891-3235	Sequence 3235, Ap
c 270	17	73.9	335	10	US-09-764-877-2742	Sequence 2742, Ap	c 343	17	73.9	693	10	US-09-764-891-87	Sequence 87, Appl
c 271	17	73.9	336	10	US-09-867-701-7075	Sequence 7075, A	344	17	73.9	728	9	US-09-986-480-87	Sequence 6039, Ap
c 272	17	73.9	339	9	US-09-918-995-17954	Sequence 17954, A	345	17	73.9	761	9	US-09-764-891-6039	Sequence 55, Appl
c 273	17	73.9	352	10	US-09-998-598-1659	Sequence 1659, Ap	c 346	17	73.9	811	9	US-09-907-969-55	Sequence 55, Appl
c 274	17	73.9	357	9	US-10-031-572-28	Sequence 28, Appl	c 347	17	73.9	811	10	US-09-884-441-55	Sequence 55, Appl
c 275	17	73.9	357	9	US-09-918-995-18791	Sequence 18791, A	c 348	17	73.9	825	9	US-10-091-504-1980	Sequence 1980, Ap
c 276	17	73.9	357	9	US-09-764-891-663	Sequence 663, App	c 349	17	73.9	825	10	US-09-764-869-1980	Sequence 5092, Ap
c 277	17	73.9	362	9	US-09-918-995-18953	Sequence 18953, A	c 350	17	73.9	828	9	US-10-198-846-5092	Sequence 814, App
c 278	17	73.9	367	9	US-09-764-872-878	Sequence 878, App	c 351	17	73.9	853	9	US-09-764-872-814	Sequence 9105, Ap
c 279	17	73.9	367	9	US-09-764-872-879	Sequence 879, App	c 352	17	73.9	853	9	US-09-764-891-9105	Sequence 6104, Ap
c 280	17	73.9	369	9	US-09-918-995-16631	Sequence 16631, A	c 353	17	73.9	853	9	US-10-198-846-6104	Sequence 1389, A
c 281	17	73.9	371	9	US-09-764-891-7616	Sequence 7616, Ap	c 354	17	73.9	859	9	US-10-023-282-18	Sequence 13, Appl
c 282	17	73.9	373	9	US-09-918-995-37769	Sequence 37769, A	c 355	17	73.9	879	10	US-09-776-724A-77	Sequence 77, Appl
c 283	17	73.9	388	9	US-10-046-935-843	Sequence 843, App	c 356	17	73.9	911	9	US-10-119-926-80	Sequence 80, Appl
c 284	17	73.9	388	9	US-09-878-178-843	Sequence 843, App	c 357	17	73.9	923	9	US-10-198-846-11389	Sequence 11389, A
c 285	17	73.9	388	9	US-10-146-502-843	Sequence 843, App	c 358	17	73.9	926	9	US-10-198-846-3411	Sequence 3411, Ap
c 286	17	73.9	388	10	US-09-867-701-7925	Sequence 7925, Ap	c 359	17	73.9	954	9	US-09-776-724A-33	Sequence 33, Appl
c 287	17	73.9	390	9	US-09-803-719-1821	Sequence 1821, Ap	c 360	17	73.9	978	9	US-09-822-830A-297	Sequence 297, App
c 288	17	73.9	391	9	US-10-198-846-12628	Sequence 12628, A	c 361	17	73.9	1020	10	US-09-764-891-5693	Sequence 5693, Ap
c 289	17	73.9	395	10	US-09-867-701-8351	Sequence 8351, Ap	c 362	17	73.9	1022	9	US-09-918-995-13908	Sequence 13908, A
c 290	17	73.9	397	10	US-09-920-300A-1579	Sequence 1579, Ap	c 363	17	73.9	1091	10	US-10-198-846-13908	Sequence 285, App
c 291	17	73.9	397	12	US-10-033-528-1579	Sequence 1579, Ap	c 364	17	73.9	1195	10	US-09-822-830A-285	Sequence 7146, Ap
c 292	17	73.9	401	9	US-09-946-807-1046	Sequence 1046, Ap	c 365	17	73.9	1241	9	US-09-764-891-7146	Sequence 817, App
c 293	17	73.9	401	9	US-09-946-807-1162	Sequence 1162, Ap	c 366	17	73.9	1300	9	US-09-764-872-817	Sequence 9108, App
c 294	17	73.9	401	10	US-09-795-668-1046	Sequence 1046, Ap	c 367	17	73.9	1300	9	US-09-764-891-9108	Sequence 363, App
c 295	17	73.9	401	10	US-09-795-668-1162	Sequence 1162, Ap	c 368	17	73.9	1364	10	US-09-822-830A-363	Sequence 253, App
c 296	17	73.9	401	10	US-09-795-668-1046	Sequence 1046, Ap	c 369	17	73.9	1453	10	US-10-072-349-253	Sequence 253, App
c 297	17	73.9	401	10	US-09-795-668-1162	Sequence 1162, Ap	c 370	17	73.9	1453	10	US-09-764-855-253	Sequence 253, App
c 298	17	73.9	404	10	US-09-867-701-5146	Sequence 5146, Ap	c 371	17	73.9	1457	9	US-09-989-920-93	Sequence 93, Appl
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c 300	17	73.9	405	10	US-09-795-668-1381	Sequence 1381, Ap	c 373	17	73.9	1560	12	US-10-068-067-20	Sequence 10306, A
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c 302	17	73.9	408	10	US-09-969-708-142	Sequence 142, App	c 375	17	73.9	1812	9	US-10-198-846-12998	Sequence 12998, A
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c 311	17	73.9	445	10	US-09-867-701-9819	Sequence 9819, Ap	c 384	17	73.9	2125	10	US-09-802-807-6	Sequence 6, Appl











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## ALIGNMENTS

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; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-921A-68
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Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22
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US-09-777-921A-69/c
; Sequence 69, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
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; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
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; NAME/KEY: variation
; LOCATION: (301)...(301)
; OTHER INFORMATION: T may be either present or absent
US-09-777-921A-69
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Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020115136A1
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; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: n = A,T,C or G
US-09-777-921A-3
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Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-764-868-1310/c
; Sequence 1310, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1310
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; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1310

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Best Local Similarity 100.0%; Pred. No. 0.03;
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RESULT 5
US-09-764-868-1311/c
; Sequence 1311, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
US-09-764-868-1311

Query Match          91.3%; Score 21; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.03;
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RESULT 6
US-09-796-692-8688/c
; Sequence 8688, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8688
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (48)
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; NAME/KEY: unsure
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US-09-796-692-8688

Query Match          91.3%; Score 21; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 AGCCAGGCATGGTGCAGGTG 22  
Db 34 AGCCAGGCATGGTGCAGGTG 14

## RESULT 7

US-10-040-862-8688/c  
; Sequence 8688, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8688  
; LENGTH: 300  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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; NAME/KEY: unsure  
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; US-10-040-862-8688

Query Match 91.3%; Score 21; DB 9; Length 300;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGCAGGTG 22  
Db 34 AGCCAGGCATGGTGCAGGTG 14

## RESULT 8

US-10-033-528-1863  
; Sequence 1863, Application US/10033528  
; Patent No. US20020131971A1  
; GENERAL INFORMATION:  
; APPLICANT: King, Gordon E.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547C1  
 CURRENT APPLICATION NUMBER: US/10/033.528  
 CURRENT FILING DATE: 2001-12-26  
 NUMBER OF SEQ ID NOS: 1896  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1863  
 LENGTH: 383  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1, 35, 37, 375  
 OTHER INFORMATION: n = A,T,C or G  
 US-10-033-528-1863

Query Match 91.3%; Score 21; DB 12; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 0.029;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22  
 Db 215 AGCCAGGCATGGTGGCAGGTG 235

# RESULT 9

US-09-946-807-876  
 Sequence 876, Application US/09946807  
 Patent No. US20020165144A1  
 GENERAL INFORMATION:  
 APPLICANT: Stefansson, Hreinn  
 APPLICANT: Steinhorsdottir, Valgerdur  
 APPLICANT: Gulcher, Jeffrey R.  
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE  
 FILE REFERENCE: 2345.2004-001  
 CURRENT APPLICATION NUMBER: US/09/946,807  
 CURRENT FILING DATE: 2001-09-05  
 PRIOR APPLICATION NUMBER: US/09/795,668  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: US 09/515,716  
 PRIOR FILING DATE: 2000-02-28  
 NUMBER OF SEQ ID NOS: 1531  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 876  
 LENGTH: 401  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-946-807-876

Query Match 91.3%; Score 21; DB 9; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.029;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22  
 Db 340 AGCCAGGCATGGTGGCAGGTG 360

# RESULT 10

US-09-946-807-877  
 Sequence 877, Application US/09946807  
 Patent No. US20020165144A1  
 GENERAL INFORMATION:  
 APPLICANT: Stefansson, Hreinn  
 APPLICANT: Steinhorsdottir, Valgerdur  
 APPLICANT: Gulcher, Jeffrey R.  
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE  
 FILE REFERENCE: 2345.2004-001  
 CURRENT APPLICATION NUMBER: US/09/946,807  
 CURRENT FILING DATE: 2001-09-05  
 PRIOR APPLICATION NUMBER: US/09/795,668  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 1531  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 877  
 LENGTH: 401  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-946-807-877

NUMBER OF SEQ ID NOS: 1531  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 877  
 LENGTH: 401  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-946-807-877

Query Match 91.3%; Score 21; DB 9; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.029;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22  
 Db 29 AGCCAGGCATGGTGGCAGGTG 49

# RESULT 11

US-09-946-807-878  
 Sequence 878, Application US/09946807  
 Patent No. US20020165144A1  
 GENERAL INFORMATION:  
 APPLICANT: Stefansson, Hreinn  
 APPLICANT: Steinhorsdottir, Valgerdur  
 APPLICANT: Gulcher, Jeffrey R.  
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE  
 FILE REFERENCE: 2345.2004-001  
 CURRENT APPLICATION NUMBER: US/09/946,807  
 CURRENT FILING DATE: 2001-09-05  
 PRIOR APPLICATION NUMBER: US/09/795,668  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: US 09/515,716  
 PRIOR FILING DATE: 2000-02-28  
 NUMBER OF SEQ ID NOS: 1531  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 878  
 LENGTH: 401  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-946-807-878

Query Match 91.3%; Score 21; DB 9; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.029;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTG 22  
 Db 27 AGCCAGGCATGGTGGCAGGTG 47

# RESULT 12

US-09-946-807-879  
 Sequence 879, Application US/09946807  
 Patent No. US20020165144A1  
 GENERAL INFORMATION:  
 APPLICANT: Stefansson, Hreinn  
 APPLICANT: Steinhorsdottir, Valgerdur  
 APPLICANT: Gulcher, Jeffrey R.  
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE  
 FILE REFERENCE: 2345.2004-001  
 CURRENT APPLICATION NUMBER: US/09/946,807  
 CURRENT FILING DATE: 2001-09-05  
 PRIOR APPLICATION NUMBER: US/09/795,668  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: US 09/515,716  
 PRIOR FILING DATE: 2000-02-28  
 NUMBER OF SEQ ID NOS: 1531  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 879  
 LENGTH: 401  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-946-807-879

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Query Match          91.3%; Score 21; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 AGCCAGGCATGGTGGCAGGTG 22  
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## RESULT 13

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US-09-795-668-876
; Sequence 876, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09795668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,131
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 1.0
; SEQ ID NO 876
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-876

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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 AGCCAGGCATGGTGGCAGGTG 22  
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## RESULT 14

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US-09-795-668-877
; Sequence 877, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; APPLICANT: Gulicher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345-2004-001
; CURRENT APPLICATION NUMBER: US/09795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US/09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
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; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-877

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Query Match          91.3%; Score 21; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 AGCCAGGCATGTTGGCAGGTG 22  
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Db 29 AGCCAGGCATGTTGGCAGGTG 49

**RESULT 15'**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 26.1364 Seconds  
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14252.028 Million cell updates/sec

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Perfect score: 23  
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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database :

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6: em\_estpl:\*

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8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

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26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 82	21	91.3	430	12	BF819892	BF819892	ME1-RT002	155	21	91.3	569	17	AQ601577	AQ601577	HS 2105 B
C 83	21	91.3	433	17	AQ592472	AQ592472	HS 5455 A	156	21	91.3	570	14	BM994846	BM994846	UI-H-DHO-
C 84	21	91.3	434	17	AQ523808	AQ523808	HS 5370 A	C 157	21	91.3	575	17	AQ234424	AQ234424	HS 2053 A
C 85	21	91.3	437	9	AA583518	AA583518	nf24g12.s	C 158	21	91.3	578	9	AI760700	AI760700	w108a04.x
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C 87	21	91.3	441	14	H72109	H72109	ys02f01.s1	160	21	91.3	583	17	AQ569782	AQ569782	HS 5334 B
C 88	21	91.3	443	10	BE677702	BE677702	7d90f07.x	161	21	91.3	593	17	AQ779286	AQ779286	HS 3185 A
C 89	21	91.3	445	12	BF772474	BF772474	IL5-IT002	C 162	21	91.3	595	17	AQ712589	AQ712589	HS 2134 A
C 90	21	91.3	445	17	AQ428107	AQ428107	CITBI-EI-	C 163	21	91.3	606	13	BI765292	BI765292	603050395
C 91	21	91.3	448	17	AQ228914	AQ228914	HS 2013 B	164	21	91.3	610	17	AQ349950	AQ349950	RPCI11-11
C 92	21	91.3	450	10	AW276769	AW276769	xp65g07.x	C 165	21	91.3	611	10	AV709937	AV709937	AV709937
C 93	21	91.3	451	17	AQ466677	AQ466677	HS 5161 B	C 166	21	91.3	620	17	AQ534862	AQ534862	RPCI-11-3
C 94	21	91.3	452	14	N33374	N33374	Y40C10.s1	C 167	21	91.3	621	17	AQ390071	AQ390071	RPCI11-15
C 95	21	91.3	453	14	R56101	R56101	Y94a06.s1	C 168	21	91.3	622	10	AW963196	AW963196	EST375269
C 96	21	91.3	453	17	AQ20765	AQ20765	CIT-HSP-2	169	21	91.3	629	14	BQ000257	BQ000257	UI-H-D10-
C 97	21	91.3	453	17	AQ708713	AQ708713	HS 5370 A	170	21	91.3	637	13	BG927341	BG927341	HNC66-1-D
C 98	21	91.3	454	10	BE148910	BE148910	CM0-HT024	171	21	91.3	643	17	AQ279940	AQ279940	CITBI-EI-
C 99	21	91.3	456	17	AQ807064	AQ807064	HS 3248 A	C 172	21	91.3	655	17	AG152442	AG152442	Pan trogl
C 100	21	91.3	461	14	H71868	H71868	YR2C03.s1	173	21	91.3	655	17	AQ480046	AQ480046	RPCI-11-2
C 101	21	91.3	461	14	R44961	R44961	Y933C08.s1	174	21	91.3	657	17	AG178656	AG178656	Pan trogl
C 102	21	91.3	462	14	BM697126	BM697126	UI-E-DWO-	175	21	91.3	658	17	AG183574	AG183574	Pan trogl
C 103	21	91.3	464	17	AQ404481	AQ404481	HS 5069 B	C 176	21	91.3	659	10	AV707441	AV707441	AV707441
C 104	21	91.3	466	17	AQ144744	AQ144744	HS 3092 A	C 177	21	91.3	661	12	BG566535	BG566535	602585562
C 105	21	91.3	468	10	AW029269	AW029269	wX08b12.x	C 178	21	91.3	663	17	AG119366	AG119366	Pan trogl
C 106	21	91.3	468	14	N57791	N57791	YV56h08.s1	179	21	91.3	663	17	AQ527989	AQ527989	RPCI-11-3
C 107	21	91.3	469	17	B82499	B82499	RPCI11-16F9	C 180	21	91.3	667	17	AQ482571	AQ482571	RPCI-11-2
C 108	21	91.3	470	14	N57770	N57770	YV56e08.s1	181	21	91.3	668	10	AV701541	AV701541	AV701541
C 109	21	91.3	471	10	AW904850	AW904850	RC5-NN106	C 182	21	91.3	669	17	AG148600	AG148600	Pan trogl
C 110	21	91.3	472	10	BE145294	BE145294	CM3-HT019	C 183	21	91.3	669	17	AG151884	AG151884	Pan trogl
C 111	21	91.3	472	17	AQ142184	AQ142184	HS 3179 B	C 184	21	91.3	670	17	AQ414253	AQ414253	RPCI-11-1
C 112	21	91.3	473	17	AQ693237	AQ693237	HS 5429 B	185	21	91.3	671	17	AG168614	AG168614	Pan trogl
C 113	21	91.3	475	17	AQ231773	AQ231773	HS 2026 A	186	21	91.3	672	17	AQ386522	AQ386522	RPCI11-14
C 114	21	91.3	479	9	AI921765	AI921765	w029h11.x	187	21	91.3	673	17	AG101374	AG101374	Pan trogl
C 115	21	91.3	482	17	AQ377523	AQ377523	RPCI11-16	C 188	21	91.3	674	12	BF817005	BF817005	MR2-C1012
C 116	21	91.3	484	17	AQ314669	AQ314669	CITBI-EI-	C 189	21	91.3	679	10	AW975969	AW975969	EST388078
C 117	21	91.3	484	17	AQ428466	AQ428466	CITBI-EI-	C 190	21	91.3	681	17	AG088220	AG088220	Pan trogl
C 118	21	91.3	485	17	AQ282171	AQ282171	RPCI11-79	C 191	21	91.3	684	17	AG115638	AG115638	Pan trogl
C 119	21	91.3	487	17	AZ694787	AZ694787	UP 390-17	C 192	21	91.3	685	17	AG056681	AG056681	Pan trogl
C 120	21	91.3	488	17	AQ351270	AQ351270	RPCI11-11	C 193	21	91.3	690	17	B68459	B68459	CIT-HSP-205
C 121	21	91.3	489	17	AQ178561	AQ178561	HS 2242 B	C 194	21	91.3	694	14	BM969614	BM969614	UI-CF-DU1
C 122	21	91.3	490	12	BF903967	BF903967	MR1-MT028	C 195	21	91.3	695	9	AL037383	AL037383	DKF2P5641
C 123	21	91.3	492	14	BM792592	BM792592	K-EST0072	C 196	21	91.3	697	14	BM989475	BM989475	UI-H-DHO-
C 124	21	91.3	493	17	AQ001060	AQ001060	CIT-HSP-2	C 197	21	91.3	697	17	AG101761	AG101761	Pan trogl
C 125	21	91.3	494	17	AQ674646	AQ674646	HS 5474 B	C 198	21	91.3	705	17	AG168762	AG168762	Pan trogl
C 126	21	91.3	495	17	AQ485341	AQ485341	RPCI-11-2	C 199	21	91.3	710	14	BM989661	BM989661	UI-H-DHO-
C 127	21	91.3	495	12	BF951417	BF951417	PM0-NN117	C 200	21	91.3	711	17	AG178705	AG178705	Pan trogl
C 128	21	91.3	501	9	AA722505	AA722505	zh31g08.s	C 201	21	91.3	713	9	AI114653	AI114653	HAI248 Hu
C 129	21	91.3	503	17	AQ555044	AQ555044	RPCI-11-4	C 202	21	91.3	715	17	AG182904	AG182904	Pan trogl
C 130	21	91.3	504	17	AQ171244	AQ171244	HS 3073 B	C 203	21	91.3	719	17	AG175181	AG175181	CITBI-EI-
C 131	21	91.3	506	17	AZ694837	AZ694837	UP 389-6N	C 204	21	91.3	724	17	AQ392119	AQ392119	CITBI-EI-
C 132	21	91.3	506	17	B42283	B42283	HS 1055-B1-	C 205	21	91.3	731	17	AG175563	AG175563	Pan trogl
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C 134	21	91.3	508	17	AQ340535	AQ340535	HS 2256 B	C 207	21	91.3	743	17	AQ391552	AQ391552	CITBI-EI-
C 135	21	91.3	510	17	AZ694838	AZ694838	UP 392-2H	C 208	21	91.3	755	17	AQ088318	AQ088318	HS 3184 A
C 136	21	91.3	511	17	AQ674545	AQ674545	HS 5476 B	C 209	21	91.3	765	12	BG571409	BG571409	602592685
C 137	21	91.3	514	17	AQ483553	AQ483553	RPCI-11-2	C 210	21	91.3	768	17	AG089754	AG089754	Pan trogl
C 138	21	91.3	515	14	BM850925	BM850925	K-EST0131	C 211	21	91.3	771	17	AG112726	AG112726	Pan trogl
C 139	21	91.3	517	17	AQ684457	AQ684457	HS 5506 B	C 212	21	91.3	775	17	AQ393755	AQ393755	CITBI-EI-
C 140	21	91.3	519	17	AQ556254	AQ556254	HS 5223 B	C 213	21	91.3	779	13	BM555512	BM555512	AGENCY
C 141	21	91.3	526	9	AL707966	AL707966	DKF2P686G	C 214	21	91.3	813	17	AG175362	AG175362	Pan trogl
C 142	21	91.3	527	17	AQ804461	AQ804461	HS 3078 A	C 215	21	91.3	835	17	AQ897779	AQ897779	HS 3144 A
C 143	21	91.3	532	12	BF155049	BF155049	QV2-BT081	C 216	21	91.3	843	14	BQ215569	BQ215569	AGENCY
C 144	21	91.3	534	10	BE147668	BE147668	RC3-HT023	C 217	21	91.3	870	12	BF695231	BF695231	602080457
C 145	21	91.3	536	17	AQ772371	AQ772371	HS 5493 B	C 218	21	91.3	872	14	BQ894318	BQ894318	AGENCY
C 146	21	91.3	538	17	AQ678329	AQ678329	HS 5529 B	C 219	21	91.3	905	12	BF970546	BF970546	602274036
C 147	21	91.3	540	9	AL712660	AL712660	DKF2P686M	C 220	21	91.3	920	12	BG121028	BG121028	602327474
C 148	21	91.3	545	14	N78122	N78122	YV73b05.r1	C 221	21	91.3	933	12	BG566706	BG566706	602585769
C 149	21	91.3	552	17	AQ754231	AQ754231	HS 5326 B	C 222	21	91.3	962	14	BQ941784	BQ941784	AGENCY
C 150	21	91.3	559	9	AL703693	AL703693	DKF2P686C	C 223	21	91.3	965	14	BQ719185	BQ719185	AGENCY
C 151	21	91.3	561	17	AQ699466	AQ699466	HS 5558 B	C 224	21	91.3	997	12	BF679103	BF679103	602153366
C 152	21	91.3	563	9	AL712057	AL712057	DKF2P686I	C 225	21	91.3	1010	12	BG679564	BG679564	602627607



C 226	21	91.3	1145	14	BM928279	AGENCOURT	299	19	82.6	219	10	BE241474
C 227	21	91.3	1210	12	BF678472	602085924	300	19	82.6	223	14	F16569
C 228	20	87.0	238	17	B41230	HS-1053-A2-	C 301	19	82.6	223	17	AQ509074
C 229	20	87.0	290	9	AA330610	EST34548	302	19	82.6	224	9	AL729254
C 230	20	87.0	307	17	AQ490922	RPCI-11-2	303	19	82.6	224	9	AL596991
C 231	20	87.0	341	10	AW844439	RC2-CN005	304	19	82.6	226	9	AA748089
C 232	20	87.0	357	17	AQ275520	RPCI-5-10	305	19	82.6	226	14	C05720
C 233	20	87.0	358	10	AV658912	AV658912	C 306	19	82.6	228	12	AQ280060
C 234	20	87.0	363	10	AW844508	RC2-CN005	C 307	19	82.6	231	12	BF295338
C 235	20	87.0	367	17	B50288	CIT-HSP-282	C 308	19	82.6	231	14	W06010
C 236	20	87.0	376	10	AQ132635	HS 3048 B	C 309	19	82.6	234	9	AI363977
C 237	20	87.0	409	12	BG897426	HOA13-1-C	C 310	19	82.6	235	9	AA176505
C 238	20	87.0	417	17	AQ061707	CIT-HSP-2	311	19	82.6	235	14	AA176505
C 239	20	87.0	421	17	B63582	RC2-CN005	312	19	82.6	239	13	BI037888
C 240	20	87.0	421	17	AQ606178	HS 5396 A	C 313	19	82.6	244	13	BG984500
C 241	20	87.0	423	17	AQ315539	RPCI-11-1	C 314	19	82.6	248	12	BF695335
C 242	20	87.0	436	17	AQ817641	HS 5265 B	C 315	19	82.6	252	9	AA369743
C 243	20	87.0	439	12	BG111039	602284720	316	19	82.6	252	12	BF945553
C 244	20	87.0	443	17	AZ521031	RPCI-11-1	317	19	82.6	253	17	AQ417185
C 245	20	87.0	443	17	AQ238984	RPCI-11-68	C 318	19	82.6	257	10	AW779204
C 246	20	87.0	452	10	AW859924	QV1-CT036	C 319	19	82.6	267	17	AQ323494
C 247	20	87.0	454	9	A1879130	au55a05.Y	320	19	82.6	268	9	AA302400
C 248	20	87.0	454	17	AQ041802	CIT-HSP-2	321	19	82.6	269	17	AQ487705
C 249	20	87.0	465	17	AQ342906	RPCI-11-12	C 322	19	82.6	270	17	AQ508046
C 250	20	87.0	465	17	AQ335335	CITBI-EI-	C 323	19	82.6	272	17	AQ628712
C 251	20	87.0	476	17	AQ053073	RPCI-11-50	C 324	19	82.6	273	9	AA516305
C 252	20	87.0	483	14	BM709802	UT-E-CK1-	C 325	19	82.6	274	12	BF948836
C 253	20	87.0	489	17	AQ695677	HS 2159 A	326	19	82.6	277	9	AA654627
C 254	20	87.0	503	17	AQ203561	HS 3103 B	327	19	82.6	277	12	BF914340
C 255	20	87.0	535	17	AZ372553	1W0124A01	C 328	19	82.6	279	17	AQ540913
C 256	20	87.0	554	17	AQ281871	RPCI-11-76	C 329	19	82.6	280	9	AA508506
C 257	20	87.0	565	17	AQ348354	RPCI-11-13	330	19	82.6	280	14	F17196
C 258	20	87.0	566	17	AQ526465	HS 5309 B	C 331	19	82.6	281	9	AI453660
C 259	20	87.0	583	17	AQ197980	RPCI-11-48	C 332	19	82.6	281	10	BE159380
C 260	20	87.0	586	17	AQ490786	RPCI-11-2	C 333	19	82.6	283	12	BF931795
C 261	20	87.0	587	17	AQ541733	RPCI-11-3	334	19	82.6	284	9	AA713720
C 262	20	87.0	661	17	AG156547	Pan trogl	C 335	19	82.6	287	9	AA643451
C 263	20	87.0	682	17	AG066350	Pan trogl	C 336	19	82.6	287	17	AQ101021
C 264	20	87.0	715	12	BE874842	601488786	C 337	19	82.6	289	12	BF772427
C 265	20	87.0	729	17	AG110850	Pan trogl	C 338	19	82.6	291	17	AQ711291
C 266	20	87.0	728	17	AG110065	Pan trogl	C 339	19	82.6	292	10	AW873951
C 267	20	87.0	747	17	AG141278	Pan trogl	340	19	82.6	292	14	T07019
C 268	20	87.0	753	14	BQ707143	AGENCOURT	341	19	82.6	293	17	AQ096010
C 269	20	87.0	775	12	BG570538	602591217	C 342	19	82.6	294	10	BE245198
C 270	20	87.0	823	17	AQ746445	HS 2278 A	C 343	19	82.6	296	9	AA995189
C 271	20	87.0	844	17	AQ888222	HS 3081 A	C 344	19	82.6	296	17	AQ592980
C 272	20	87.0	861	17	AQ741554	HS 5567 B	345	19	82.6	300	9	AA668148
C 273	19	82.6	57	12	BF542036	602069193	C 346	19	82.6	300	9	AA668148
C 274	19	82.6	103	10	BE165639	CM1-HT048	C 347	19	82.6	303	9	AA718906
C 275	19	82.6	121	10	AW838339	XC35H05.X	C 348	19	82.6	304	9	AA551777
C 276	19	82.6	124	10	AW885941	RC4-OT007	C 349	19	82.6	304	9	AA573543
C 277	19	82.6	135	13	BI059889	IL3-UT011	C 350	19	82.6	305	12	BF830366
C 278	19	82.6	149	13	BG982074	MR3-CN014	351	19	82.6	305	12	BF912307
C 279	19	82.6	152	10	AW793990	MR1-UM000	C 352	19	82.6	309	10	AW079301
C 280	19	82.6	152	17	AQ262347	CITBI-EI-	353	19	82.6	310	9	AA090387
C 281	19	82.6	160	17	B42150	HS-1055-A2-	C 354	19	82.6	313	14	BQ311827
C 282	19	82.6	163	17	AQ283089	RPCI-11-79	C 355	19	82.6	315	17	B75820
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C 285	19	82.6	171	12	BF927273	CM1-NT024	C 358	19	82.6	330	12	BG154184
C 286	19	82.6	180	14	H65170	601488786	359	19	82.6	331	9	AI190960
C 287	19	82.6	182	9	AA821616	ny87a06.S	C 360	19	82.6	336	12	BF871261
C 288	19	82.6	184	9	AA885578	o131a12.S	361	19	82.6	336	17	AQ066842
C 289	19	82.6	187	9	AA908328	oq75d01.S	362	19	82.6	336	17	AQ067768
C 290	19	82.6	187	9	AA903195	110234.8e	C 363	19	82.6	336	17	AQ057181
C 291	19	82.6	194	14	F25733	HSPD12316 H	C 364	19	82.6	337	9	AI453155
C 292	19	82.6	196	13	BG978412	RC4-CI019	365	19	82.6	337	9	AI453155
C 293	19	82.6	198	17	AQ075272	CIT-HSP-2	C 366	19	82.6	338	13	BI496293
C 294	19	82.6	200	10	AW277235	xg80c03.X	367	19	82.6	338	14	F37291
C 295	19	82.6	208	14	T05426	EST03315 Fe	C 368	19	82.6	340	17	AQ478365
C 296	19	82.6	213	9	AA714477	nw06g03.S	C 369	19	82.6	342	9	AA484022
C 297	19	82.6	213	12	BF904023	MR1-NT028	C 370	19	82.6	343	12	BF896334
C 298	19	82.6	215	9	AA366961	EST77975	C 371	19	82.6	346	13	BG982460

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AL596991	DKPZP313M
AA748089	nx58h02.S
C05720	C05720 Huma
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BF295338	QV3-NT021
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AI363977	qz35a03.X
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BF695335	IL3-ET011
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BF945553	PM3-NN108
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AQ323494	RPCI-11-10
AA302400	EST15536
AQ487705	RPCI-11-2
AQ508046	RPCI-11-2
AQ628712	RPCI-11-4
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AQ057181	RPCI-11-3
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C 372	19	82.6	348	9	AA491862	AA491862 ne72a09.s	C 445	19	82.6	415	14	C06141	C06141 C06141 Huma
C 373	19	82.6	349	10	AW874331	AW874331 hq45e12.x	446	19	82.6	415	17	B63136	B63136 CIT978SK-A-
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C 375	19	82.6	349	17	AQ472121	AQ472121 CITBI-EI-	448	19	82.6	418	9	AA307292	AA307292 EST178209
C 376	19	82.6	351	17	AQ151158	AQ151158 HS 2186_A	449	19	82.6	418	17	BH614821	BH614821 UP 535-10
C 377	19	82.6	352	9	AA491650	AA491650 ne80f07.s	C 450	19	82.6	418	17	AQ556945	AQ556945 HS 5328_A
C 378	19	82.6	352	17	AQ389958	AQ389958 RPTC11-15	C 451	19	82.6	419	10	AW403829	AW403829 UT-HT-BKO
C 379	19	82.6	352	17	AQ007136	AQ007136 CIT-HSP-2	C 452	19	82.6	419	10	BE155302	BE155302 PM1-HT035
C 380	19	82.6	356	17	AQ0803519	AQ0803519 HS 3178_A	C 453	19	82.6	419	17	AQ036584	AQ036584 CIT-HSP-2
C 381	19	82.6	357	9	A1338350	A1338350 qq96g12.x	C 454	19	82.6	420	9	AW17989	AW17989 as93a02.x
C 382	19	82.6	359	17	AQ085420	AQ085420 HS 2270_B	C 455	19	82.6	421	9	AA653154	AA653154 ag64c05.s
C 383	19	82.6	360	13	BI712069	BI712069 i601c02.x	C 456	19	82.6	421	10	AW975904	AW975904 EST388013
C 384	19	82.6	360	17	AQ682145	AQ682145 HS 5503_B	C 457	19	82.6	421	14	H59066	H59066 y33b02.s1
C 385	19	82.6	360	17	AZ515814	AZ515814 RPTC11-11	C 458	19	82.6	422	9	AL601258	AL601258 DKEZP313K
C 386	19	82.6	361	17	AQ471450	AQ471450 CITBI-EI-	C 459	19	82.6	423	9	AA226047	AA226047 nc09e01.s
C 387	19	82.6	361	17	AQ936459	AQ936459 RPTC11-11-S	C 460	19	82.6	423	13	BM506690	BM506690 in24a11.x
C 388	19	82.6	361	17	AQ116881	AQ116881 HS 2175_B	C 461	19	82.6	423	14	R82650	R82650 yJ20d04.s1
C 389	19	82.6	362	13	BI496292	BI496292 df124b09.	C 462	19	82.6	425	9	A1491867	A1491867 t001f10.x
C 390	19	82.6	363	12	BF917688	BF917688 IL3-UT011	C 463	19	82.6	427	17	AQ060020	AQ060020 CIT-HSP-2
C 391	19	82.6	364	9	AA508103	AA508103 ng93d10.s	C 464	19	82.6	428	9	AA648979	AA648979 ns41f01.s
C 392	19	82.6	365	9	AA834683	AA834683 cd99a05.s	C 465	19	82.6	430	9	AA488746	AA488746 as95h05.r
C 393	19	82.6	365	14	T06598	T06598 EST04487 Fe	C 466	19	82.6	432	17	AQ057431	AQ057431 CIT-HSP-2
C 394	19	82.6	365	17	AQ030530	AQ030530 HS 3178_A	C 467	19	82.6	432	17	AQ225898	AQ225898 HS 2011_B
C 395	19	82.6	366	17	AQ388598	AQ388598 RPTC11-15	C 468	19	82.6	433	9	AA302979	AA302979 EST113212
C 396	19	82.6	367	9	A1521525	A1521525 t064b10.x	C 469	19	82.6	433	17	AQ234523	AQ234523 HS 2052_B
C 397	19	82.6	367	17	AQ146635	AQ146635 HS 2233_B	C 470	19	82.6	433	17	B92880	B92880 CIT-HSP-216
C 398	19	82.6	369	14	W93917	W93917 zd97g02.r1	C 471	19	82.6	433	17	AQ245629	AQ245629 HS 2064_A
C 399	19	82.6	369	17	AQ349605	AQ349605 RPTC11-11	C 472	19	82.6	434	9	A1929627	A1929627 au61g01.y
C 400	19	82.6	370	9	A1282511	A1282511 qv04e04.x	C 473	19	82.6	435	9	AA228877	AA228877 nc16g03.r
C 401	19	82.6	370	14	F25593	F25593 HSPD12698 H	C 474	19	82.6	435	14	N69462	N69462 zal8a08.s1
C 402	19	82.6	373	9	AA468271	AA468271 nc76a08.r	C 475	19	82.6	436	9	AA259174	AA259174 nc17a08.r
C 403	19	82.6	373	17	AQ132907	AQ132907 HS 3045_B	C 476	19	82.6	436	14	R98406	R98406 yq65b12.s1
C 404	19	82.6	374	12	BF817826	BF817826 MK2-C1012	C 477	19	82.6	437	13	BM72501	BM72501 i942901.y
C 405	19	82.6	376	17	AQ284447	AQ284447 RPTC11-90	C 478	19	82.6	437	17	AQ759739	AQ759739 HS 2257_A
C 406	19	82.6	377	9	AA719073	AA719073 zh33a05.s	C 479	19	82.6	439	9	AA604751	AA604751 no84e04.s
C 407	19	82.6	377	17	AQ547053	AQ547053 CITBI-EI-	C 480	19	82.6	439	17	AQ936180	AQ936180 RPTC11-S
C 408	19	82.6	378	14	N52480	N52480 yv51b10.s1	C 481	19	82.6	440	9	AA767297	AA767297 nz81c06.s
C 409	19	82.6	378	14	T62539	T62539 yc04d04.s1	C 482	19	82.6	440	13	BM127350	BM127350 i988b10.x
C 410	19	82.6	380	10	BE155299	BE155299 PM1-HT035	C 483	19	82.6	441	17	AQ798736	AQ798736 HS 3032_A
C 411	19	82.6	380	12	BF840062	BF840062 IL0-HT106	C 484	19	82.6	441	17	AQ557783	AQ557783 HS 2083_A
C 412	19	82.6	380	17	AQ119439	AQ119439 HS 2165_B	C 485	19	82.6	442	12	BF871533	BF871533 IL5-ET011
C 413	19	82.6	383	9	AA877992	AA877992 oh95h04.s	C 486	19	82.6	442	12	BF871533	BF871533 IL5-ET011
C 414	19	82.6	385	14	T90080	T90080 yd39b07.s1	C 487	19	82.6	443	17	AQ233796	AQ233796 HS 2046_B
C 415	19	82.6	386	13	EG939818	EG939818 cr63a05.x	C 488	19	82.6	443	17	AQ222139	AQ222139 HS 2193_A
C 416	19	82.6	386	13	EG939828	EG939828 cr63b11.x	C 489	19	82.6	444	17	AQ112607	AQ112607 CIT-HSP-2
C 417	19	82.6	386	13	EG939834	EG939834 cr63c11.x	C 490	19	82.6	445	17	AQ183180	AQ183180 HS 3132_A
C 418	19	82.6	387	9	A1537368	A1537368 tp07g09.x	C 491	19	82.6	446	17	AQ552491	AQ552491 RPTC11-4
C 419	19	82.6	387	10	AW338506	AW338506 xw71g01.x	C 492	19	82.6	448	17	AQ035361	AQ035361 CIT-HSP-2
C 420	19	82.6	388	14	BQ268842	BQ268842 ik21c02.x	C 493	19	82.6	448	17	AQ280660	AQ280660 CITBI-E1-
C 421	19	82.6	389	17	AQ263739	AQ263739 CITBI-EI-	C 494	19	82.6	449	13	BI714784	BI714784 ic31h04.x
C 422	19	82.6	391	9	AA311522	AA311522 EST18266	C 495	19	82.6	449	9	AA705333	AA705333 zj97f12.s
C 423	19	82.6	392	17	AQ380122	AQ380122 RPTC11-13	C 496	19	82.6	450	13	BM264564	BM264564 i936h10.x
C 424	19	82.6	395	9	AA663786	AA663786 ae72f07.s	C 497	19	82.6	450	13	BM310600	BM310600 i950b09.x
C 425	19	82.6	397	10	AW020150	AW020150 df05a09.y	C 498	19	82.6	450	17	AQ381517	AQ381517 RPTC11-16
C 426	19	82.6	397	12	BG896311	BG896311 HOA29-1-C	C 499	19	82.6	452	17	AQ595781	AQ595781 HS 2131_B
C 427	19	82.6	400	10	AW028403	AW028403 wv88f09.x	C 500	19	82.6	452	17	AQ770491	AQ770491 HS 5372_A
C 428	19	82.6	400	17	AQ755528	AQ755528 HS 2210_B	C 501	19	82.6	453	17	AQ815097	AQ815097 HS 5361_B
C 429	19	82.6	401	9	AL048983	AL048983 DKEZp434M	C 502	19	82.6	453	17	AQ180278	AQ180278 HS 3209_B
C 430	19	82.6	401	17	AQ412443	AQ412443 RPTC11-11	C 503	19	82.6	454	14	C06481	C06481 C06481 Huma
C 431	19	82.6	403	17	AQ129179	AQ129179 HS 3037_B	C 504	19	82.6	455	17	AQ178894	AQ178894 tu70f09.x
C 432	19	82.6	403	17	AQ020701	AQ020701 RPTC11-57	C 505	19	82.6	457	9	BE045897	BE045897 hq54d11.x
C 433	19	82.6	404	9	A1366729	A1366729 qy95c09.x	C 506	19	82.6	458	10	BE045897	BE045897 hq54d11.x
C 434	19	82.6	404	13	BI491182	BI491182 df05a09.w	C 507	19	82.6	459	17	AQ284359	AQ284359 RPTC11-91
C 435	19	82.6	404	14	N22161	N22161 yw33g10.s1	C 508	19	82.6	459	17	AQ586397	AQ586397 RPTC11-4
C 436	19	82.6	404	17	AQ733664	AQ733664 HS 5558_A	C 509	19	82.6	460	10	AW088563	AW088563 xdl7f02.x
C 437	19	82.6	405	9	AA070539	AA070539 zm70b04.r	C 510	19	82.6	460	17	AQ382314	AQ382314 RPTC11-13
C 438	19	82.6	406	12	BF871325	BF871325 CM0-ET012	C 511	19	82.6	464	9	A1571512	A1571512 tr95a12.x
C 439	19	82.6	408	14	H57192	H57192 y08a05.r1	C 512	19	82.6	464	17	B42459	B42459 HS-1055-B2-
C 440	19	82.6	408	17	AQ101931	AQ101931 HS 3017_B	C 513	19	82.6	465	17	AQ340477	AQ340477 HS 2236_B
C 441	19	82.6	410	14	W93102	W93102 zh45e02.s1	C 514	19	82.6	466	17	AQ817627	AQ817627 HS 5285_B
C 442	19	82.6	410	17	AQ132151	AQ132151 HS 3001_B	C 515	19	82.6	467	12	BG007715	BG007715 RC2-GN026
C 443	19	82.6	411	14	BQ778298	BQ778298 il44f02.x	C 516	19	82.6	467	17	AZ517949	AZ517949 RPTC11-9
C 444	19	82.6	412	9	A1654529	A1654529 tq91h04.x	C 517	19	82.6	467	17	AQ491297	AQ491297 RPTC11-2

C 518	19	82.6	469	14	BQ890690	BQ890690 AGENCOURT	C 591	19	82.6	517	17	AQ323115	AQ323115 RPC111-96
C 519	19	82.6	470	9	AL299694	AL299694 qm37a09.x	C 592	19	82.6	519	17	AQ678348	AQ678348 HS 5529 B
C 520	19	82.6	470	9	AL707371	AL707371 DKFZp686F	C 593	19	82.6	520	9	AL710725	AL710725 DKFZp686L
C 521	19	82.6	470	10	AW265393	AW265393 xp46d12.x	C 594	19	82.6	521	9	AL711809	AL711809 DKFZp686C
C 522	19	82.6	471	9	A1570212	A1570212 to76d03.x	C 595	19	82.6	522	9	AQ150128	AQ150128 HS 3194 A
C 523	19	82.6	471	10	AW501334	AW501334 UI-HF-BPO	C 596	19	82.6	524	13	BM310899	BM310899 i950809.y
C 524	19	82.6	472	10	AW238345	AW238345 xp21c10.x	C 597	19	82.6	525	17	AQ726076	AQ726076 HS 5403 B
C 525	19	82.6	472	17	AQ310879	AQ310879 CIT-HSP-2	C 598	19	82.6	525	17	AQ370935	AQ370935 HS 5048 A
C 526	19	82.6	473	9	A1039738	A1039738 ox33h10.s	C 599	19	82.6	525	17	AQ532727	AQ532727 RPC111-3
C 527	19	82.6	473	17	AQ278752	AQ278752 CITBI-E1-	C 600	19	82.6	526	9	A1871225	A1871225 w180b08.x
C 528	19	82.6	474	9	A1989390	A1989390 wt80f04.x	C 601	19	82.6	527	17	AQ785290	AQ785290 HS 3214 A
C 529	19	82.6	474	17	AQ387376	AQ387376 RC111-14	C 602	19	82.6	530	10	BE042846	BE042846 ho29f03.x
C 530	19	82.6	475	17	AQ569138	AQ569138 HS 5332 A	C 603	19	82.6	531	17	AQ483271	AQ483271 RPC111-2
C 531	19	82.6	476	9	A1377567	A1377567 tc37f04.x	C 604	19	82.6	532	9	AA844930	AA844930 ak61a09.s
C 532	19	82.6	477	12	BF906470	BF906470 ILO-OT012	C 605	19	82.6	532	10	AV754589	AV754589 AV754589
C 533	19	82.6	477	12	BF906470	BF906470 ILO-OT012	C 606	19	82.6	532	10	AV754589	AV754589 AV754589
C 534	19	82.6	479	17	AQ792336	AQ792336 CIT-HSP-2	C 607	19	82.6	533	17	AQ310799	AQ310799 CITBI-E1-
C 535	19	82.6	480	17	B43116	B43116 HS-1057-A1-	C 608	19	82.6	535	10	AW975164	AW975164 EST397270
C 536	19	82.6	481	10	AV743288	AV743288 AV743288	C 609	19	82.6	536	9	AL043804	AL043804 DKFZp434P
C 537	19	82.6	482	17	B94693	B94693 CIT-HSP-216	C 610	19	82.6	536	17	AQ839321	AQ839321 HS 5258 A
C 538	19	82.6	483	9	AL701275	AL701275 DKFZp686C	C 611	19	82.6	537	13	BI714785	BI714785 iG31h05.x
C 539	19	82.6	483	10	AW188419	AW188419 xj98a02.x	C 612	19	82.6	537	17	AQ311201	AQ311201 CITBI-E1-
C 540	19	82.6	483	10	AW499719	AW499719 UI-HF-BRO	C 613	19	82.6	539	12	BQ291183	BQ291183 602398621
C 541	19	82.6	484	14	R12604	R12604 yf57a01.r1	C 614	19	82.6	539	17	AQ391351	AQ391351 CITBI-E1-
C 542	19	82.6	484	17	AQ223415	AQ223415 HS 2014 B	C 615	19	82.6	540	17	AQ694862	AQ694862 HS 5471 B
C 543	19	82.6	484	17	AQ240423	AQ240423 CIT-HSP-2	C 616	19	82.6	540	17	AQ883528	AQ883528 HS 5478 A
C 544	19	82.6	485	12	BF874197	BF874197 MR1-ET014	C 617	19	82.6	542	14	BM822753	BM822753 K-EST0092
C 545	19	82.6	486	14	C06154	C06154 C06154 Huma	C 618	19	82.6	544	9	AL047247	AL047247 DKFZp586A
C 546	19	82.6	487	17	AQ789011	AQ789011 HS 3044 B	C 619	19	82.6	544	17	AQ394650	AQ394650 CITBI-E1-
C 547	19	82.6	487	17	B59081	B59081 CIT-HSP-201	C 620	19	82.6	545	10	AW852727	AW852727 PMI-CT024
C 548	19	82.6	487	17	AQ332988	AQ332988 CITBI-E1-	C 621	19	82.6	545	17	AQ408978	AQ408978 HS 5065 B
C 549	19	82.6	488	14	BM763572	BM763572 K-EST0044	C 622	19	82.6	546	17	AQ417654	AQ417654 RPC111-2
C 550	19	82.6	489	10	AW172908	AW172908 xj05e10.x	C 623	19	82.6	547	17	AQ536020	AQ536020 RPC111-3
C 551	19	82.6	489	17	AQ276084	AQ276084 CITBI-E1-	C 624	19	82.6	548	9	AU144688	AU144688 AU144688
C 552	19	82.6	489	17	AQ406744	AQ406744 HS 5103 B	C 625	19	82.6	549	17	AQ333394	AQ333394 HS 5009 B
C 553	19	82.6	491	12	BF754060	BF754060 IL5-CT052	C 626	19	82.6	549	17	AQ558170	AQ558170 HS 2067 B
C 554	19	82.6	491	17	AQ882875	AQ882875 HS 5448 B	C 627	19	82.6	551	10	AW938578	AW938578 PM2-DT006
C 555	19	82.6	492	17	AQ134773	AQ134773 HS 3053 A	C 628	19	82.6	552	14	BM688309	BM688309 UI-E-CL0-
C 556	19	82.6	492	9	A1377556	A1377556 tc37e04.x	C 629	19	82.6	553	17	B92301	B92301 CIT-HSP-217
C 557	19	82.6	493	17	AQ894221	AQ894221 HS 3114 A	C 630	19	82.6	553	17	AQ415061	AQ415061 RPC111-2
C 558	19	82.6	494	14	H29241	H29241 ym59f09.e1	C 631	19	82.6	553	17	AQ417207	AQ417207 RPC111-2
C 559	19	82.6	495	17	AQ246931	AQ246931 HS 2016 B	C 632	19	82.6	554	9	AU146713	AU146713 AU146713
C 560	19	82.6	495	17	AQ338555	AQ338555 HS 3118 B	C 633	19	82.6	554	10	BE151208	BE151208 RC4-HT027
C 561	19	82.6	496	9	AU121297	AU121297 AU121297	C 634	19	82.6	555	17	AQ463998	AQ463998 HS 5087 A
C 562	19	82.6	497	12	BF814066	BF814066 MR2-CI018	C 635	19	82.6	557	12	BF816011	BF816011 MR2-CI012
C 563	19	82.6	497	14	T52020	T52020 yb29h03.s1	C 636	19	82.6	557	12	AQ267977	AQ267977 RPC111-72
C 564	19	82.6	498	10	AW658184	AW658184 EST390379	C 637	19	82.6	558	10	AW974167	AW974167 EST396270
C 565	19	82.6	498	17	B82435	B82435 RPC111-15M3	C 638	19	82.6	558	17	AQ149657	AQ149657 HS 3171 B
C 566	19	82.6	499	10	AW469098	AW469098 hc77b02.x	C 639	19	82.6	559	9	AU148234	AU148234 AU148234
C 567	19	82.6	499	14	BQ416803	BQ416803 iK41g12.x	C 640	19	82.6	559	14	BM822827	BM822827 K-EST0093
C 568	19	82.6	499	17	AQ263708	AQ263708 CITBI-E1-	C 641	19	82.6	559	17	AQ487105	AQ487105 RPC111-2
C 569	19	82.6	500	17	AQ040474	AQ040474 CIT-HSP-2	C 642	19	82.6	560	14	BQ271553	BQ271553 iK15d04.x
C 570	19	82.6	502	17	AQ758821	AQ758821 HS 3024 B	C 643	19	82.6	561	17	AQ346608	AQ346608 RPC111-12
C 571	19	82.6	504	14	BM673489	BM673489 UI-E-CRI-	C 644	19	82.6	565	17	AQ349314	AQ349314 RPC111-12
C 572	19	82.6	505	9	A1377505	A1377505 tc37d04.x	C 645	19	82.6	567	10	AV718449	AV718449 AV718449
C 573	19	82.6	505	14	BQ640608	BQ640608 hc30h04.y	C 646	19	82.6	567	12	BG142238	BG142238 iA52e02.y
C 574	19	82.6	509	10	AW504832	AW504832 UI-HF-BNO	C 647	19	82.6	568	17	AQ377281	AQ377281 RPC111-1
C 575	19	82.6	510	17	AQ140446	AQ140446 HS 3110 B	C 648	19	82.6	568	17	AQ532926	AQ532926 RPC111-3
C 576	19	82.6	510	17	AQ279719	AQ279719 CITBI-E1-	C 649	19	82.6	570	17	BI5271	BI5271 344117.TV C
C 577	19	82.6	511	13	BM353779	BM353779 i956a11.y	C 650	19	82.6	570	17	AQ306219	AQ306219 HS 2041 A
C 578	19	82.6	511	17	AQ263778	AQ263778 CITBI-E1-	C 651	19	82.6	571	17	AQ775679	AQ775679 HS 2173 B
C 579	19	82.6	511	17	AQ488409	AQ488409 RPC111-2	C 652	19	82.6	572	17	B49180	B49180 RPC111-5C23
C 580	19	82.6	511	17	AQ488409	AQ488409 RPC111-2	C 653	19	82.6	573	13	BM263650	BM263650 i928g07.y
C 581	19	82.6	512	14	BQ640398	BQ640398 hc28a08.y	C 654	19	82.6	573	17	AQ037313	AQ037313 CIT-HSP-2
C 582	19	82.6	513	10	BE151195	BE151195 RC4-HT027	C 655	19	82.6	573	17	AQ059773	AQ059773 RPC111-42
C 583	19	82.6	513	17	AQ027663	AQ027663 CIT-HSP-2	C 656	19	82.6	575	17	AQ503749	AQ503749 RPC111-2
C 584	19	82.6	513	17	AQ353226	AQ353226 CITBI-E1-	C 657	19	82.6	576	9	AA570010	AA570010 nm48h01.s
C 585	19	82.6	515	9	AA665160	AA665160 nu83b08.s	C 658	19	82.6	576	12	BF812525	BF812525 MR2-CI018
C 586	19	82.6	515	14	BQ026454	BQ026454 UI-1-BB0-	C 659	19	82.6	577	17	B01006	B01006 cSRL-123b7-
C 587	19	82.6	515	17	AQ738319	AQ738319 HS 2260 B	C 660	19	82.6	579	9	A1525172	A1525172 promrna-9
C 588	19	82.6	516	9	A1978650	A1978650 wr57g08.x	C 661	19	82.6	579	10	AW851317	AW851317 IL3-CT022
C 589	19	82.6	516	17	AQ207747	AQ207747 HS 5560 A	C 662	19	82.6	579	17	AQ531851	AQ531851 RPC111-3
C 590	19	82.6	516	17	AQ293549	AQ293549 HS_3024_A	C 663	19	82.6	582	10	BE045902	BE045902 hc54f03.x

664	19	82.6	585	17	AQ423630	CITBI-E1-	737	19	82.6	690	17	AG146194	Pan trogl
C 665	19	82.6	587	10	AW150781	XG39503.x	C 738	19	82.6	691	17	AQ051709	RPCI11-49
666	19	82.6	588	10	AV759047	AV759047	739	19	82.6	691	17	AQ001893	Homo sapi
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668	19	82.6	588	14	BM992270	UT-H-DF1-	741	19	82.6	693	10	AG001472	Homo sapi
C 669	19	82.6	592	10	AV718791	AV718791	C 742	19	82.6	696	10	AV731842	AV731842
C 670	19	82.6	594	9	AA668309	ab79d02.s	C 743	19	82.6	696	17	AG009915	Homo sapi
C 671	19	82.6	594	17	AQ319274	RPCI11-99	C 744	19	82.6	698	17	AQ013971	RPCI11-23
C 672	19	82.6	596	17	AQ379242	RPCI11-11-1	C 745	19	82.6	698	17	AQ059526	CIT-HSP-2
C 673	19	82.6	598	17	AQ350160	RPCI11-10	746	19	82.6	698	17	AQ009905	Homo sapi
674	19	82.6	601	17	B83348	B83348	747	19	82.6	698	17	AQ009905	Homo sapi
C 675	19	82.6	604	17	AQ285763	RPCI11-89	748	19	82.6	699	17	AG180770	Pan trogl
C 676	19	82.6	614	17	AQ051953	AQ051953	749	19	82.6	702	17	AG171475	Pan trogl
C 677	19	82.6	621	17	AG012061	Homo sapi	C 750	19	82.6	706	17	AG124119	Pan trogl
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## ALIGNMENTS

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LOCUS      HA2479 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION      A1174766
VERSION      A1174766.1 GI:63611145
KEYWORDS      EST.
SOURCE      human.

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ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 217)
AUTHORS      Yu.Y., Zhang.C., Luo.L., Ouyang.S., Li.W., Wu.J., Zhou.S., Liu.M.
and He.F.
TITLE      Expression profile analysis of a human fetal liver cDNA library
JOURNAL      Unpublished (1998)
COMMENT      Contact: Chenggang Zhang
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Email: zhang.chenggang@hotmail.com.
FEATURES      source
              1..217
              Location/Qualifiers

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/db xref="taxon:9606"
/clone_lib="Human fetal liver cDNA library"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/P3"
/notes="Vector: pCDNA1"

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BASE COUNT      69 a 49 c 55 g 44 t
ORIGIN

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Query Match      95.7%; Score 22; DB 9; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 1 CAGCCAGGCATGGTGGCAGGTG 22
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Db 44 CAGCCAGGCATGGTGGCAGGTG 65
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RESULT 2
AA372667
LOCUS

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DEFINITION      AA372667      237 bp mrna linear EST 21-APR-1997
to EST84797 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar
to EST containing Alu repeat, mRNA sequence.
ACCESSION      AA372667
VERSION      AA372667.1 GI:20251575
KEYWORDS      EST.
SOURCE      human.

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## ORGANISM

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Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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## REFERENCE

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1 (bases 1 to 237)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Shall,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li.Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li.H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu.C., Yu.G.L., Ruben,S.M., Dillion,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tcdb/hgi/hgi.html)
Seq primer: M13 Reverse.
              Location/Qualifiers
              1..237
              /organism="Homo sapiens"
              /db xref="taxon:9606"
              /clone_lib="Colon adenocarcinoma IV"
              /dev_stage="adult"
              /note="Organ: colon; Vector: pBluescript SK-; Site_1:
              EcoRI; Site_2: XhoI"

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## FEATURES

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source
1..237
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="Colon adenocarcinoma IV"
/dev_stage="adult"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

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BASE COUNT      68 a      50 c      67 g      52 t
ORIGIN
Query Match      95.7%; Score 22; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 152 AGCCAGGCATGGTGGCAGGTGT 173

RESULT 3
AQ102785      361 bp      DNA      linear      GSS 27-AUG-1998
LOCUS
DEFINITION
HS 3055 A2 C10 MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3055 Col=20 Row=E, DNA sequence.
ACCESSION
AQ102785
VERSION
AQ102785.1 GI:3473814
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 361)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
9380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3055 row: E column: 20
Class: BAC ends
High quality sequence stop: 361.
Location/Qualifiers
1. 361
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT      112 a      77 c      98 g      73 t      1 others
ORIGIN
Query Match      95.7%; Score 22; DB 17; Length 361;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23
|||||
Db 150 AGCCAGGCATGGTGGCAGGTGT 171

RESULT 4
BG960515      375 bp      mRNA      linear      EST 12-JUN-2001
LOCUS
DEFINITION
IL3-CT0674-060401-492-D11 CT0674 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG960515
VERSION
BG960515.1 GI:14378673
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 375)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0674-
060401-492-D11&t3=2001-04-06&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 375.
Location/Qualifiers
1. 375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0674"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (O.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT      109 a      82 c      91 g      93 t
ORIGIN
Query Match      95.7%; Score 22; DB 13; Length 375;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCAGGCATGGTGGCAGGTG 22
|||||
Db 297 CAGCCAGGCATGGTGGCAGGTG 318

RESULT 5
BF084762      538 bp      mRNA      linear      EST 18-OCT-2000
LOCUS
DEFINITION
MR1-CT0529-140900-002-e06 CT0529 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF084762
VERSION
BF084762.1 GI:10878592
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 538)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

```



MEDLINE  
COMMENT  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR1-CT0529-140  
900-002-e06&t3=2000-09-14&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 3  
High quality sequence stop: 538.  
Location/Qualifiers  
FEATURES  
source  
1. .538  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0529"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 170 a 116 c 107 g 144 t 1 others  
ORIGIN  
Query Match 95.7%; Score 22; DB 12; Length 538;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAGCCAGGCATGGTGGCAGGTG 22  
Db 512 CAGCCAGGCATGGTGGCAGGTG 533  
RESULT 6  
A0714377/c  
LOCUS  
DEFINITION HS\_5426\_A2\_H11\_T7A\_RPC1-11 Human Male BAC Library Homo sapiens  
Genomic clone Plate=1002 Col=22 Row=O, DNA sequence.  
ACCESSION A0714377  
VERSION A0714377.1 GI:5463693  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 587)  
Mahaitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
MEDLINE  
COMMENT 99380589  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPC1-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)  
or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu  
Plate: 1002 Row: O Column: 22  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 587.  
Location/Qualifiers  
FEATURES  
source  
1. .587  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="RPC1-11 Human Male BAC Library"  
/sex="male"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"  
BASE COUNT 159 a 137 c 108 g 166 t 17 others  
ORIGIN  
Query Match 95.7%; Score 22; DB 17; Length 587;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 AGCCAGGCATGGTGGCAGGTG 23  
Db 386 AGCCAGGCATGGTGGCAGGTG 365  
RESULT 7  
AG034167  
LOCUS  
DEFINITION Pan troglodytes DNA, clone: PTB-009G22.F, genomic survey sequence.  
ACCESSION AG034167  
VERSION AG034167.1 GI:16561040  
KEYWORDS GSS.  
SOURCE Pan troglodytes male lymphoblast DNA, clone lib:PTB Chimpanzee Male  
BAC Library clone:PTB-009G22.F.  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE  
1  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 674)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimps@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
FEATURES  
source  
1. .674  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-009G22.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"  
BASE COUNT 264 a 134 c 142 g 133 t 1 others



## ORIGIN

Query Match 95.7%; Score 22; DB 17; Length 674;  
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23  
 |||||  
 Db 149 AGCCAGGCATGGTGGCAGGTGT 170

## RESULT 8

AG096453/c  
 LOCUS Homo sapiens  
 DEFINITION Pan troglodytes DNA, clone: PTB-097N07.F, genomic survey sequence.  
 ACCESSION AG096453  
 VERSION AG096453.1 GI:16716970  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male

## ORGANISM

Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

## REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 679)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB. This BAC end

was generated during the R&D process and may have higher chance of

clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.

Location/Qualifiers

1. 679

/organism="Pan troglodytes"

/db xref="taxon:9598"

/clone="PTB-097N07.F"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

131 a 180 c 173 g 195 t

## BASE COUNT

## ORIGIN

Query Match 95.7%; Score 22; DB 17; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23  
 |||||  
 Db 417 AGCCAGGCATGGTGGCAGGTGT 396

## RESULT 9

BG617547  
 LOCUS Homo sapiens  
 DEFINITION 602615028F1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4733982 5',  
 mRNA sequence.

## ACCESSION

BG617547

VERSION BG617547.1 GI:13668918

## KEYWORDS

## SOURCE

human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 723)

NIH-MGC http://mgs.nci.nih.gov/.

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI596 row: g column: 07

High quality sequence stop: 706.

## FEATURES

## source

1. 723  
 /organism="Homo sapiens"  
 /db xref="taxon:9606"  
 /clone="IMAGE:4733982"  
 /clone\_lib="NIH\_MGC\_76"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccgcctcgcc); Site 2: SfiI (ggccattatggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGGCATATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.85  
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH MGC Library."

BASE COUNT 235 a 138 c 137 g 213 t

## ORIGIN

Query Match 95.7%; Score 22; DB 12; Length 723;  
 Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0;

Qy 2 AGCCAGGCATGGTGGCAGGTGT 23  
 |||||

Db 128 AGCCAGGCATGGTGGCAGGTGT 149

## RESULT 10

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## human.

## ORGANISM

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

```

http://image.llnl.gov
Plate: L1CM1067 row: 1 column: 22
High quality sequence stop: 239.
Location/Qualifiers
1. 766
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cln="IMAGE:4248741"
/clone_lib="NIH_MGC_83"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfII (ggcgctggcc); Site 2: SfII (ggccattggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGGCACATG-dT(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 207 a 186 c 211 g 162 t
ORIGIN

Query Match 95.7%; Score 22; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGGCGATGGTGGCAGGTG 22
|||||
Db 128 CAGCAGGCGATGGTGGCAGGTG 149

RESULT 11
AA089829
LOCUS
DEFINITION chn1495.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
CDNA 5', mRNA sequence.
ACCESSION AA089829
VERSION AA089829.1 GI:1636321
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 144)
Liew, C.C.
CDNAs from fetal heart (1996)
Unpublished (1996)
JOURNAL
COMMENT Bringham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6179750995
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: 5' CCAAGTCTGAATTAACCTCACTAAGGG 3'
PCR Primers
FORWARD: 5' CCAAGTCTGAATTAACCTCACTAAGGG 3'
BACKWARD: 5' CCAAGTCTGAATTAACCTCACTAAGGG 3'
Seq primer: 5' GAAATTAACCTCACTAAGGG 3'.
Location/Qualifiers
1. 144
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dt
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI for directional cloning into
predigested lambda ZAP Express."
BASE COUNT 37 a 34 c 45 g 28 t
ORIGIN

Query Match 91.3%; Score 21; DB 9; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCGATGGTGGCAGGTG 22
|||||
Db 5 AGCCAGGCGATGGTGGCAGGTG 25

RESULT 12
N84649/c
LOCUS
DEFINITION N84649 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
clone J0399 5' similar to REPETITIVE ELEMENT ALU, mRNA sequence.
ACCESSION N84649
VERSION N84649.1 GI:1260274
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 150)
Liew, C.C.
CDNAs from fetal heart (1996)
Unpublished (1996)
JOURNAL
COMMENT Bringham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6179750995
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: GAAATTAACCTCACTAAGGG.
Location/Qualifiers
1. 150
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dt
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI for directional cloning into
predigested lambda ZAP Express."
BASE COUNT 35 a 40 c 31 g 44 t
ORIGIN

Query Match 91.3%; Score 21; DB 14; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCGATGGTGGCAGGTG 22
|||||
Db 72 AGCCAGGCGATGGTGGCAGGTG 52

RESULT 13
T28260
LOCUS
DEFINITION T28260 Human Embryo Homo sapiens cDNA 5' end similar to
alcohol/hydroxysteroid sulfotransferase (HT:2595), mRNA sequence.
ACCESSION T28260
VERSION T28260.1 GI:610358
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 152)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

```

C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.B., Hanna, W.C., Hedblom, E., Hinkley, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

**TITLE** Initial Assessment of Human Gene Diversity and Expression Patterns  
**JOURNAL** Based Upon 83 Million Basepairs of cDNA Sequence  
**MEDLINE** Nature 377, 3-174 (1995)  
**COMMENT** 96026280

**CONTACT:** Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@db.tigr.org)

Seq primer: M13 Reverse.

Location/Qualifiers

1. .152

/organism="Homo sapiens"

/db\_xref="ATCC (inhost):101723"

/db\_xref="taxon:9606"

/clone\_lib="Human Embryo"

/tissue\_type="embryo"

/note="Organ: colon"

BASE COUNT 39 a 34 c 52 t

ORIGIN

Query Match 91.3%; Score 21; DB 14; Length 152;

Best Local Similarity 100.0%; Pred. No. 0.95;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGTCGCGAGGTG 22

Db 130 AGCCAGGCATGTCGCGAGGTG 150

RESULT 14

AI925839/c

LOCUS

DEFINITION

w052h09.x1 NCI\_CGAP Gas4 Homo sapiens cDNA clone IMAGE:2459009 3'

similar to contains Alu repetitive element; contains element PTR5

repetitive element ; mRNA sequence.

AI925839

ACCESSION

VERSION

AI925839.1 GI:5661803

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 170)

REFERENCE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgap@remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Insert length: 2114 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 141.

Location/Qualifiers

1. .170

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2459009"

/clone\_lib="NCI CGAP Gas4"

/tissue\_type="poorly\_differentiated adenocarcinoma with

signet ring cell features"

/lab\_host="DH10B"

/notes="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

BASE COUNT 32 a 52 c 39 g 47 t

ORIGIN

Query Match 91.3%; Score 21; DB 9; Length 170;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCCAGGCATGTCGCGAGGTG 22

Db 151 AGCCAGGCATGTCGCGAGGTG 131

RESULT 15

BE179910/c

LOCUS

DEFINITION

IL3-HT0618-110500-133-Fl2 HT0618 Homo sapiens cDNA, mRNA sequence.

BE179910

ACCESSION

BE179910.1 GI:8658971

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 183)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zsago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

COMMENT

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL3-HT0618-110

500-133-Fl2&t3=2000-05-11&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 183.

Location/Qualifiers

1. .183

/organism="Homo sapiens"

/db\_xref="taxon:9606"

**FEATURES**

source

1. .183

/organism="Homo sapiens"

/db\_xref="taxon:9606"

**TITLE**

JOURNAL

MEDLINE

COMMENT

```

/clone_lib="HT0618"
/dev_stage="Adult"
/site="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      35 a      49 c      38 g      61 t
ORIGIN

```

```

Query Match      91.3%; Score 21; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AGCCAGGCATGGTGGCAGGTG 22
      |||||
Db      165 AGCCAGGCATGGTGGCAGGTG 145

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Search completed: June 17, 2003, 06:24:11  
Job time : 74.3864 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 4429.72 Seconds  
(without alignments)  
15794.017 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_4514\_6917

Perfect score: 2404

Sequence: 1 agagggagcgcgaggtgc.....gacagggtctgtctgtcc 2404

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_man.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2404	100.0	9108	9	AF123653	Homo sapi
2	1966	81.8	5492	9	AF123659	Homo sapi
3	1338	55.7	173264	2	AC025853	Homo sapi
4	373	15.5	1722	9	AF123658	Homo sapi
5	283	11.8	1692	9	AF123657	Homo sapi
6	254	10.6	1614	9	AF123655	Homo sapi
7	219	9.1	1515	9	AF123656	Homo sapi
8	80	3.3	633	9	AF123654	Homo sapi
9	76	3.2	231	9	AF123652	Homo sapi
10	52	2.2	227884	2	AC114995	Mus muscu
c 11	52	2.2	263546	2	AC099416	Mus muscu
12	49	2.0	162178	9	AC093491	Homo sapi
c 13	49	2.0	195952	9	AC012184	Homo sapi
14	43	1.8	129435	9	AL391314	Human DNA
c 15	43	1.8	140179	2	AC084688	Homo sapi
16	43	1.8	178785	9	AC068139	Homo sapi
17	43	1.8	203484	2	AC010194	Homo sapi
18	42	1.7	26478	9	AL445307	Human DNA
19	42	1.7	42159	9	AP000950	Homo sapi
c 20	42	1.7	104357	9	AL392123	Human DNA
21	42	1.7	138006	2	AC068246	Homo sapi
22	42	1.7	144784	9	AC009224	Homo sapi
23	42	1.7	145528	9	AC003665	Homo sapi
c 24	42	1.7	147244	9	AC005969	Homo sapi
25	42	1.7	147525	2	AC060754	Homo sapi
26	42	1.7	154708	2	AC024443	Homo sapi
27	42	1.7	157289	9	AC009234	Homo sapi
c 28	42	1.7	159070	2	AC131160	Homo sapi
29	42	1.7	160604	9	AL449305	Human DNA
30	42	1.7	167998	9	AL353662	Human DNA
31	42	1.7	168738	2	AC093632	Homo sapi
32	42	1.7	169149	9	AL445930	Human DNA
33	42	1.7	171731	2	AC091659	Papio cyn
34	42	1.7	175952	2	AC009195	Homo sapi
c 35	42	1.7	178688	9	AC068644	Homo sapi
c 36	42	1.7	180231	9	AC009161	Homo sapi
c 37	42	1.7	181049	9	AC093131	Papio cyn
38	42	1.7	187064	9	AC011476	Homo sapi
39	42	1.7	187822	9	AC015674	Homo sapi
c 40	42	1.7	203006	9	HS1145123	Human DNA
41	42	1.7	203912	9	AC008755	Homo sapi
42	42	1.7	204340	2	AC019238	Homo sapi
c 43	42	1.7	247335	2	AC084794	Homo sapi
c 44	42	1.7	257967	2	AL365337	Mus muscu
45	42	1.7	340000	9	AP001688	Homo sapi
46	41	1.7	87471	9	AC041005	Homo sapi
c 47	41	1.7	103819	9	HSJ775C13	Human DNA
48	41	1.7	122564	9	HSJ899B16	Human DNA
c 49	41	1.7	150829	2	AC009092	Homo sapi
c 50	41	1.7	162559	9	AL360230	Human DNA
c 51	41	1.7	164602	9	AC022001	Homo sapi
c 52	41	1.7	165398	2	AC012086	Homo sapi
c 53	41	1.7	166206	2	AC016927	Homo sapi
54	41	1.7	167238	9	AC024903	Homo sapi
55	41	1.7	167245	9	AC099521	Homo sapi
c 56	41	1.7	169969	2	AL390727	Homo sapi
c 57	41	1.7	173317	9	AC016637	Homo sapi
c 58	41	1.7	177834	9	AC018811	Homo sapi
c 59	41	1.7	181646	9	AC009162	Homo sapi
c 60	41	1.7	182452	9	AL161731	Human DNA
61	41	1.7	186202	9	AC108516	Homo sapi
c 62	41	1.7	191308	9	AC034243	Homo sapi
c 63	41	1.7	195191	9	AC024339	Homo sapi
c 64	41	1.7	201599	2	AC068790	Homo sapi
c 65	41	1.7	210067	2	AC026358	Homo sapi

C 66	41	1-7	212659	2	AL390737	AL390737 Homo sapi	C 139	38	1-6	59561	2	AC009011	AC009011 Homo sapi
C 67	41	1-7	243587	2	AL591179	AL591179 Homo sapi	C 140	38	1-6	62944	6	AX334775	AX334775 Sequence
C 68	40	1-7	105880	9	HS127820	Z83838 Human DNA s	C 141	38	1-6	62944	6	AX336090	AX336090 Sequence
C 69	39	1-6	105880	9	AL158062	AL158062 Human DNA s	C 142	38	1-6	62944	9	HS127820	HS127820 Sequence
C 70	39	1-6	119638	9	AC024575	AC024575 Homo sapi	C 143	38	1-6	63459	2	AC115224	AC115224 Homo sapi
C 71	39	1-6	130416	9	AC008851	AC008851 Homo sapi	C 144	38	1-6	65435	2	AC104587	AC104587 Homo sapi
C 72	39	1-6	148656	9	AC005482	AC005482 Homo sapi	C 145	38	1-6	65961	2	AC090266	AC090266 Homo sapi
C 73	39	1-6	150107	2	AC027582	AC027582 Homo sapi	C 146	38	1-6	66597	2	AC090850	AC090850 Homo sapi
C 74	39	1-6	154370	2	AC108106	AC108106 Homo sapi	C 147	38	1-6	67066	2	AC126358	AC126358 Homo sapi
C 75	39	1-6	162350	9	AC008118	AC008118 Homo sapi	C 148	38	1-6	67236	2	AC021282	AC021282 Homo sapi
C 76	39	1-6	177381	2	AC083805	AC083805 Homo sapi	C 149	38	1-6	67550	2	AC016452	AC016452 Homo sapi
C 77	39	1-6	180672	9	AC011451	AC011451 Homo sapi	C 150	38	1-6	67908	2	AC103998	AC103998 Homo sapi
C 78	39	1-6	184053	9	AC011900	AC011900 Homo sapi	C 151	38	1-6	68517	2	AC107935	AC107935 Homo sapi
C 79	39	1-6	194716	2	AL136227	AL136227 Homo sapi	C 152	38	1-6	68517	2	AL107935	AL107935 Homo sapi
C 80	39	1-6	198161	9	HS232K4	AL021938 Homo sapi	C 153	38	1-6	68525	2	AL845464	AL845464 Homo sapi
C 81	39	1-6	202457	2	AC121759	AC121759 Homo sapi	C 154	38	1-6	70416	9	AC095039	AC095039 Homo sapi
C 82	39	1-6	203530	9	AC025097	AC025097 Homo sapi	C 155	38	1-6	70435	2	AC116909	AC116909 Homo sapi
C 83	39	1-6	212103	9	CNS01DV4	AL133453 Human Chr	C 156	38	1-6	70972	2	AC130332	AC130332 Homo sapi
C 84	39	1-6	217328	2	AC007513	AC007513 Homo sapi	C 157	38	1-6	71263	9	HS1014D13	AL022311 Human DNA
C 85	39	1-6	217668	2	AC020561	AC020561 Homo sapi	C 158	38	1-6	72461	9	AC073322	AC073322 Homo sapi
C 86	39	1-6	239008	2	AC022460	AC022460 Homo sapi	C 159	38	1-6	72754	9	AC011398	AC011398 Homo sapi
C 87	39	1-6	309805	2	AC026340	AC026340 Homo sapi	C 160	38	1-6	72847	2	AC023563	AC023563 Homo sapi
C 88	39	1-6	313264	2	AC023053	AC023053 Homo sapi	C 161	38	1-6	73201	9	AC011388	AC011388 Homo sapi
C 89	38	1-6	394	11	HUMUT6516	L30644 Human STRs U	C 162	38	1-6	73845	2	AL356478	AL356478 Homo sapi
C 90	38	1-6	1408	9	AK026097	AK026097 Homo sapi	C 163	38	1-6	75001	9	AC093167	AC093167 Homo sapi
C 91	38	1-6	1513	9	BC002820	BC002820 Homo sapi	C 164	38	1-6	76200	9	AC008616	AC008616 Homo sapi
C 92	38	1-6	1566	9	HS127820	AL049434 Homo sapi	C 165	38	1-6	76200	9	AP005401	AP005401 Homo sapi
C 93	38	1-6	1636	9	AK024527	AK024527 Homo sapi	C 166	38	1-6	76702	9	HS756P4	AL035072 Human DNA
C 94	38	1-6	2081	9	BC017096	BC017096 Homo sapi	C 167	38	1-6	76763	2	AL157705	AL157705 Human DNA
C 95	38	1-6	2131	9	AF092925	AF092925 Homo sapi	C 168	38	1-6	77313	2	AC022855	AC022855 Homo sapi
C 96	38	1-6	2306	9	AK054811	AK054811 Homo sapi	C 169	38	1-6	77425	9	AF068862	AF068862 Homo sapi
C 97	38	1-6	2340	9	HS127820	AL833636 Homo sapi	C 170	38	1-6	77529	2	AL611948	AL611948 Homo sapi
C 98	38	1-6	2467	9	HSCDGEN	X74984 H. sapiens S	C 171	38	1-6	78233	9	AC004636	AC004636 Homo sapi
C 99	38	1-6	2598	6	BD012292	BD012292 Genes rel	C 172	38	1-6	78373	2	AC026519	AC026519 Homo sapi
C 100	38	1-6	2598	9	AK027382	AK027382 Homo sapi	C 173	38	1-6	79305	9	AC005200	AC005200 Homo sapi
C 101	38	1-6	2598	23	BD004972	BD004972 Genes rel	C 174	38	1-6	79810	9	AC005543	AC005543 Homo sapi
C 102	38	1-6	4192	9	AF305083	AF305083 Homo sapi	C 175	38	1-6	80846	9	AL512489	AL512489 Human DNA
C 103	38	1-6	4652	9	AF187725	AF187725 Homo sapi	C 176	38	1-6	80869	9	HS127820	AL096794 Human DNA
C 104	38	1-6	4652	9	AF189367	AF189367 Homo sapi	C 177	38	1-6	82117	9	AP000338	AP000338 Homo sapi
C 105	38	1-6	6799	9	AB051447	AB051447 Homo sapi	C 178	38	1-6	83329	2	AC073860	Continuation (4 of
C 106	38	1-6	8231	9	AC110808	AC110808 Homo sapi	C 179	38	1-6	84450	2	AC091431	AC091431 Homo sapi
C 107	38	1-6	8231	9	AC110808	AC110808 Homo sapi	C 180	38	1-6	85874	9	AC073150	AC073150 Homo sapi
C 108	38	1-6	8922	9	AC112176	AC112176 Homo sapi	C 181	38	1-6	86451	2	AC107037	AC107037 Pan trogl
C 109	38	1-6	20539	9	HS349E10	AL022341 Human DNA	C 182	38	1-6	89218	9	AC005902	AC005902 Homo sapi
C 110	38	1-6	26078	9	AF376770	AF376770 Homo sapi	C 183	38	1-6	89921	2	AF170802	AF170802 Homo sapi
C 111	38	1-6	27273	9	AL365206	AL365206 Homo sapi	C 184	38	1-6	89944	9	AC093127	AC093127 Papio cyn
C 112	38	1-6	28265	9	HSR314	HSR314 Homo sapi	C 185	38	1-6	90109	2	AC002557	AC002557 Homo sapi
C 113	38	1-6	30632	9	AL160051	AL160051 Human DNA s	C 186	38	1-6	90136	9	HS330012	HS330012 Human DNA
C 114	38	1-6	32269	9	HSRA36	Z69720 Human DNA s	C 187	38	1-6	90143	9	AL669876	AL669876 Human DNA
C 115	38	1-6	32918	2	AC007445	AC007445 Homo sapi	C 188	38	1-6	90780	2	AC093202	AC093202 Homo sapi
C 116	38	1-6	34182	9	HSU197H3	Z74409 Human DNA s	C 189	38	1-6	91187	9	AC023790	AC023790 Homo sapi
C 117	38	1-6	34346	9	AC090632	AC090632 Homo sapi	C 190	38	1-6	91388	9	AC005994	AC005994 Homo sapi
C 118	38	1-6	36230	9	AP001059	AP001059 Homo sapi	C 191	38	1-6	91835	9	HS26H23	Z84467 Human DNA s
C 119	38	1-6	37718	9	AC004034	AC004034 Homo sapi	C 192	38	1-6	93285	9	AL159174	AL159174 Human DNA
C 120	38	1-6	38250	2	AC012006	AC012006 Homo sapi	C 193	38	1-6	93296	9	AL136363	AL136363 Human DNA
C 121	38	1-6	38727	9	AC006693	AC006693 Homo sapi	C 194	38	1-6	93324	9	AL139119	AL139119 Human DNA
C 122	38	1-6	3383	9	AC022149	AC022149 Homo sapi	C 195	38	1-6	93976	9	AP000474	AP000474 Homo sapi
C 123	38	1-6	40893	9	AL589952	AL589952 Human DNA	C 196	38	1-6	94060	2	AF216673	AF216673 Homo sapi
C 124	38	1-6	44544	9	AC004262	AC004262 Homo sapi	C 197	38	1-6	95484	2	AC015854	AC015854 Homo sapi
C 125	38	1-6	44733	2	AC006171	AC006171 Homo sapi	C 198	38	1-6	97218	9	AC092385	AC092385 Homo sapi
C 126	38	1-6	45373	9	AL158092	AL158092 Human DNA	C 199	38	1-6	97601	9	AC073190	AC073190 Homo sapi
C 127	38	1-6	47338	9	AL355990	AL355990 Human DNA	C 200	38	1-6	98104	9	HS127820	AL132774 Human DNA
C 128	38	1-6	47854	9	HS839M1	AL034485 Human DNA	C 201	38	1-6	99074	9	HS560B9	Z98751 Human DNA s
C 129	38	1-6	50651	9	AC004762	AC004762 Homo sapi	C 202	38	1-6	99799	9	AL445184	AL445184 Human DNA
C 130	38	1-6	50660	9	AP000657	AP000657 Homo sapi	C 203	38	1-6	100000	9	AB020865	AB020865 Homo sapi
C 131	38	1-6	52737	2	AC007800	AC007800 Homo sapi	C 204	38	1-6	100000	9	AP000216	AP000216 Homo sapi
C 132	38	1-6	53168	9	HS109G6	AL023879 Human DNA	C 205	38	1-6	100167	9	HSJ189G13	AL121916 Human DNA
C 133	38	1-6	53415	2	AC111176	AC111176 Homo sapi	C 206	38	1-6	100793	9	AF070717	AF070717 Homo sapi
C 134	38	1-6	53942	9	HS056G2A	Z82901 Human DNA s	C 207	38	1-6	102117	9	AC098823	AC098823 Homo sapi
C 135	38	1-6	54166	9	AC126119	AC126119 Homo sapi	C 208	38	1-6	102259	2	AC015916	AC015916 Homo sapi
C 136	38	1-6	54407	2	AC021817	AC021817 Homo sapi	C 209	38	1-6	102484	9	HS510H16	AL008635 Human DNA
C 137	38	1-6	57408	9	AL670471	AL670471 Human DNA	C 210	38	1-6	104082	9	AC011503	AC011503 Homo sapi
C 138	38	1-6	58884	9	AL359512	AL359512 Human DNA	C 211	38	1-6	104357	9	AL392123	AL392123 Human DNA

c 212	38	1.6 104679	9	AL353706	Human DNA
c 213	38	1.6 105955	9	AC074136	Homo sapi
c 214	38	1.6 106008	9	HS0506	Human DNA
c 215	38	1.6 106506	9	AL358235	Human DNA
c 216	38	1.6 106508	9	AC005102	Homo sapi
c 217	38	1.6 106954	9	AC104651	Homo sapi
c 218	38	1.6 107527	9	AC005018	Homo sapi
c 219	38	1.6 108315	9	HS41P2	Human DNA
c 220	38	1.6 108500	9	AP001624	Homo sapi
c 221	38	1.6 108965	9	AF191069	Homo sapi
c 222	38	1.6 109239	2	AC104521	Homo sapi
c 223	38	1.6 109488	9	HS2988J15	Human DNA
c 224	38	1.6 109864	9	AF096876	Homo sapi
c 225	38	1.6 110000	2	AC073860	Continuation (3 of
c 226	38	1.6 110000	2	AC092789	Continuation (3 of
c 227	38	1.6 110000	2	AC125635	Continuation (2 of
c 228	38	1.6 110000	2	AL390072	Continuation (3 of
c 229	38	1.6 110000	2	AL693885	Continuation (2 of
c 230	38	1.6 110000	2	AL732359	Continuation (5 of
c 231	38	1.6 110000	2	AC026673	Continuation (4 of
c 232	38	1.6 110159	2	AC068178	Homo sapi
c 233	38	1.6 110271	9	AC024576	Homo sapi
c 234	38	1.6 111123	9	AP000365	Homo sapi
c 235	38	1.6 111321	2	AC026718	Homo sapi
c 236	38	1.6 111738	2	AL592304	Homo sapi
c 237	38	1.6 111962	9	AP000890	Homo sapi
c 238	38	1.6 113117	9	AL512288	Human DNA
c 239	38	1.6 113213	9	AC016554	Homo sapi
c 240	38	1.6 113370	9	AL591493	Human DNA
c 241	38	1.6 113929	9	AF196969	Homo sapi
c 242	38	1.6 113982	2	AF192303	Homo sapi
c 243	38	1.6 114231	9	HS390C10	Human DNA
c 244	38	1.6 114842	9	AC002996	Homo sapi
c 245	38	1.6 115297	2	U82207	Homo sapi
c 246	38	1.6 115644	2	AC124056	Homo sapi
c 247	38	1.6 115928	2	AC037475	Homo sapi
c 248	38	1.6 115948	2	AC027727	Homo sapi
c 249	38	1.6 115958	9	AC004736	Human DNA
c 250	38	1.6 116311	9	AL360181	Human DNA
c 251	38	1.6 116334	2	AC084172	Homo sapi
c 252	38	1.6 117034	2	AC026329	Homo sapi
c 253	38	1.6 117587	2	AC107375	Homo sapi
c 254	38	1.6 118047	9	HS0513M9	Human DNA
c 255	38	1.6 118218	2	AP000670	Homo sapi
c 256	38	1.6 118582	2	AC115989	Homo sapi
c 257	38	1.6 119760	9	AC025458	Homo sapi
c 258	38	1.6 120015	2	AL354860	Homo sapi
c 259	38	1.6 120166	9	AC091390	Homo sapi
c 260	38	1.6 120387	9	AC003051	Homo sapi
c 261	38	1.6 120821	9	AC004702	Homo sapi
c 262	38	1.6 121143	9	AF312915	Homo sapi
c 263	38	1.6 121460	2	AC027330	Homo sapi
c 264	38	1.6 121478	9	AL365229	Human DNA
c 265	38	1.6 121520	9	AC006477	Homo sapi
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c 268	38	1.6 122140	2	AC082647	Homo sapi
c 269	38	1.6 123288	9	AP000547	Homo sapi
c 270	38	1.6 123661	9	AC095048	Homo sapi
c 271	38	1.6 125108	9	AF030453	Homo sapi
c 272	38	1.6 125641	9	HSJ234P15	Human DNA
c 273	38	1.6 125653	9	AL133517	Human DNA
c 274	38	1.6 125922	9	AL731566	Human DNA
c 275	38	1.6 126392	2	AC018785	Homo sapi
c 276	38	1.6 126491	9	AL589764	Human DNA
c 277	38	1.6 126615	9	AC005180	Homo sapi
c 278	38	1.6 126792	9	AC008102	Homo sapi
c 279	38	1.6 127661	2	AP001261	Homo sapi
c 280	38	1.6 128398	9	AC004817	Homo sapi
c 281	38	1.6 128779	9	HS29K1	Human DNA
c 282	38	1.6 128871	9	AL157838	Human DNA
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c 285	38	1.6 129435	9	AL391314	Human DNA
c 286	38	1.6 129541	9	AC004999	Homo sapi
c 287	38	1.6 129584	9	AL355385	Human DNA
c 288	38	1.6 131078	9	HSU80017	Homo sapi
c 289	38	1.6 132070	9	AC003663	Homo sapi
c 290	38	1.6 132290	9	AL627402	Human DNA
c 291	38	1.6 132875	9	AC112907	Homo sapi
c 292	38	1.6 133337	2	AC016231	Homo sapi
c 293	38	1.6 133814	2	AC027550	Homo sapi
c 294	38	1.6 134011	2	AC068269	Homo sapi
c 295	38	1.6 134040	2	AC044856	Homo sapi
c 296	38	1.6 134091	2	AC023349	Homo sapi
c 297	38	1.6 134250	9	AL139044	Human DNA
c 298	38	1.6 134999	2	AC040894	Homo sapi
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c 300	38	1.6 137730	9	HS365E2	Human DNA
c 301	38	1.6 137806	2	AC026372	Homo sapi
c 302	38	1.6 137922	2	AC073398	Homo sapi
c 303	38	1.6 137935	9	AL662884	Human DNA
c 304	38	1.6 138221	9	AL391422	Human DNA
c 305	38	1.6 138347	9	AL389889	Human DNA
c 306	38	1.6 138764	9	AC006387	Homo sapi
c 307	38	1.6 138932	9	AL662828	Human DNA
c 308	38	1.6 139327	2	AC025017	Homo sapi
c 309	38	1.6 139966	9	AC004820	Homo sapi
c 310	38	1.6 140207	9	AL356390	Human DNA
c 311	38	1.6 140403	2	AC109444	Homo sapi
c 312	38	1.6 140446	9	AL355581	Human DNA
c 313	38	1.6 140974	9	AC088533	Homo sapi
c 314	38	1.6 140999	9	AL356415	Human DNA
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c 331	38	1.6 144578	9	AC016588	Homo sapi
c 332	38	1.6 144620	9	AC023787	Homo sapi
c 333	38	1.6 144735	2	AL161458	Homo sapi
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c 336	38	1.6 145173	9	AC005599	Homo sapi
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c 341	38	1.6 145726	2	AC021807	Homo sapi
c 342	38	1.6 146004	9	AC019144	Homo sapi
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c 344	38	1.6 146572	2	AC024983	Homo sapi
c 345	38	1.6 146776	2	AC093486	Homo sapi
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c 348	38	1.6 147280	9	AC067747	Homo sapi
c 349	38	1.6 147760	9	AC011846	Homo sapi
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c 351	38	1.6 148507	2	AC011263	Homo sapi
c 352	38	1.6 148606	9	AC104692	Homo sapi
c 353	38	1.6 148819	9	AC006996	Homo sapi
c 354	38	1.6 148980	2	AC105105	Homo sapi
c 355	38	1.6 149170	2	AC110603	Homo sapi
c 356	38	1.6 149271	9	AC022144	Homo sapi
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C 358	38	1.6 149660	9	AC027449	AC027449 Homo sapi	C 431	38	1.6 161445	2	AP000938	AP000938 Homo sapi
C 359	38	1.6 149930	9	AL136084	Human DNA	C 432	38	1.6 161575	2	AC025233	AC025233 Homo sapi
C 360	38	1.6 150005	9	AL450344	Human DNA	C 433	38	1.6 161723	9	AC079790	AC079790 Homo sapi
C 361	38	1.6 150036	9	AP000557	Human DNA	C 434	38	1.6 161775	9	AC099512	AC099512 Homo sapi
C 362	38	1.6 150199	9	AC087568	Human DNA	C 435	38	1.6 161920	2	AP002502	AP002502 Homo sapi
C 363	38	1.6 150222	9	AC092296	Human DNA	C 436	38	1.6 161990	2	AL135713	AL135713 Homo sapi
C 364	38	1.6 150489	2	AC068854	Human DNA	C 437	38	1.6 162126	9	AL354711	AL354711 Homo sapi
C 365	38	1.6 150562	2	AC069420	Human DNA	C 438	38	1.6 162377	9	AL683870	AL683870 Human DNA
C 366	38	1.6 150572	2	GNS01R1C	Human chr	C 439	38	1.6 162638	2	AC096537	AC096537 Homo sapi
C 367	38	1.6 150668	9	AC027314	Human sapi	C 440	38	1.6 162728	9	AP002906	AP002906 Homo sapi
C 368	38	1.6 150681	9	AP001251	Human sapi	C 441	38	1.6 162959	2	AC019255	AC019255 Homo sapi
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C 370	38	1.6 151133	9	AC013355	Human sapi	C 443	38	1.6 163711	2	AC013245	AC013245 Homo sapi
C 371	38	1.6 151358	2	AL590437	Human sapi	C 444	38	1.6 164168	9	AL135927	AL135927 Human DNA
C 372	38	1.6 151445	9	AL354943	Human DNA	C 445	38	1.6 164176	2	AC080147	AC080147 Homo sapi
C 373	38	1.6 151606	9	AC087441	Human sapi	C 446	38	1.6 164179	9	AC007227	AC007227 Homo sapi
C 374	38	1.6 151630	2	AC005154	Human sapi	C 447	38	1.6 164342	2	AC073982	AC073982 Homo sapi
C 375	38	1.6 151736	2	AC024439	Human sapi	C 448	38	1.6 164500	9	AC037433	AC037433 Homo sapi
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C 377	38	1.6 152118	2	AC013263	Human sapi	C 450	38	1.6 164598	2	AC093212	AC093212 Homo sapi
C 378	38	1.6 152454	2	AC067909	Human sapi	C 451	38	1.6 164937	2	AC090804	AC090804 Homo sapi
C 379	38	1.6 152719	2	AC012545	Human sapi	C 452	38	1.6 165028	9	AC110758	AC110758 Homo sapi
C 380	38	1.6 152867	9	AC027671	Human sapi	C 453	38	1.6 165197	9	AC002070	AC002070 Human BAC
C 381	38	1.6 153299	9	AC073593	Human sapi	C 454	38	1.6 165282	2	AC092037	AC092037 Homo sapi
C 382	38	1.6 153748	9	AC110719	Human sapi	C 455	38	1.6 165341	2	AC022448	AC022448 Homo sapi
C 383	38	1.6 153993	9	AC012262	Human sapi	C 456	38	1.6 165434	2	AC023038	AC023038 Homo sapi
C 384	38	1.6 154516	9	AC090324	Human sapi	C 457	38	1.6 165531	2	AC116004	AC116004 Homo sapi
C 385	38	1.6 154518	2	AC011619	Human sapi	C 458	38	1.6 165562	2	AC087273	AC087273 Homo sapi
C 386	38	1.6 154604	2	AC104974	Human sapi	C 459	38	1.6 165866	2	AC073200	AC073200 Homo sapi
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C 390	38	1.6 155306	2	AC010272	Human sapi	C 463	38	1.6 166076	2	AC092993	AC092993 Homo sapi
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C 394	38	1.6 156207	2	AC025507	Human sapi	C 467	38	1.6 166702	2	AC125612	AC125612 Homo sapi
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C 402	38	1.6 157122	2	AC028235	Human sapi	C 475	38	1.6 167592	2	AC012473	AC012473 Homo sapi
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C 423	38	1.6 160433	9	AC093296	Human sapi	C 496	38	1.6 169740	2	AC018794	AC018794 Homo sapi
C 424	38	1.6 160604	9	AL449305	Human DNA	C 497	38	1.6 170138	2	AC092983	AC092983 Homo sapi
C 425	38	1.6 160658	9	AC024258	Human sapi	C 498	38	1.6 170514	2	AP000894	AP000894 Homo sapi
C 426	38	1.6 160676	2	AC022920	Human sapi	C 499	38	1.6 170522	9	AC026410	AC026410 Homo sapi
C 427	38	1.6 161053	9	AL356608	Human DNA	C 500	38	1.6 170591	2	AC034163	AC034163 Homo sapi
C 428	38	1.6 161308	2	AC067818	Human sapi	C 501	38	1.6 170630	9	AL592284	AL592284 Human DNA
C 429	38	1.6 161421	2	AC068114	Human sapi	C 502	38	1.6 170669	9	AC044907	AC044907 Homo sapi
C 430	38	1.6 161433	2	AC079199	Human sapi	C 503	38	1.6 170793	9		



C 504	38	1.6	170793	9	AC044907	AC044907 Homo sapi
C 505	38	1.6	170827	2	AC007950	AC007950 Homo sapi
C 506	38	1.6	170847	2	AL357135	AL357135 Homo sapi
C 507	38	1.6	171273	9	AC079141	AC079141 Homo sapi
C 508	38	1.6	171418	2	AC023591	AC023591 Homo sapi
C 509	38	1.6	171461	9	AC092041	AC092041 Homo sapi
C 510	38	1.6	171545	9	AC008394	AC008394 Homo sapi
C 511	38	1.6	171625	2	AC008750	AC008750 Homo sapi
C 512	38	1.6	171742	30	AC069495	AC069495 Homo sapi
C 513	38	1.6	172136	2	AC023959	AC023959 Homo sapi
C 514	38	1.6	172402	9	AC091672	AC091672 Homo sapi
C 515	38	1.6	172507	9	AC092960	AC092960 Homo sapi
C 516	38	1.6	172657	9	AC004386	AC004386 Homo sapi
C 517	38	1.6	172797	9	AC105411	AC105411 Homo sapi
C 518	38	1.6	173119	9	AL359986	AL359986 Human DNA
C 519	38	1.6	173346	9	AC112184	AC112184 Homo sapi
C 520	38	1.6	173717	9	AC005695	AC005695 Homo sapi
C 521	38	1.6	173729	9	AC012236	AC012236 Homo sapi
C 522	38	1.6	173893	9	AC010150	AC010150 Homo sapi
C 523	38	1.6	173911	9	AC092490	AC092490 Homo sapi
C 524	38	1.6	174034	9	AC020908	AC020908 Homo sapi
C 525	38	1.6	174539	9	AC103558	AC103558 Homo sapi
C 526	38	1.6	174713	2	AC079083	AC079083 Homo sapi
C 527	38	1.6	174776	9	AL592546	AL592546 Human DNA
C 528	38	1.6	174991	2	AC015935	AC015935 Homo sapi
C 529	38	1.6	175011	2	AC105339	AC105339 Homo sapi
C 530	38	1.6	175056	2	AP002368	AP002368 Homo sapi
C 531	38	1.6	175265	2	AC063964	AC063964 Homo sapi
C 532	38	1.6	175339	9	AC005772	AC005772 Homo sapi
C 533	38	1.6	175403	9	AC093268	AC093268 Homo sapi
C 534	38	1.6	175419	2	AP000788	AP000788 Homo sapi
C 535	38	1.6	175550	2	AC009863	AC009863 Homo sapi
C 536	38	1.6	175561	9	AC012636	AC012636 Homo sapi
C 537	38	1.6	175822	2	AC068402	AC068402 Homo sapi
C 538	38	1.6	175940	9	HS015217	HS015217 Human DNA
C 539	38	1.6	176155	2	AC012149	AC012149 Homo sapi
C 540	38	1.6	176222	9	AC011825	AC011825 Homo sapi
C 541	38	1.6	176388	2	AC025273	AC025273 Homo sapi
C 542	38	1.6	176616	2	AC114489	AC114489 Homo sapi
C 543	38	1.6	176634	2	AC116163	AC116163 Homo sapi
C 544	38	1.6	176636	2	AC024936	AC024936 Homo sapi
C 545	38	1.6	176845	2	AC023509	AC023509 Homo sapi
C 546	38	1.6	177017	2	AL662924	AL662924 Homo sapi
C 547	38	1.6	177019	9	AL158194	AL158194 Human DNA
C 548	38	1.6	177066	9	AC091001	AC091001 Homo sapi
C 549	38	1.6	177160	9	AC019089	AC019089 Homo sapi
C 550	38	1.6	177178	2	AC013791	AC013791 Homo sapi
C 551	38	1.6	177257	2	AL807789	AL807789 Homo sapi
C 552	38	1.6	177379	2	AC079826	AC079826 Homo sapi
C 553	38	1.6	177384	9	AC097639	AC097639 Homo sapi
C 554	38	1.6	177444	2	AC024617	AC024617 Homo sapi
C 555	38	1.6	177750	2	AC040947	AC040947 Homo sapi
C 556	38	1.6	177785	9	AP005431	AP005431 Homo sapi
C 557	38	1.6	177893	9	AC005089	AC005089 Homo sapi
C 558	38	1.6	177995	9	AC016700	AC016700 Homo sapi
C 559	38	1.6	178199	2	AC018772	AC018772 Homo sapi
C 560	38	1.6	178217	9	AC022080	AC022080 Homo sapi
C 561	38	1.6	178367	9	AC006115	AC006115 Homo sapi
C 562	38	1.6	178714	2	AC017008	AC017008 Homo sapi
C 563	38	1.6	179149	2	AC063948	AC063948 Homo sapi
C 564	38	1.6	179202	2	AC025935	AC025935 Homo sapi
C 565	38	1.6	179220	9	AC114493	AC114493 Homo sapi
C 566	38	1.6	179369	9	AP000842	AP000842 Homo sapi
C 567	38	1.6	179491	2	AC020673	AC020673 Homo sapi
C 568	38	1.6	179599	2	AC013278	AC013278 Homo sapi
C 569	38	1.6	179974	2	AC021704	AC021704 Homo sapi
C 570	38	1.6	180360	9	AC011139	AC011139 Homo sapi
C 571	38	1.6	180538	2	AC073514	AC073514 Homo sapi
C 572	38	1.6	180650	9	AC109474	AC109474 Homo sapi
C 573	38	1.6	180702	9	AC018557	AC018557 Homo sapi
C 574	38	1.6	181427	2	AC027209	AC027209 Homo sapi
C 575	38	1.6	181652	9	CNS01DUS	AL133367 Human chr
C 576	38	1.6	181663	9	AC010894	AC010894 Homo sapi
C 577	38	1.6	181858	2	AC079822	AC079822 Homo sapi
C 578	38	1.6	181858	2	AC084856	AC084856 Homo sapi
C 579	38	1.6	182048	2	AC027439	AC027439 Homo sapi
C 580	38	1.6	182084	2	AC026615	AC026615 Homo sapi
C 581	38	1.6	182323	9	AL512307	AL512307 Human DNA
C 582	38	1.6	182448	2	AC090323	AC090323 Homo sapi
C 583	38	1.6	182557	2	AC091942	AC091942 Homo sapi
C 584	38	1.6	182763	9	AC091806	AC091806 Homo sapi
C 585	38	1.6	183176	9	AC106894	AC106894 Homo sapi
C 586	38	1.6	183382	9	AL157388	AL157388 Human DNA
C 587	38	1.6	183687	9	AC064864	AC064864 Homo sapi
C 588	38	1.6	183726	2	AC099535	AC099535 Homo sapi
C 589	38	1.6	183763	2	AC026900	AC026900 Homo sapi
C 590	38	1.6	183928	2	AC020773	AC020773 Homo sapi
C 591	38	1.6	183946	2	AC009164	AC009164 Homo sapi
C 592	38	1.6	184000	2	AC010892	AC010892 Homo sapi
C 593	38	1.6	184053	9	AC011900	AC011900 Homo sapi
C 594	38	1.6	184289	9	AL359878	AL359878 Human DNA
C 595	38	1.6	184436	9	AP000919	AP000919 Homo sapi
C 596	38	1.6	184439	2	AP003085	AP003085 Homo sapi
C 597	38	1.6	184598	9	AL139406	AL139406 Human DNA
C 598	38	1.6	184683	2	AP001640	AP001640 Homo sapi
C 599	38	1.6	184787	2	AC087354	AC087354 Homo sapi
C 600	38	1.6	185029	2	AC068986	AC068986 Homo sapi
C 601	38	1.6	185121	2	AC069105	AC069105 Homo sapi
C 602	38	1.6	185161	9	AC006059	AC006059 Homo sapi
C 603	38	1.6	185380	2	AC021739	AC021739 Homo sapi
C 604	38	1.6	185408	2	AC021053	AC021053 Homo sapi
C 605	38	1.6	185420	2	AC021973	AC021973 Homo sapi
C 606	38	1.6	185590	2	AC118137	AC118137 Homo sapi
C 607	38	1.6	185720	2	AC093286	AC093286 Homo sapi
C 608	38	1.6	185759	2	AC084026	AC084026 Homo sapi
C 609	38	1.6	185799	9	AC091296	AC091296 Pan trogl
C 610	38	1.6	186024	2	AC084225	AC084225 Homo sapi
C 611	38	1.6	186238	9	AC090671	AC090671 Homo sapi
C 612	38	1.6	186239	30	AC067874	AC067874 Homo sapi
C 613	38	1.6	186349	2	AC073420	AC073420 Homo sapi
C 614	38	1.6	186403	9	AC022558	AC022558 Homo sapi
C 615	38	1.6	186563	9	AC104452	AC104452 Homo sapi
C 616	38	1.6	186616	2	AC026294	AC026294 Homo sapi
C 617	38	1.6	186838	2	AC092947	AC092947 Homo sapi
C 618	38	1.6	186925	2	AC087503	AC087503 Homo sapi
C 619	38	1.6	187064	2	AP001379	AP001379 Homo sapi
C 620	38	1.6	187200	2	AC011476	AC011476 Homo sapi
C 621	38	1.6	187272	2	AC069076	AC069076 Homo sapi
C 622	38	1.6	187332	9	AC053544	AC053544 Homo sapi
C 623	38	1.6	187543	9	AC005678	AC005678 Homo sapi
C 624	38	1.6	187568	9	AP002967	AP002967 Homo sapi
C 625	38	1.6	187574	9	AC018622	AC018622 Homo sapi
C 626	38	1.6	187955	30	AC067759	AC067759 Homo sapi
C 627	38	1.6	187950	9	AP000866	AP000866 Homo sapi
C 628	38	1.6	188119	9	AC119673	AC119673 Homo sapi
C 629	38	1.6	188207	9	AC027644	AC027644 Homo sapi
C 630	38	1.6	188255	2	AC061991	AC061991 Homo sapi
C 631	38	1.6	188257	2	AC118755	AC118755 Homo sapi
C 632	38	1.6	188353	9	AC009480	AC009480 Homo sapi
C 633	38	1.6	188450	2	AC010542	AC010542 Homo sapi
C 634	38	1.6	188478	9	CNS05TF4	AL135294 Human chr
C 635	38	1.6	188582	2	AC013720	AC013720 Homo sapi
C 636	38	1.6	188784	2	AC090154	AC090154 Homo sapi
C 637	38	1.6	189174	9	AC092687	AC092687 Homo sapi
C 638	38	1.6	189796	2	AC068015	AC068015 Homo sapi
C 639	38	1.6	190162	9	AC009244	AC009244 Homo sapi
C 640	38	1.6	190189	2	AC027181	AC027181 Homo sapi
C 641	38	1.6	190357	2	AC012259	AC012259 Homo sapi
C 642	38	1.6	190385	9	AC012305	AC012305 Homo sapi
C 643	38	1.6	190739	2	AP001361	AP001361 Homo sapi
C 644	38	1.6	190773	9	AC018513	AC018513 Homo sapi
C 645	38	1.6	190848	9	AC113416	AC113416 Homo sapi
C 646	38	1.6	190871	9	AC044797	AC044797 Homo sapi
C 647	38	1.6	191027	2	AC022271	AC022271 Homo sapi
C 648	38	1.6	191141	2	AC069374	AC069374 Homo sapi
C 649	38	1.6	191923	2	AP001846	AP001846 Homo sapi

650	38	1.6	191970	2	AC073334	Homo sapi	AC073334	38	1.6	222106	2	AC018570	Homo sapi
651	38	1.6	192298	9	AP000943	Homo sapi	AP000943	38	1.6	223284	2	AC108373	Pan trogl
652	38	1.6	192404	9	CNS01DNO	Human chr	AL136296	38	1.6	223606	2	AC103479	Homo sapi
653	38	1.6	192491	2	AC103705	Homo sapi	AC103705	38	1.6	224068	9	CNS01DUU	
654	38	1.6	192799	9	ALS83841	Human DNA	ALS83841	38	1.6	226171	9	AP003730	Homo sapi
655	38	1.6	192834	2	AC069503	Homo sapi	AC069503	38	1.6	229379	9	AC010746	Homo sapi
656	38	1.6	193118	2	AC067728	Homo sapi	AC067728	38	1.6	230392	9	AC026672	Homo sapi
657	38	1.6	193358	2	AC130473	Homo sapi	AC130473	38	1.6	231379	2	AC091717	Pan trogl
658	38	1.6	193605	2	AC130472	Homo sapi	AC130472	38	1.6	233250	9	AC053527	Homo sapi
659	38	1.6	194197	9	AC064871	Homo sapi	AC064871	38	1.6	233877	9	AC093798	Homo sapi
660	38	1.6	194523	9	HS323M22	Human DNA	AL022476	38	1.6	234481	2	AC022214	Homo sapi
661	38	1.6	194523	9	AC018642	Homo sapi	AC018642	38	1.6	235968	9	AC087393	Homo sapi
662	38	1.6	195029	2	AC007902	Homo sapi	AC007902	38	1.6	239008	2	AC022460	Homo sapi
663	38	1.6	195323	2	AC026612	Homo sapi	AC026612	38	1.6	241674	2	AC068641	Homo sapi
664	38	1.6	195325	2	AC125616	Homo sapi	AC125616	38	1.6	252015	9	AC008382	Homo sapi
665	38	1.6	195766	9	CNS01DVC	Human chr	AL135744	38	1.6	256073	9	AE006464	Homo sapi
666	38	1.6	195900	2	AC021184	Homo sapi	AC021184	38	1.6	258002	9	AE006462	Homo sapi
667	38	1.6	196973	9	AP000926	Homo sapi	AP000926	38	1.6	273403	9	AE011498	Homo sapi
668	38	1.6	197811	2	AC009833	Homo sapi	AC009833	38	1.6	283396	2	AC093024	Homo sapi
669	38	1.6	198068	9	AC087240	Homo sapi	AC087240	38	1.6	297235	2	AL499603	Homo sapi
670	38	1.6	198248	2	AP001487	Homo sapi	AP001487	38	1.6	298575	2	HSBA22B4	Homo sapi
671	38	1.6	198418	9	AC007496	Homo sapi	AC007496	38	1.6	304623	2	AC021052	Homo sapi
672	38	1.6	198888	9	AC087728	Papio cyn	AC087728	38	1.6	320902	2	AL161456	Homo sapi
673	38	1.6	199208	2	AC019236	Homo sapi	AC019236	38	1.6	321438	2	AC104989	Homo sapi
674	38	1.6	199240	2	AC010287	Homo sapi	AC010287	38	1.6	330250	9	AF049895	Homo sapi
675	38	1.6	199287	2	AC068659	Homo sapi	AC068659	38	1.6	340000	9	AP001679	Homo sapi
676	38	1.6	199906	2	AC021764	Homo sapi	AC021764	38	1.6	340000	9	AP001684	Homo sapi
677	38	1.6	200221	2	AC069454	Homo sapi	AC069454	38	1.6	340000	9	AP001689	Homo sapi
678	38	1.6	200445	2	AC105137	Homo sapi	AC105137	38	1.6	340000	9	AP001707	Homo sapi
679	38	1.6	200477	9	AC079271	Homo sapi	AC079271	38	1.6	340000	9	AP001746	Homo sapi
680	38	1.6	200493	9	AP005270	Homo sapi	AP005270	38	1.6	340000	9	AP001753	Homo sapi
681	38	1.6	200680	2	AC023891	Homo sapi	AC023891	38	1.6	340000	9	AP001760	Homo sapi
682	38	1.6	200685	2	AP001455	Homo sapi	AP001455	38	1.6	345524	9	AF235103	Homo sapi
683	38	1.6	200771	9	AC093668	Homo sapi	AC093668	38	1.6	345524	9	AF235103	Homo sapi
684	38	1.6	200799	2	AL445648	Homo sapi	AL445648	38	1.5	1808	9	AK094860	Homo sapi
685	38	1.6	201948	2	AP001026	Homo sapi	AP001026	38	1.5	3107	9	AK023883	Homo sapi
686	38	1.6	202544	9	AC104447	Homo sapi	AC104447	38	1.5	6458	9	AF332857S1	Homo sapi
687	38	1.6	202889	9	AC010552	Homo sapi	AC010552	38	1.5	10304	9	AF332750	Homo sapi
688	38	1.6	203010	9	AC006530	Homo sapi	AC006530	38	1.5	13472	9	AF020057	Homo sapi
689	38	1.6	203038	9	AC076968	Homo sapi	AC076968	38	1.5	14266	9	HS3140G5	Homo sapi
690	38	1.6	203040	2	AC128674	Homo sapi	AC128674	38	1.5	18388	9	AB034990	Homo sapi
691	38	1.6	203050	2	HS44N10	Homo sapi	297197	38	1.5	26550	9	AF421855	Homo sapi
692	38	1.6	203169	9	AL390785	Human DNA	AL390785	38	1.5	28567	9	HS413269S	Homo sapi
693	38	1.6	203228	9	AC092718	Homo sapi	AC092718	38	1.5	35122	9	AP000302	Homo sapi
694	38	1.6	203790	9	AC010422	Homo sapi	AC010422	38	1.5	35122	9	AP000302	Homo sapi
695	38	1.6	203838	2	AC026840	Homo sapi	AC026840	38	1.5	36542	9	AC006117	Homo sapi
696	38	1.6	203926	2	AC011122	Homo sapi	AC011122	38	1.5	36705	9	AC005340	Homo sapi
697	38	1.6	204340	2	AC019238	Homo sapi	AC019238	38	1.5	38939	9	AC004578	Homo sapi
698	38	1.6	204917	9	AC008040	Homo sapi	AC008040	38	1.5	39673	9	AL672238	Human DNA
699	38	1.6	205715	2	AC007604	Homo sapi	AC007604	38	1.5	40149	9	AL672238	Human DNA
700	38	1.6	205866	2	AC055833	Homo sapi	AC055833	38	1.5	40198	9	AL672238	Human DNA
701	38	1.6	206624	9	AC097662	Homo sapi	AC097662	38	1.5	41055	9	AC006930	Homo sapi
702	38	1.6	207086	2	AC034290	Homo sapi	AC034290	38	1.5	41220	9	AC004777	Homo sapi
703	38	1.6	208024	9	AC010900	Homo sapi	AC010900	38	1.5	41229	9	AC097942	Homo sapi
704	38	1.6	208612	2	AC108668	Homo sapi	AC108668	38	1.5	42513	9	AL592438	Human DNA
705	38	1.6	208823	9	AC022532	Homo sapi	AC022532	38	1.5	42513	9	AC005578	Homo sapi
706	38	1.6	209907	2	AC078778	Homo sapi	AC078778	38	1.5	43297	9	AC005578	Homo sapi
707	38	1.6	210805	2	AC026333	Homo sapi	AC026333	38	1.5	43297	9	AC005578	Homo sapi
708	38	1.6	211767	2	AC110813	Homo sapi	AC110813	38	1.5	44145	9	AL501129	Homo sapi
709	38	1.6	212505	2	AC027220	Homo sapi	AC027220	38	1.5	44145	9	AL501129	Homo sapi
710	38	1.6	212656	9	AC007957	Homo sapi	AC007957	38	1.5	44942	9	AL589691	Human DNA
711	38	1.6	213599	2	AC104785	Homo sapi	AC104785	38	1.5	46965	2	AC006183	Homo sapi
712	38	1.6	215081	2	AC087501	Homo sapi	AC087501	38	1.5	46965	2	AC006183	Homo sapi
713	38	1.6	215339	9	AL160278	Human DNA	AL160278	38	1.5	47833	9	AF334400	Homo sapi
714	38	1.6	215509	2	AC079794	Homo sapi	AC079794	38	1.5	48032	9	AC003963	Homo sapi
715	38	1.6	216268	2	AC026986	Homo sapi	AC026986	38	1.5	48032	9	AC003963	Homo sapi
716	38	1.6	216877	9	AC106791	Homo sapi	AC106791	38	1.5	48680	9	AC091799	Homo sapi
717	38	1.6	217900	9	AC091809	Homo sapi	AC091809	38	1.5	51932	9	AC114275	Homo sapi
718	38	1.6	218445	2	AC083959	Homo sapi	AC083959	38	1.5	51932	9	AC114275	Homo sapi
719	38	1.6	220719	2	AC116353	Homo sapi	AC116353	38	1.5	5386	9	AC002117	Genomic s
720	38	1.6	220995	2	AC010687	Homo sapi	AC010687	38	1.5	5386	9	AC002117	Genomic s
721	38	1.6	221222	2	AC023794	Homo sapi	AC023794	38	1.5	56386	9	AC002117	Genomic s
722	38	1.6	221673	2	AC012183	Homo sapi	AC012183	38	1.5	56386	9	AC002117	Genomic s

796	37	1.5	68001	9	AP001442	Homo sapi
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798	37	1.5	70111	9	AP000263	Homo sapi
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808	37	1.5	81364	2	AC021072 <sub>3</sub>	Continuation (4 of
809	37	1.5	81437	2	AC002353	Homo sapi
810	37	1.5	82939	9	AL135928	Human DNA
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812	37	1.5	83549	9	AC004752	Homo sapi
813	37	1.5	85195	2	AL136093	Human DNA
814	37	1.5	86975	2	AC048340	Homo sapi
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816	37	1.5	87543	9	HSWENG2	Homo sapi
817	37	1.5	87974	2	AC021283	Homo sapi
818	37	1.5	90108	2	AC021611	Homo sapi
819	37	1.5	90108	2	AC021611	Homo sapi
820	37	1.5	90476	9	AC015910	Homo sapi
821	37	1.5	91202	2	AC006186	Homo sapi
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828	37	1.5	96201	9	AC079601	Homo sapi
829	37	1.5	96227	9	AC008026	Homo sapi
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831	37	1.5	98804	2	AC106723 <sub>3</sub>	Continuation (4 of
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LOCUS

5492 bp mRNA linear PRI 07-APR-1999

DEFINITION Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.  
ACCESSION AF123659  
VERSION AF123659.1 GI:4572475  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 5492)  
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,  
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.  
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
and its expression is altered in multiple human tumors  
Proc Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
JOURNAL 99199287  
MEDLINE 10097140  
PUBMED  
REFERENCE 2 (bases 1 to 5492)  
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,  
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.  
Direct Submision  
TITLE Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
JOURNAL Institute, 233S 10th street, Philadelphia, PA 19107, USA  
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## RESULT 3

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DEFINITION Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING
IN PROGRESS ***, 3 unordered pieces.
ACCESSION AC025853
VERSION AC025853.13 GI:21431202
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
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## ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collimore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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## REFERENCE

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1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collimore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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## AUTHORS

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1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
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## TITLE

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1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
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Collimore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
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## JOURNAL

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1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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## AUTHORS

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1 (bases 1 to 173264)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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## FEATURES

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## Direct Submission

Submitted (16-WAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## 3 (bases 1 to 173264)

Birren,B., Linton,L., Nuebaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzgerald,M., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tessaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## JOURNAL

On Jun 17, 2002 this sequence version replaced gi:21321864.

## COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L7454

Center clone name: 353\_K\_12

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved

\* 1 39461: contig of 39461 bp in length  
\* 39462 39561: gap of 100 bp  
\* 39562 108347: contig of 68786 bp in length  
\* 108348 108447: gap of 100 bp  
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Location/Qualifiers

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DEFINITION complete cds.
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VERSION AF123658.1 GI:4572473
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1722)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1722)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
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DEFINITION complete cds.
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VERSION AF123657.1 GI:4572471
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1692)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1692)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
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VERSION AF123655.1 GI:4572467
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1614)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
INSTITUTE, 233S 10th street, Philadelphia, PA 19107, USA
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DEFINITION complete cds.
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VERSION AF123656.1 GI:4572469
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SOURCE Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1515)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 1515)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
INSTITUTE, 233S 10th street, Philadelphia, PA 19107, USA
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/translation="MGSVSLISGHSFHKCRASQYKLRKSSHLKLNRYSDGLLRF  
GFSQDSHGKSGKMGSEDFYIKVQKARGSHHDPYATLSSGDLGGQAGVDFDPST  
ELKPGLCGALSDSGRNSKMGKAVRPTAPKPLVLRSGAILHSSPESASHQLHPAPDPKPEQ  
LQKLSRFEKELASLAYERPRRCDELEGPCKGNLKOASOKSORAOQVLHQL  
VLQKQKRLQRLSLKMEQDLLETKLRSYEREKTSFQPALEETONEVCQKSGEIS  
LLKQQLKESQTEVNAKASEILGLKQKLDTRKLEGLLETRTDLEGLALRTKGLLEVC  
ENLQSQSYVAMYQNRLEKALQQLARGDSAGEPLEVDLEGADIPYEDIIATEI"  
BASE COUNT 336 a 483 c 482 g 214 t  
ORIGIN

Query Match 9.1%; Score 219; DB 9; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 2.4e-109;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGGTGTCAGGAGTACAGGCGAGATCTCCCTCTGAAGCAGCAGCTCAAGAGTCCACGA 396  
DB 1148 AGGTGTCAGGAGTACAGGCGAGATCTCCCTCTGAAGCAGCAGCTCAAGAGTCCACGA 1207  
QY 397 CGGAGGTGAACGCGCAAGGCTAGCGAGATCTCTGGGTCTCAAGGCACAGCTGAAGGACACGC 456  
DB 1208 CGGAGGTGAACGCGCAAGGCTAGCGAGATCTCTGGGTCTCAAGGCACAGCTGAAGGACACGC 1267  
QY 457 GGGCAGCTGGAGGCGCTCGAGCTGAGGACCCAGCAGCTGGAGGCGCCCTGGCGACCA 516  
DB 1268 GGGCAGCTGGAGGCGCTCGAGCTGAGGACCCAGCAGCTGGAGGCGCCCTGGCGACCA 1327  
QY 517 AGGCGCTGGAGCTGGAGCTCTGTGAGATGAGCTGACGC 555  
DB 1328 AGGCGCTGGAGCTGGAGCTCTGTGAGATGAGCTGACGC 1366

RESULT 8  
AF123654  
LOCUS  
DEFINITION  
Homo sapiens clone E264162 FEZ1 (FEZ1) mRNA, alternatively spliced,  
complete cds.  
AF123654  
VERSION  
AF123654.1 GI:4572465  
KEYWORDS  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 633)  
AUTHORS  
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,  
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.  
TITLE  
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
and its expression is altered in multiple human tumors  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
MEDLINE  
99199287  
PUBMED  
10097140  
REFERENCE  
2 (bases 1 to 633)  
AUTHORS  
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,  
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
Institute, 233S 10th street, Philadelphia, PA 19107, USA  
FEATURES  
source  
1. .231  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="8"  
/map="8p22"  
/clone="E16T8"  
1. .231  
gene

FEATURES  
source  
Institute, 233S 10th street, Philadelphia, PA 19107, USA  
Location/Qualifiers  
1. .1515  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="8"  
/map="8p22"  
/clone="D14"  
1. .1515  
/genes="FEZ1"  
1. .1515  
/genes="FEZ1"  
/notes="alternatively spliced"  
/codon\_start=1  
/product="FEZ1"  
/protein\_id="AAD23837.1"  
/db\_xref="GI:4572470"  
/translation="MGSVSLISGHSFHKCRASQYKLRKSSHLKLNRYSDGLLRF  
GFSQDSHGKSGKMGSEDFYIKVQKARGSHHDPYATLSSGDLGGQAGVDFDPST  
ELKPGLCGALSDSGRNSKMGKAVRPTAPKPLVLRSGAILHSSPESASHQLHPAPDPKPEQ  
LQKLSRFEKELASLAYERPRRCDELEGPCKGNLKOASOKSORAOQVLHQL  
VLQKQKRLQRLSLKMEQDLLETKLRSYEREKTSFQPALEETONEVCQKSGEIS  
LLKQQLKESQTEVNAKASEILGLKQKLDTRKLEGLLETRTDLEGLALRTKGLLEVC  
ENLQSQSYVAMYQNRLEKALQQLARGDSAGEPLEVDLEGADIPYEDIIATEI"  
BASE COUNT 336 a 483 c 482 g 214 t  
ORIGIN

Query Match 9.1%; Score 219; DB 9; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 2.4e-109;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGGTGTCAGGAGTACAGGCGAGATCTCCCTCTGAAGCAGCAGCTCAAGAGTCCACGA 396  
DB 1148 AGGTGTCAGGAGTACAGGCGAGATCTCCCTCTGAAGCAGCAGCTCAAGAGTCCACGA 1207  
QY 397 CGGAGGTGAACGCGCAAGGCTAGCGAGATCTCTGGGTCTCAAGGCACAGCTGAAGGACACGC 456  
DB 1208 CGGAGGTGAACGCGCAAGGCTAGCGAGATCTCTGGGTCTCAAGGCACAGCTGAAGGACACGC 1267  
QY 457 GGGCAGCTGGAGGCGCTCGAGCTGAGGACCCAGCAGCTGGAGGCGCCCTGGCGACCA 516  
DB 1268 GGGCAGCTGGAGGCGCTCGAGCTGAGGACCCAGCAGCTGGAGGCGCCCTGGCGACCA 1327  
QY 517 AGGCGCTGGAGCTGGAGCTCTGTGAGATGAGCTGACGC 555  
DB 1328 AGGCGCTGGAGCTGGAGCTCTGTGAGATGAGCTGACGC 1366

RESULT 8  
AF123654  
LOCUS  
DEFINITION  
Homo sapiens clone E264162 FEZ1 (FEZ1) mRNA, alternatively spliced,  
complete cds.  
AF123654  
VERSION  
AF123654.1 GI:4572465  
KEYWORDS  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 633)  
AUTHORS  
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,  
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.  
TITLE  
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
and its expression is altered in multiple human tumors  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
MEDLINE  
99199287  
PUBMED  
10097140  
REFERENCE  
2 (bases 1 to 633)  
AUTHORS  
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,  
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.



```

misc_feature 402..5831
/note="assembly_fragment"
misc_feature 5932..173029
/note="assembly_fragment"
misc_feature 173130..210061
/note="assembly_fragment"
misc_feature 210162..227884
/note="assembly_fragment
clone_end:T7
vector_side:right"
BASE COUNT 65784 a 48825 c 49502 g 62967 t 402 others
ORIGIN
Query Match 2.2%; Score 52; DB 2; Length 227884;
Best Local Similarity 100.0%; Pred.No. 1e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 939 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGCTGCT 990
Db 87977 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGCTGCT 88028

RESULT 11
AC099416/c
LOCUS AC099416 263546 bp DNA linear HTG 23-MAY-2002
DEFINITION Mus musculus chromosome UNK clone RP23-122M11, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
ACCESSION AC099416
VERSION AC099416.2 GI:21105058
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (14-NOV-2001) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 263546)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 23, 2002 this sequence version replaced gi:16924178.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: M BA0122M11
----- Summary Statistics -----
Sequencing vector: M13; 32%
Sequencing vector: plasmid; 68%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 278310 bases at least Q40
Consensus quality: 282938 bases at least Q30
Consensus quality: 286149 bases at least Q20
Insert size: 250000; agarose-fp
Insert size: 387570; sum-of-contigs
Quality coverage: 25.74 in Q20 bases; agarose-fp
Quality coverage: 16.86 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently

```

\* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

1 1204: contig of 1204 bp in length
* 1205: gap of unknown length
* 1305: contig of 1220 bp in length
* 2525: gap of unknown length
* 2625: contig of 1512 bp in length
* 4137: gap of unknown length
* 4237: contig of 12198 bp in length
* 16435: gap of unknown length
* 16535: contig of 15572 bp in length
* 32107: gap of unknown length
* 32207: contig of 108018 bp in length
* 140225: gap of unknown length
* 140325: contig of 122369 bp in length
* 262694: gap of unknown length
* 262794: contig of 753 bp in length.

```

## FEATURES

## Location/Qualifiers

## source

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1..263546
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-122M11"

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## misc\_feature

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1..1204
/note="assembly_name:Contig127"

```

## misc\_feature

```

1305..2524
/note="assembly_name:Contig157"

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## misc\_feature

```

2625..4136
/note="assembly_name:Contig360"

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## misc\_feature

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4237..16434
/note="assembly_name:Contig396"

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## misc\_feature

```

16535..32106
/note="assembly_name:Contig397"

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## misc\_feature

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32207..140224
/note="assembly_name:Contig398"

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## misc\_feature

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140325..262693
/note="assembly_name:Contig399"

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## misc\_feature

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262794..263546
/note="assembly_name:Contig154"

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BASE COUNT 76628 a 56149 c 55623 g 74436 t 710 others

## ORIGIN

```

Query Match 2.2%; Score 52; DB 2; Length 263546;
Best Local Similarity 100.0%; Pred.No. 1e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 939 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGCTGCT 990

Db 246909 GCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGCTGCT 246958

## RESULT 12

## AC093491

```

LOCUS AC093491 162178 bp DNA linear PRI 02-NOV-2001
DEFINITION Homo sapiens chromosome 16 clone RP11-410N2, complete sequence.
ACCESSION AC093491 AC024237
VERSION AC093491.2 GI:16596544
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162178)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
REFERENCE 2 (bases 1 to 162178)
AUTHORS DOE Joint Genome Institute.

```

**TITLE**  
JOURNAL  
**REFERENCE**  
AUTHORS  
**TITLE**  
JOURNAL  
**COMMENT**

Direct Submission  
Submitted (28-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 162178)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Nov 2, 2001 this sequence version replaced gi:15320919.

**Sequence Quality Assessment:**  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

**Sequence Quality Assessment:**  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

**FEATURES**  
source  
Location/Qualifiers  
1. 162178  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/clone="RP11-410N2"  
BASE COUNT 41546 a 39076 c 39454 g 42102 t  
ORIGIN

Query Match 2.0%; Score 49; DB 9; Length 162178;  
Best Local Similarity 100.0%; Pred. No. 4.6e-15;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGAGCGGAGGTTTCAGTGAGCCCAAGATCAGCCACTACACCCAGCCT 54  
|||||  
Db 100265 GGAGCGGAGGTTTCAGTGAGCCCAAGATCAGCCACTACACCCAGCCT 100313  
|||||

**RESULT 13**  
AC012184/c  
LOCUS  
DEFINITION  
AC012184  
VERSION  
AC012184.6 GI:20486391  
KEYWORDS  
HTG.  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
AUTHORS  
**TITLE**  
JOURNAL  
**REFERENCE**  
AUTHORS  
**TITLE**  
JOURNAL  
**REFERENCE**  
AUTHORS  
**TITLE**  
JOURNAL  
**COMMENT**

AC012184 195952 bp DNA linear PRI 07-MAY-2002  
Homo sapiens chromosome 16 clone RP11-529K1, complete sequence.  
AC012184.6 GI:20486391  
HTG.  
Homo sapiens.  
Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
DOE Joint Genome Institute.  
Sequencing of Human Chromosome 16  
Unpublished  
2 (bases 1 to 195952)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (21-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 195952)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (07-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On May 7, 2002 this sequence version replaced gi:13786348.

**Sequence Quality Assessment:**  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

**Sequence Quality Assessment:**  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

**FEATURES**  
source  
Location/Qualifiers  
1. 195952  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/clone="RP11-529K1"  
BASE COUNT 48977 a 48735 c 48253 g 49987 t  
ORIGIN

Query Match 2.0%; Score 49; DB 9; Length 195952;  
Best Local Similarity 100.0%; Pred. No. 4.6e-15;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGAGCGGAGGTTTCAGTGAGCCCAAGATCAGCCACTACACCCAGCCT 54  
|||||  
Db 32583 GGAGCGGAGGTTTCAGTGAGCCCAAGATCAGCCACTACACCCAGCCT 32535  
|||||

**RESULT 14**  
AL391314  
LOCUS  
DEFINITION  
AL391314  
Human DNA sequence from clone RP11-477H7 on chromosome 10, complete sequence.  
AL391314  
VERSION  
AL391314.21 GI:17426471  
KEYWORDS  
HTG.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Tracey, A.  
1 (bases 1 to 129435)  
Direct Submission  
Submitted (06-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
On Dec 8, 2001 this sequence version replaced gi:17402352.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP

database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 10, constructed by the Sanger Centre Chromosome 10  
 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr10>  
 RP11-477H7 is from the library RPI1-11.2 constructed by the group  
 of Pictet de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone  
 RP11-477H7 it may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true right end of clone RP11-477H7 is at 129435 in this  
 sequence. The true left end of clone RP11-481B7 is at 30248 in this  
 sequence. The true right end of clone RP11-186N15 is at 2000 in  
 this sequence.

FEATURES  
 Location/Qualifiers  
 1..129435  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-477H7"  
 /clone\_lib="RPI1-11.2"  
 99418..99422  
 /note="Sequence from uni-directional dGTP big dye  
 terminator reads only."

BASE COUNT 32508 a 29205 c 30709 g 37013 t  
 ORIGIN

Query Match 1.8%; Score 43; DB 9; Length 129435;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-12;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGGGAGCGGAGGTTGCAGTCAGCCAGATCACGCCACTACAC 46  
 |||||

Db 92566 GGGGAGCGGAGGTTGCAGTCAGCCAGATCACGCCACTACAC 92508  
 |||||

RESULT 15  
 AC084688/c  
 LOCUS  
 DEFINITION Homo sapiens chromosome 1 clone RP11-25F12 map 1, WORKING DRAFT  
 SEQUENCE, 41 unordered pieces.  
 AC084688  
 AC084688.2 GI:11875300  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 140179)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 1, clone RP11-25F12  
 Unpublished

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 2 (bases 1 to 140179)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Bada,F., Boguslavskiy,L.,  
 Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,  
 Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,  
 Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,  
 FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,  
 Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,  
 Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,  
 Lamazares,R., Landers,T., Lechoczy,J., Levine,R., Lieu,C., Liu,G.,  
 Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,  
 McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
 Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,  
 O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,  
 Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,  
 Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,  
 Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,  
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,  
 Zimmer,A. and Zody,M.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

Direct Submission  
 Submitted (05-NOV-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 140179)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,  
 Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,  
 Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,  
 Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,  
 Lechoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,  
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 Zembek,L., Zimmer,A. and Zody,M.

TITLE  
 JOURNAL  
 COMMENT

Direct Submission  
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Dec 16, 2000 this sequence version replaced gi:11095466.  
 All repeats were identified using RepeatMasker:  
 Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L11244

Center clone name: 25\_F\_12

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 122426 bases at least Q40

Consensus quality: 130754 bases at least Q30

Consensus quality: 133913 bases at least Q20

Insert size: 165000; agarose-fp

Insert size: 136179; sum-of-contigs

Quality coverage: 3.4 in Q20 bases; agarose-fp

Quality coverage: 4.2 in Q20 bases; sum-of-contigs

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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 41 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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C 382	31	1.3	12149	22	AAK36758	Human cardiovascular
C 383	31	1.3	12247	22	AAK73076	Human immune/haema
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C 385	31	1.3	12409	22	AAK30238	DNA encoding rena
C 386	31	1.3	13058	22	AAK29194	Genomic sequence #
C 387	31	1.3	13058	22	AAK79325	Human immune/haema
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C 408	31	1.3	16596	22	AAK33396	DNA encoding human
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C 412	31	1.3	17073	21	AAK34876	Human adenosine re
C 413	31	1.3	17138	22	AAK41577	Human protease gen
C 414	31	1.3	17138	22	ABL41524	Entire genomic seq
C 415	31	1.3	17170	22	AAK77880	Human immune/haema
C 416	31	1.3	17173	22	AAK77881	Human immune/haema
C 417	31	1.3	17200	22	AAK73025	Human musculocele
C 418	31	1.3	18887	22	AAK18543	DNA encoding UDP g
C 419	31	1.3	19125	22	AAK36440	Human musculocele
C 420	31	1.3	19191	22	AAK67485	Human immune/haema
C 421	31	1.3	19883	21	AAK20999	Human low adenosin
C 422	31	1.3	19943	21	AAK34877	Human adenosine re
C 423	31	1.3	20188	22	AAK73082	Human immune/haema
C 424	31	1.3	20188	22	AAK87550	Human nervous syst
C 425	31	1.3	20869	22	ABAL6245	Human cardiovascular
C 426	31	1.3	20869	22	AAK36927	Human immune/haema
C 427	31	1.3	20869	22	AAK85001	Human immune/haema
C 428	31	1.3	20991	22	AAK87545	Human immune/haema
C 429	31	1.3	21358	22	AAK39919	Genomic sequence #
C 430	31	1.3	21358	22	AAK06419	Human reproductive
C 431	31	1.3	21358	22	AAK73090	Human immune/haema
C 432	31	1.3	21358	22	AAK87446	Human immune/haema
C 433	31	1.3	21358	22	AAK87558	Human immune/haema
C 434	31	1.3	21358	22	AAK90363	Human digestive sy
C 435	31	1.3	21676	22	AAK39918	Genomic sequence #
C 436	31	1.3	21676	22	AAK06418	Human reproductive
C 437	31	1.3	21676	22	AAK73081	Human immune/haema
C 438	31	1.3	21676	22	AAK87445	Human immune/haema
C 439	31	1.3	21676	22	AAK87549	Human immune/haema
C 440	31	1.3	21676	22	AAK90362	Human digestive sy
C 441	31	1.3	22401	22	AAK71911	Human immune/haema
C 442	31	1.3	22402	22	AAK71912	Human immune/haema
C 443	31	1.3	22645	22	AAK04985	Human reproductive
C 444	31	1.3	22645	22	AAK05495	Human reproductive
C 445	31	1.3	22645	22	AAK89727	Human digestive sy
C 446	31	1.3	22645	23	ABL97878	Human testicular a
C 447	31	1.3	22645	23	ABL98348	Human testicular a
448	31	1.3	23075	22	ABAL9112	Human nervous syst
449	31	1.3	23580	22	AAK66230	Human immune/haema
C 450	31	1.3	23580	22	AAK83578	Human immune/haema
C 451	31	1.3	23603	22	AAK71829	Human immune/haema
C 452	31	1.3	23603	22	AAK73089	Human immune/haema
C 453	31	1.3	23603	22	AAK87557	Human immune/haema
C 454	31	1.3	23603	22	AAI62936	Human genomic DNA
C 455	31	1.3	23613	22	AAK71823	Human immune/haema
C 456	31	1.3	23613	22	AAK73085	Human immune/haema
C 457	31	1.3	23613	22	AAK87553	Human immune/haema
C 458	31	1.3	23613	22	AAI62930	Human genomic DNA
C 459	31	1.3	24102	22	AAK74877	Human immune/haema
C 460	31	1.3	24218	22	AAK71828	Human immune/haema
C 461	31	1.3	24218	22	AAK73088	Human immune/haema
C 462	31	1.3	24218	22	AAK87556	Human immune/haema
C 463	31	1.3	24218	22	AAI62935	Human genomic DNA
C 464	31	1.3	25837	22	AAK85952	Human immune/haema
C 465	31	1.3	25895	22	AAK77832	Human immune/haema
C 466	31	1.3	26928	22	ABA82620	Human HBM gene reg
C 467	31	1.3	26928	24	ABK22779	Human high bone ma
C 468	31	1.3	26995	22	AAK229963	Human lung antigen
C 469	31	1.3	29163	22	AAU05121	Human reproductive
C 470	31	1.3	29163	23	ABL98013	Human testicular a
C 471	31	1.3	29449	22	AAD16646	Human novel protei
C 472	31	1.3	29449	22	AAK30243	DNA encoding rena
C 473	31	1.3	31871	23	ABK42516	Genomic sequence #
C 474	31	1.3	32145	22	AAK68491	Human immune/haema
C 475	31	1.3	32145	22	AAK68575	Human immune/haema
C 476	31	1.3	32187	22	AAK89946	Human digestive sy
C 477	31	1.3	32190	22	AAI62927	Human genomic DNA
C 478	31	1.3	32195	22	AAK36517	Human cardiovascular
C 479	31	1.3	32207	22	ABAL9666	Human nervous syst
C 480	31	1.3	32219	22	AAK36516	Human cardiovascular
C 481	31	1.3	32249	22	AAI62932	Human genomic DNA
C 482	31	1.3	33795	24	ABN95686	Gene #2184 used to
C 483	31	1.3	33968	22	AAK71820	Human immune/haema
C 484	31	1.3	33968	22	AAK73078	Human immune/haema
C 485	31	1.3	39068	22	AAK85294	Human immune/haema
C 486	31	1.3	39068	22	AAK87544	Human immune/haema
C 487	31	1.3	39110	22	AAK71825	Human immune/haema
C 488	31	1.3	39110	22	AAK73087	Human immune/haema
C 489	31	1.3	39110	22	AAK87555	Human immune/haema
C 490	31	1.3	39887	22	AAK79153	Human immune/haema
C 491	31	1.3	39887	22	AAK81263	Human immune/haema
C 492	31	1.3	40742	22	AAK68089	Human immune/haema
C 493	31	1.3	40742	22	AAK79886	Human immune/haema
C 494	31	1.3	42324	22	AAK84724	Human immune/haema
C 495	31	1.3	44354	22	AAK77833	Human immune/haema
C 496	31	1.3	44354	22	AAK77836	Human immune/haema
C 497	31	1.3	44354	22	AAK77837	Human immune/haema
C 498	31	1.3	45000	22	AAK12437	DNA encoding 1-ami
C 499	31	1.3	45300	22	AAK73079	Human immune/haema
C 500	31	1.3	45300	22	AAK87547	Human immune/haema
C 501	31	1.3	47090	22	AAK68725	Human immune/haema
C 502	31	1.3	47090	22	AAK78219	Human immune/haema
C 503	31	1.3	48037	22	AAK84729	Human immune/haema
C 504	31	1.3	48037	22	AAK85983	Human immune/haema
C 505	31	1.3	48045	22	AAK84730	Human immune/haema
C 506	31	1.3	48045	22	AAK85984	Human immune/haema
C 507	31	1.3	49998	20	AAK23518	Human kidney amino
C 508	31	1.3	50849	24	ABN87883	Human glutathione
C 509	31	1.3	51402	22	AAK72363	Human immune/haema
C 510	31	1.3	53552	22	AAK13655	Genomic DNA sequen
C 511	31	1.3	57296	22	AAK78170	Human immune/haema
C 512	31	1.3	57296	22	AAK78847	Human immune/haema
C 513	31	1.3	57296	22	AAK79364	Human immune/haema
C 514	31	1.3	57296	22	AAK86799	Human immune/haema
C 515	31	1.3	62944	24	ABL66947	Lung cancer relate
C 516	31	1.3	62944	24	ABL68262	Kidney cancer rela
C 517	31	1.3	65854	22	AAK86282	Human immune/haema
C 518	31	1.3	66566	21	AAA53450	Human thioredoxin
C 519	31	1.3	72928	20	AAK21835	Human ASTH1J 5' ge
C 520	31	1.3	72928	21	AAA80253	Human ASTH1J 5' ge

C 521	31	1.3	81001	22	AAF30035	Human apolipoprote	c 594	30	1.2	402	22	AAI91321	Human polynucleoti
C 522	31	1.3	97835	24	ABQ84796	Human CDNA differe	C 595	30	1.2	404	23	ABV43752	Human prostate exp
C 523	31	1.3	100301	24	ABQ88176	Human osteoblast d	C 596	30	1.2	405	23	ABV34903	Human prostate exp
C 524	31	1.3	107820	22	AAI16230	Human ATP-binding	C 597	30	1.2	412	24	ABL83673	Human ovarian canc
C 525	31	1.3	109906	24	ABK94411	DNA encoding endot	C 598	30	1.2	420	21	ABV36507	Human prostate exp
C 526	31	1.3	110096	24	ABN95044	Gene #1542 used to	C 599	30	1.2	431	22	AAK84332	Human immune/haema
C 527	31	1.3	125439	24	ABQ88177	Human osteoblast d	C 600	30	1.2	432	22	AAK84331	Human immune/haema
C 528	31	1.3	136284	24	ABK83575	Human CDNA differe	C 601	30	1.2	432	22	AAK84331	DNA encoding novel
C 529	31	1.3	139389	24	ABK84795	Human CDNA differe	C 602	30	1.2	432	22	AAK84331	Human immune/haema
C 530	31	1.3	139904	24	ABK83562	Human CDNA differe	C 603	30	1.2	436	21	AAK25662	Human secreted pro
C 531	31	1.3	143899	24	AAI38336	Genomic sequence e	C 604	30	1.2	437	24	ABN65729	Human cancer relat
C 532	31	1.3	145831	24	ABL62309	Colon adenocarcino	C 605	30	1.2	448	22	AAK57663	Human immune/haema
C 533	31	1.3	145831	24	ABL66806	Lung cancer relate	C 606	30	1.2	455	22	AAK56418	Human immune/haema
C 534	31	1.3	145831	24	ABL68588	Kidney cancer rela	C 607	30	1.2	470	22	AAH10091	Human CDNA clone (
C 535	31	1.3	145831	24	ABL69213	Prostate cancer re	C 608	30	1.2	471	23	ABV35684	Human prostate exp
C 536	31	1.3	147708	24	ABQ88154	Human osteoblast d	C 609	30	1.2	471	23	ABV44489	Human prostate exp
C 537	31	1.3	160755	23	AAH88704	Human DNA sequence	C 610	30	1.2	477	23	ABV04621	Human prostate exp
C 538	31	1.3	160771	24	ABQ88179	Human osteoblast d	C 611	30	1.2	478	22	AAK67984	Human immune/haema
C 539	31	1.3	183999	22	AAK92831	Human ABC1 genomic	C 612	30	1.2	478	22	AAK67985	Human immune/haema
C 540	31	1.3	198161	24	ABK93564	Human CDNA differe	C 613	30	1.2	482	24	ABL85825	Human ovarian canc
C 541	31	1.3	220895	24	ABK84798	Human CDNA differe	C 614	30	1.2	485	23	ABV38047	Human prostate exp
C 542	31	1.3	235033	19	AAV57926	Hereditary haemoch	C 615	30	1.2	495	22	ABV53854	Human prostate exp
C 543	31	1.3	237326	19	AAV57903	Hereditary haemoch	C 616	30	1.2	496	22	ABA14124	Human nervous syst
C 544	31	1.3	452237	24	ABQ87681	Human osteogen re	C 617	30	1.2	527	24	ABN62961	Human cancer relat
C 545	31	1.3	452237	24	ABA90193	Human osteogen re	C 618	30	1.2	536	24	ABN64923	Human cancer relat
C 546	31	1.3	1503900	22	AAK95240	Human neuregulin-1	C 619	30	1.2	538	23	ABV16597	Human prostate exp
C 547	31	1.3	1503900	22	AAK96733	Human neuregulin-1	C 620	30	1.2	544	23	ABV50544	Human prostate exp
C 548	30	1.2	51	22	AAI76249	Human silent SNP c	C 621	30	1.2	546	24	ABL85722	Human ovarian canc
C 549	30	1.2	51	22	AAI76251	Human silent SNP c	C 622	30	1.2	550	22	AAH09740	Human CDNA clone (
C 550	30	1.2	51	22	AAH89405	Human coding sequ	C 623	30	1.2	553	23	ABV57690	Human prostate exp
C 551	30	1.2	73	22	AAK90007	Human upstream Alu	C 624	30	1.2	564	22	AAH10031	Human CDNA clone (
C 552	30	1.2	101	22	AAK82622	Human immune/haema	C 625	30	1.2	566	22	AAH10007	Human CDNA clone (
C 553	30	1.2	103	22	AAK73577	Human immune/haema	C 626	30	1.2	569	22	AAH13412	Human CDNA clone (
C 554	30	1.2	107	22	AAI04735	Human reproductive	C 627	30	1.2	574	24	ABL66172	Lung cancer relate
C 555	30	1.2	107	22	AAI04738	Human reproductive	C 628	30	1.2	585	23	ABV51184	Human prostate exp
C 556	30	1.2	107	23	ABL97640	Human testicular a	C 629	30	1.2	586	22	AAK36781	Human cardiovascular
C 557	30	1.2	107	23	ABL97643	Human testicular a	C 630	30	1.2	586	23	AAK36781	Human cardiovascular
C 558	30	1.2	110	22	AAK85751	Human immune/haema	C 631	30	1.2	587	23	ABV08133	Human immune/haema
C 559	30	1.2	111	22	AAK73576	Human immune/haema	C 632	30	1.2	587	23	ABV23699	Human prostate exp
C 560	30	1.2	112	22	AAK73582	Human immune/haema	C 633	30	1.2	587	23	ABV29568	Human prostate exp
C 561	30	1.2	114	22	AAK36217	Human cardiovascular	C 634	30	1.2	592	22	AAK72482	Human immune/haema
C 562	30	1.2	116	22	AAK73326	Human immune/haema	C 635	30	1.2	593	22	AAK36778	Human cardiovascular
C 563	30	1.2	119	22	AAK73566	Human immune/haema	C 636	30	1.2	593	22	AAK36780	Human cardiovascular
C 564	30	1.2	119	22	AAK73569	Human immune/haema	C 637	30	1.2	604	22	ABA21237	Human nervous syst
C 565	30	1.2	127	22	AAI36925	Human musculoskele	C 638	30	1.2	611	24	ABN62702	Human cancer relat
C 566	30	1.2	127	22	AAI36925	Human musculoskele	C 639	30	1.2	619	23	ABV05824	Human prostate exp
C 567	30	1.2	127	22	AAK65153	Human genomic DNA	C 640	30	1.2	620	23	ABV14993	Human prostate exp
C 568	30	1.2	133	22	AAK77877	Human immune/haema	C 641	30	1.2	622	23	ABV51983	Human prostate exp
C 569	30	1.2	133	22	AAK77879	Human immune/haema	C 642	30	1.2	632	22	AAK70386	Human immune/haema
C 570	30	1.2	134	22	ABA16899	Human nervous syst	C 643	30	1.2	632	22	AAK70386	Human immune/haema
C 571	30	1.2	134	22	ABA18331	Human nervous syst	C 644	30	1.2	661	23	ABV39076	Human prostate exp
C 572	30	1.2	136	22	AAK68049	Human nervous syst	C 645	30	1.2	661	23	ABV44862	Human prostate exp
C 573	30	1.2	140	22	AAK65590	Human immune/haema	C 646	30	1.2	671	23	ABV46395	Human prostate exp
C 574	30	1.2	151	22	AAK86194	Human immune/haema	C 647	30	1.2	691	22	AAK56390	Human immune/haema
C 575	30	1.2	157	20	AAH86639	Human single nucle	C 648	30	1.2	700	22	AAH92156	Human inflammatory
C 576	30	1.2	167	22	AAI89783	Human polynucleoti	C 649	30	1.2	700	22	AAH92420	Human inflammatory
C 577	30	1.2	248	22	AAI98905	Human excretory re	C 650	30	1.2	708	22	AAH92572	Human inflammatory
C 578	30	1.2	248	22	AAI63255	Human kidney relat	C 651	30	1.2	723	22	AAH07283	Human CDNA clone (
C 579	30	1.2	294	21	AAI63305	Human secreted pro	C 652	30	1.2	723	22	AAH07283	hFIX gene AB3' age
C 580	30	1.2	308	22	AAI63305	Human secreted pro	C 653	30	1.2	726	22	AAH89444	Human digestive sy
C 581	30	1.2	312	24	ABL80501	Human musculoskele	C 654	30	1.2	739	22	AAH98158	Human EST-derived
C 582	30	1.2	313	24	ABL84842	Human ovarian canc	C 655	30	1.2	763	22	AAI95299	Human neuroblastom
C 583	30	1.2	321	22	AAI223397	Human breast canc	C 656	30	1.2	791	23	AAK568432	DNA encoding novel
C 584	30	1.2	323	24	ABK45452	cDNA encoding colo	C 657	30	1.2	797	23	ABV13790	Human prostate exp
C 585	30	1.2	335	14	AAO59473	Human brain Expres	C 658	30	1.2	800	22	AAH04460	Human CDNA clone (
C 586	30	1.2	341	22	AAI88329	Human polynucleoti	C 659	30	1.2	847	22	AAK67359	Human immune/haema
C 587	30	1.2	341	22	AAH19245	Human secreted pro	C 660	30	1.2	856	23	ABV14606	Human prostate exp
C 588	30	1.2	351	22	AAI36757	Novel human diagno	C 661	30	1.2	1000	20	AAZ27733	Human DNA marker c
C 589	30	1.2	358	22	AAI84944	Human polynucleoti	C 662	30	1.2	1001	21	AAH51279	Human GSHS related
C 590	30	1.2	369	22	ABA15271	Human nervous syst	C 663	30	1.2	1001	21	AAH51293	Human GLCL related
C 591	30	1.2	380	24	ABL84503	Human ovarian canc	C 664	30	1.2	1001	21	AAH51294	Human GLCL related
C 592	30	1.2	401	22	AAK96009	Human neuregulin g	C 665	30	1.2	1001	21	AAH51559	Human GLCL related
C 593	30	1.2	401	22	AAK97502	Human neuregulin g	C 666	30	1.2	1002	22	AAH06938	Human reproductive

c 667	30	1.2	1041	22	AAI86080	Human polynucleoti
c 668	30	1.2	1083	22	AAI04506	Human reproductive
c 669	30	1.2	1145	23	ABV21468	Human prostate exp
c 670	30	1.2	1145	23	ABV27286	Human prostate exp
c 671	30	1.2	1321	22	AAH19195	Human secreted pro
c 672	30	1.2	1432	22	AAH131350	Human CDNA encodin
c 673	30	1.2	1432	24	ABQ66674	Human polynucleoti
c 674	30	1.2	1494	22	AAI06935	Human reproductive
c 675	30	1.2	1496	22	AAI03200	Human reproductive
c 676	30	1.2	1496	22	AAI06934	Human reproductive
c 677	30	1.2	1496	22	AAI06941	Human reproductive
c 678	30	1.2	1591	22	AAH79923	Human immune/haema
c 679	30	1.2	1646	22	AAH15532	Human CDNA sequenc
c 680	30	1.2	1654	22	AAH13895	Human CDNA sequenc
c 681	30	1.2	1704	22	AAI60361	Human polynucleoti
c 682	30	1.2	1724	21	AAI68105	Human secreted pro
c 683	30	1.2	1734	22	AAH16375	Human CDNA sequenc
c 684	30	1.2	1770	24	ABQ55059	Human ovarian anti
c 685	30	1.2	1782	22	AAH75827	Human immune/haema
c 686	30	1.2	1782	22	AAH75828	Human immune/haema
c 687	30	1.2	1782	22	AAH75829	Human immune/haema
c 688	30	1.2	1817	24	AAI33245	Human secreted pro
c 689	30	1.2	1819	22	AAH73699	Human immune/haema
c 690	30	1.2	1840	22	AAH17364	Human CDNA sequenc
c 691	30	1.2	1849	24	AAI62511	CDNA sequence #298
c 692	30	1.2	1926	20	AAH98020	Human secreted pro
c 693	30	1.2	1946	22	AAI58575	Human polynucleoti
c 694	30	1.2	1946	22	AAH18694	Human CDNA sequenc
c 695	30	1.2	1956	22	AAH17398	Human CDNA sequenc
c 696	30	1.2	1965	24	ABK34980	Human CDNA encodin
c 697	30	1.2	2012	22	AAH16700	Human CDNA sequenc
c 698	30	1.2	2103	22	AAH17435	Human CDNA sequenc
c 699	30	1.2	2109	22	AAK91478	Human digestive sy
c 700	30	1.2	2109	22	AAI57788	Human colorectal c
c 701	30	1.2	2123	22	AAH17323	Human CDNA sequenc
c 702	30	1.2	2136	22	AAH18289	Human CDNA sequenc
c 703	30	1.2	2185	22	AAK83299	Human immune/haema
c 704	30	1.2	2244	22	AAH14757	Human CDNA sequenc
c 705	30	1.2	2266	22	AAK89548	Human digestive sy
c 706	30	1.2	2290	24	ABK35014	Human CDNA encodin
c 707	30	1.2	2297	22	AAK77678	Human immune/haema
c 708	30	1.2	2471	23	ABV23397	Human prostate exp
c 709	30	1.2	2471	23	ABV29253	Human prostate exp
c 710	30	1.2	2685	23	ABV22723	Human prostate exp
c 711	30	1.2	2685	23	ABV28548	Human prostate exp
c 712	30	1.2	2692	24	AAI33268	Human secreted pro
c 713	30	1.2	2749	22	AAH18717	Human CDNA sequenc
c 714	30	1.2	2771	22	AAH17350	Human CDNA sequenc
c 715	30	1.2	2816	22	AAK83109	Human immune/haema
c 716	30	1.2	2972	22	AAI33260	Human 39406 CDNA
c 717	30	1.2	3270	22	AAK26707	Human genomic DNA
c 718	30	1.2	3309	22	AAK74687	Human immune/haema
c 719	30	1.2	3309	22	AAK74688	Human immune/haema
c 720	30	1.2	3543	22	AAK83495	Human immune/haema
c 721	30	1.2	3788	22	AAK71131	Human immune/haema
c 722	30	1.2	4087	22	ABA20446	Human nervous syst
c 723	30	1.2	4385	22	AAI32674	Human CDNA encodin
c 724	30	1.2	4447	22	AAK75249	Human immune/haema
c 725	30	1.2	4752	22	AAK81040	Human immune/haema
c 726	30	1.2	4837	22	AAI36474	Human musculoskele
c 727	30	1.2	4963	22	AAI328260	Genomic sequence #
c 728	30	1.2	4963	22	AAI31527	Human DNA for a no
c 729	30	1.2	4963	24	ABQ66851	Human polynucleoti
c 730	30	1.2	5096	22	AAI32234	Human DNA repair a
c 731	30	1.2	5150	22	ABAO7960	Human ovarian and
c 732	30	1.2	5150	22	AAI03872	Human reproductive
c 733	30	1.2	5151	22	ABA07961	Human ovarian and
c 734	30	1.2	5151	22	AAI03873	Human reproductive
c 735	30	1.2	5441	22	AAI98937	Human excretory re
c 736	30	1.2	5441	22	AAI63287	Human kidney relat
c 737	30	1.2	6040	22	AAI28595	Genomic sequence #
c 738	30	1.2	6284	22	AAI37278	Human musculoskele
c 739	30	1.2	6461	22	AAI31467	Human DNA for a no
c 740	30	1.2	740	24	ABQ66791	Human polynucleoti
c 741	30	1.2	6708	22	ABA07966	Human ovarian and
c 742	30	1.2	6708	22	AAI03878	Human reproductive
c 743	30	1.2	6713	22	AAK65822	Human immune/haema
c 744	30	1.2	6713	22	AAK73821	Human immune/haema
c 745	30	1.2	6767	22	AAK83147	Human immune/haema
c 746	30	1.2	6801	22	AAK77606	Human immune/haema
c 747	30	1.2	6801	22	AAK77607	Human immune/haema
c 748	30	1.2	7023	22	AAI36437	Human musculoskele
c 749	30	1.2	7062	22	AAI37524	Human musculoskele
c 750	30	1.2	7218	22	AAK85312	Human immune/haema
c 751	30	1.2	7588	22	AAI07036	Human reproductive
c 752	30	1.2	7588	22	AAI62714	Human breast or ov
c 753	30	1.2	8067	22	AAK71945	Human immune/haema
c 754	30	1.2	8082	22	AAI28672	Genomic sequence #
c 755	30	1.2	8387	22	ABA14892	Human nervous syst
c 756	30	1.2	8387	22	AAK84548	Human immune/haema
c 757	30	1.2	8734	22	AAK72027	Human immune/haema
c 758	30	1.2	8782	22	AAK811381	Human immune/haema
c 759	30	1.2	8821	22	AAI27837	DNA encoding novel
c 760	30	1.2	9192	22	AAI33461	DNA encoding human
c 761	30	1.2	9358	24	ABK84319	Human CDNA differe
c 762	30	1.2	9358	24	ABL61905	Colon adenocarcino
c 763	30	1.2	9556	22	AAK80290	Human immune/haema
c 764	30	1.2	9831	22	ABA07250	Human pancreatic c
c 765	30	1.2	9831	22	AAK89891	Human digestive sy
c 766	30	1.2	9899	22	AAK85825	Human immune/haema
c 767	30	1.2	9979	22	AAK81194	Human immune/haema
c 768	30	1.2	10012	24	ABL55889	Human small induci
c 769	30	1.2	10283	24	ABL56821	Human immediate ea
c 770	30	1.2	10445	22	AAI03692	Human reproductive
c 771	30	1.2	10563	22	AAI26706	Human genomic DNA
c 772	30	1.2	10709	22	AAI97858	Human neuroblastom
c 773	30	1.2	11006	22	AAK66281	Human immune/haema
c 774	30	1.2	11079	22	AAK90954	Human digestive sy
c 775	30	1.2	11079	22	AAK91989	Human liver associ
c 776	30	1.2	11079	24	ABN90344	Human liver anti
c 777	30	1.2	11096	22	ABA18278	Human nervous syst
c 778	30	1.2	11101	24	ABN83947	Human transporter
c 779	30	1.2	11176	22	AAK83662	Human immune/haema
c 780	30	1.2	11337	22	AAI36286	Human musculoskele
c 781	30	1.2	11618	22	AAI07202	Human reproductive
c 782	30	1.2	11618	22	AAK87088	Human immune/haema
c 783	30	1.2	11618	22	AAI33447	DNA encoding human
c 784	30	1.2	11742	22	ABA20557	Human nervous syst
c 785	30	1.2	11742	22	AAK76069	Human immune/haema
c 786	30	1.2	11870	22	AAI07328	Human reproductive
c 787	30	1.2	11870	22	AAI07329	Human reproductive
c 788	30	1.2	11870	22	AAK82242	Human immune/haema
c 789	30	1.2	11870	22	AAK82243	Human immune/haema
c 790	30	1.2	11870	22	AAK84792	Human immune/haema
c 791	30	1.2	11870	22	AAK84793	Human immune/haema
c 792	30	1.2	11948	22	AAK90588	Human digestive sy
c 793	30	1.2	11953	22	AAK90589	Human digestive sy
c 794	30	1.2	11967	22	AAI97863	Human neuroblastom
c 795	30	1.2	12232	22	AAI06946	Human reproductive
c 796	30	1.2	12301	22	AAI34544	Human DNA for a no
c 797	30	1.2	12438	22	AAI32819	Human genomic DNA
c 798	30	1.2	12452	22	ABA21062	Human nervous syst
c 799	30	1.2	12452	22	AAI37624	Human musculoskele
c 800	30	1.2	12562	22	AAI36095	Human musculoskele
c 801	30	1.2	12562	22	AAK72631	Human immune/haema
c 802	30	1.2	12600	24	AAI25770	Human APOBEC2 gene
c 803	30	1.2	12600	24	AAI25817	Human APOBEC2 gene
c 804	30	1.2	12970	22	AAK65917	Human immune/haema
c 805	30	1.2	12970	22	AAK85145	Human immune/haema
c 806	30	1.2	13158	18	AAI75288	Nucleotide sequenc
c 807	30	1.2	13467	22	AAI05944	Human reproductive
c 808	30	1.2	13467	22	AAI27670	DNA encoding novel
c 809	30	1.2	13467	22	AAI27838	DNA encoding novel
c 810	30	1.2	13467	22	AAI27838	Human immune/haema
c 811	30	1.2	13467	23	ABI98508	Human testicular a
c 812	30	1.2	13646	22	AAI97857	Human neuroblastom

C 813	30	1.2	13824	22	AAL37127	Human musculoskele	886	30	1.2	24887	24	ABK14141	Human aminolevulin
C 814	30	1.2	14040	22	ABA08209	Human ovarian and	C 887	30	1.2	25012	22	ABA15431	DNA nervous syst
C 815	30	1.2	14040	22	AAL02790	Human reproductive	C 888	30	1.2	25715	22	AAS33462	DNA encoding human
C 816	30	1.2	14040	22	AAL07517	Human reproductive	C 889	30	1.2	25785	22	AAK78465	Human immune/haema
C 817	30	1.2	14063	22	AAK82933	Human immune/haema	C 890	30	1.2	25971	22	AAK86336	Human immune/haema
C 818	30	1.2	14063	22	AAK82934	Human immune/haema	C 891	30	1.2	26191	22	AAK86339	Human immune/haema
C 819	30	1.2	14175	22	AAS27814	DNA encoding novel	C 892	30	1.2	26201	24	ABK14039	Human 3-hydroxy-3-
C 820	30	1.2	14175	22	AAK78859	Human immune/haema	C 893	30	1.2	26201	24	ABK14446	Human HMGL gene,
C 821	30	1.2	14299	22	AAK90955	Human digestive sy	C 894	30	1.2	26372	22	AAK77103	Human immune/haema
C 822	30	1.2	14299	22	AAS31990	Human liver associ	C 895	30	1.2	27289	22	AAS34624	Human DNA for a no
C 823	30	1.2	14299	22	ABN90345	Human liver antige	C 896	30	1.2	27435	22	AAK65476	Human immune/haema
C 824	30	1.2	14403	22	AAL07146	Human reproductive	C 897	30	1.2	27435	22	AAK65476	Human immune/haema
C 825	30	1.2	14633	22	ABA10066	Human nervous syst	C 898	30	1.2	27841	22	AAS29820	Human cytoskeletal
C 826	30	1.2	14633	22	AAK83608	Human immune/haema	C 899	30	1.2	28772	24	ABK83555	Human cDNA differe
C 827	30	1.2	14970	22	AAS42037	Genomic sequence #	C 900	30	1.2	28974	22	AAK32821	Human genomic DNA
C 828	30	1.2	14976	22	AAS42038	Genomic sequence #	C 901	30	1.2	28974	22	AAK69977	Human immune/haema
C 829	30	1.2	15554	22	AAK73537	Human immune/haema	C 902	30	1.2	29411	22	AAK76613	Human immune/haema
C 830	30	1.2	15555	22	AAK73539	Human immune/haema	C 903	30	1.2	30568	22	AAK37486	Human musculoskele
C 831	30	1.2	15558	22	AAK73538	Human immune/haema	C 904	30	1.2	30709	24	ABK87217	Human lipase, horm
C 832	30	1.2	15580	22	ABA15958	Human nervous syst	C 905	30	1.2	30967	17	AAK72454	Calpain large subu
C 833	30	1.2	15589	22	AAK80921	Human immune/haema	C 906	30	1.2	31853	22	AAI98993	Human excretory re
C 834	30	1.2	15610	22	AAL07072	Human reproductive	C 907	30	1.2	31853	22	AAI63343	Human kidney relat
C 835	30	1.2	15610	22	AAK80920	Human immune/haema	C 908	30	1.2	32167	22	AAI05509	Human reproductive
C 836	30	1.2	15650	22	ABA15903	Human nervous syst	C 909	30	1.2	32188	22	AAS28365	Genomic sequence #
C 837	30	1.2	15650	22	ABA16364	Human nervous syst	C 910	30	1.2	32190	22	AAS29937	Human lung antigen
C 838	30	1.2	15651	22	AAK81510	Human immune/haema	C 911	30	1.2	32190	22	AAK89689	Human digestive sy
C 839	30	1.2	15734	22	AAS36422	Human cardiovascular	C 912	30	1.2	32192	22	AAK37292	Human musculoskele
C 840	30	1.2	15843	22	AAS36896	Human cardiovascular	C 913	30	1.2	32192	22	AAI07103	Human reproductive
C 841	30	1.2	15843	22	AAK67635	Human immune/haema	C 914	30	1.2	32193	22	AAS29936	Human lung antigen
C 842	30	1.2	16057	22	AAS35935	Human immune/haema	C 915	30	1.2	32249	22	AAS29938	Human lung antigen
C 843	30	1.2	16086	22	AAL36020	Human cardiovascular	C 916	30	1.2	33513	22	AAK78746	Human immune/haema
C 844	30	1.2	16086	22	AAK36921	Human musculoskele	C 917	30	1.2	34634	24	AAK31198	Human WKL-1 Genomi
C 845	30	1.2	16106	22	AAK83468	Human immune/haema	C 918	30	1.2	34917	22	AAK70686	Human immune/haema
C 846	30	1.2	16161	22	AAK83469	Human immune/haema	C 919	30	1.2	36221	22	AAK00624	Human death-associ
C 847	30	1.2	16181	22	AAL04268	Human reproductive	C 920	30	1.2	36797	24	AAK26738	Human synaptosomal
C 848	30	1.2	16181	23	ABK42539	Genomic sequence #	C 921	30	1.2	36797	24	AAK26738	Human SNAP29 gene
C 849	30	1.2	16774	22	AAS36895	Human cardiovascular	C 922	30	1.2	37314	22	AAK71358	Human immune/haema
C 850	30	1.2	16774	22	AAS36898	Human cardiovascular	C 923	30	1.2	37449	22	AAK66874	Human immune/haema
C 851	30	1.2	16774	22	AAK67634	Human immune/haema	C 924	30	1.2	37925	22	AAK72372	Human immune/haema
C 852	30	1.2	16774	22	AAK67637	Human immune/haema	C 925	30	1.2	38059	22	AAK72372	Human immune/haema
C 853	30	1.2	17000	22	AAK86254	Human immune/haema	C 926	30	1.2	38059	22	AAK54018	Human factor IX (h
C 854	30	1.2	17000	22	AAK90956	Human digestive sy	C 927	30	1.2	38059	24	ABN95627	Gene #2125 used to
C 855	30	1.2	17000	22	AAS31991	Human liver associ	C 928	30	1.2	38186	20	AAK32028	Human METH1 relate
C 856	30	1.2	17000	24	ABN90346	Human liver associ	C 929	30	1.2	38186	22	AAK90085	AC004449 cDNA clon
C 857	30	1.2	17047	22	AAK81251	Human liver antige	C 930	30	1.2	38844	24	AAK40255	Genomic DNA encodi
C 858	30	1.2	17197	22	AAK79870	Human immune/haema	C 931	30	1.2	41159	22	AAK65631	Human immune/haema
C 859	30	1.2	17245	22	AAK83897	Human immune/haema	C 932	30	1.2	41765	22	AAK76675	Human immune/haema
C 860	30	1.2	17245	22	AAK83897	Human immune/haema	C 933	30	1.2	41772	22	AAK76676	Human immune/haema
C 861	30	1.2	17286	22	AAK36869	Human musculoskele	C 934	30	1.2	43950	24	AAK366022	Human kinase genom
C 862	30	1.2	17462	22	ABA15655	Human nervous syst	C 935	30	1.2	44820	24	AAS19703	Reference sequence
C 863	30	1.2	17538	21	AAZ29204	Human myelin oligo	C 936	30	1.2	44820	24	AAS19703	Reference sequence
C 864	30	1.2	17947	22	AAK77679	Human immune/haema	C 937	30	1.2	45546	20	AAK23520	Human kidney amino
C 865	30	1.2	18534	24	ABK84757	Human cDNA differe	C 938	30	1.2	45993	24	AAK36070	Human liver glucok
C 866	30	1.2	18564	22	AAK65368	Human immune/haema	C 939	30	1.2	47319	22	AAK64813	Human immune/haema
C 867	30	1.2	18564	22	AAK65368	Human immune/haema	C 940	30	1.2	47319	22	AAK72230	Human immune/haema
C 868	30	1.2	18576	22	AAS29819	Human cytoskeletal	C 941	30	1.2	48203	22	AAK70161	Human immune/haema
C 869	30	1.2	18660	22	AAK79108	Human immune/haema	C 942	30	1.2	48203	22	AAK81663	Human immune/haema
C 870	30	1.2	18671	22	AAK90763	Human digestive sy	C 943	30	1.2	48203	22	AAK82628	Human immune/haema
C 871	30	1.2	18925	22	ABA81553	Human phospholipid	C 944	30	1.2	48204	22	AAK70164	Human immune/haema
C 872	30	1.2	18925	24	AAS94555	Human phospholipid	C 945	30	1.2	48204	22	AAK81666	Human immune/haema
C 873	30	1.2	19596	22	AAS94692	Human phospholipid	C 946	30	1.2	48204	22	AAK82630	Human immune/haema
C 874	30	1.2	19596	22	AAK73967	Human immune/haema	C 947	30	1.2	48908	22	AAK82338	Human immune/haema
C 875	30	1.2	19597	22	AAK73968	Human immune/haema	C 948	30	1.2	50196	22	AAK79598	Human immune/haema
C 876	30	1.2	20067	22	AAK66735	Human immune/haema	C 949	30	1.2	51474	22	AAK97846	Human neuroblastom
C 877	30	1.2	20068	22	AAK66733	Human immune/haema	C 950	30	1.2	52216	22	AAH28355	Nucleotide sequenc
C 878	30	1.2	20323	22	AAK66731	Human immune/haema	C 951	30	1.2	52216	22	AAH28355	Human musashi prom
C 879	30	1.2	21596	22	AAK71582	Human immune/haema	C 952	30	1.2	54863	22	AAK86025	Human immune/haema
C 880	30	1.2	21982	22	AAK67644	Human immune/haema	C 953	30	1.2	54877	22	AAK86026	Human immune/haema
C 881	30	1.2	22081	22	AAK97862	Human neuroblastom	C 954	30	1.2	57248	24	ABK83563	Human cDNA differe
C 882	30	1.2	22086	22	AAL37362	Human musculoskele	C 955	30	1.2	59065	24	ABL42416	Human serine/threo
C 883	30	1.2	22916	22	AAK55305	Human immune/haema	C 956	30	1.2	59747	24	ABQ88209	Human osteoblast d
C 884	30	1.2	23164	22	AAK79678	Human immune/haema	C 957	30	1.2	65608	24	ABL62910	Breast cancer rela
C 885	30	1.2	24843	24	AAS17764	Human Genomic DNA	C 958	30	1.2	65608	24	ABL64414	Stomach cancer rel
												ABL67668	Oesophagus cancer



c 959 30 1-2 76798 24 ABLN97454  
c 960 30 1-2 84495 24 AAS20588  
c 961 30 1-2 84495 24 AAS20588  
c 962 30 1-2 84539 24 ABL64158  
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c 971 30 1-2 112460 24 ABL61995  
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c 994 30 1-2 325791 22 AAS43104  
c 995 30 1-2 1503900 22 AAK95240  
c 996 30 1-2 1503900 22 AAK96733  
c 997 29 1-2 51 22 AAI78842  
c 998 29 1-2 84 22 AAK73246  
c 999 29 1-2 88 22 AAK73246  
c1000 29 1-2 89 22 ABA20476

## ALIGNMENTS

RESULT 1  
AAA64507  
ID AAA64507 standard; DNA; 9048 BP.

AC AAA64507;

XX 02-JAN-2001 (first entry)

DE Nucleotide sequence comprising the human FEZ1 gene.

XX Human; FEZ1 gene; tumour suppressor gene; 9p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein E1-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

OS WO2000050565-A2.

PN 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -

XX Claim 2; Fig 5A; 255pp; English.

XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour  
CC suppressor gene, located at chromosome location 8p22. Decreased or no  
CC expression of FEZ1 is detected in a variety of cancer cells. Expression  
CC of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts  
CC with tubulin, with microtubules, and with protein E1-gamma.

CC Post-translational phosphorylation and dephosphorylation modulates the  
CC effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are  
CC useful for inducing cells to proliferate. Compounds which modulate FEZ1  
CC association with tubulin are useful for alleviating tubulin hyper- or  
CC hypo- polymerisation disorders, such as those associated with aberrant  
CC initiation of mitosis, modulation of the initiation and rate of cell  
CC proliferation and cell growth, modulation of cell shape, cell rigidity,  
CC cell motility, rate and stage of cellular DNA replication, intracellular  
CC distribution of organelles, metastatic potential of cell and cellular  
CC transformation from a non-cancerous to cancerous phenotype. Compounds  
CC which modulate FEZ1 binding and phosphorylation are also useful for  
CC alleviating a disorder, such as tumorigenesis, tumour survival, growth  
CC and metastasis.

XX Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;

Query Match 100.0%; Score 2404; DB 21; Length 9048;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAGGGGAGCGGAGGTTGAGTGAGCCAGAGTACGCCACTACACCCAGCCTAGGTGA 60

Db 4514 AGAGGGGAGCGGAGGTTGAGTGAGCCAGAGTACGCCACTACACCCAGCCTAGGTGA 4573

Qy 61 CAAAGCGAGACTTCTCAATATTAACAATAATAATATATATATATATATATATATATAT 120

Db 4574 CAAAGCGAGACTTCTCAATATTAACAATAATAATATATATATATATATATATATAT 4633

Qy 121 ATTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 180

Db 4634 ATTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 4693

Qy 181 CAATGTTTACGTTTACTTTTACGTTTACTTTTACGTTTACTTTTACGTTTACTTTTACG 240

Db 4694 CAATGTTTACGTTTACTTTTACGTTTACTTTTACGTTTACTTTTACGTTTACTTTTACG 4753

Qy 241 ATCCGAGTGGCTTGGTTTATTTTAGGAGTGGAGTGTCTACTTCTCCCTGGGTAGGACACT 300

Db 4754 ATCCGAGTGGCTTGGTTTATTTTAGGAGTGGAGTGTCTACTTCTCCCTGGGTAGGACACT 4813

Qy 301 CACCTTTTGGAGTCTTCTTCCACCCACCCCTGGAGGTTGTCAGAGTTCAGAGTTCAGAGT 360

Db 4814 CACCTTTTGGAGTCTTCTTCCACCCACCCCTGGAGGTTGTCAGAGTTCAGAGTTCAGAGT 4873

Qy 361 TCTCCCTCTTGAAGCAGCAGTGAAGGAGTCCACAGCGGAGGTGAAGCAGCGGAGTGAAG 420

Db 4874 TCTCCCTCTTGAAGCAGCAGTGAAGGAGTCCACAGCGGAGGTGAAGCAGCGGAGTGAAG 4933

Qy 421 AGATCTCTGGGTCTCAAGGACAGTGAAGGACAGCGCGGGGCAAGCTGGAGGCTGGAGC 480

Db 4934 AGATCTCTGGGTCTCAAGGACAGTGAAGGACAGCGCGGGGCAAGCTGGAGGCTGGAGC 4993

Qy 481 TGAGGACCCAGGACCTGGAGGGGCGCCCTGGCACCACAGGGGCTGGAGTGGAGTCTGTG 540

Db 4994 TGAGGACCCAGGACCTGGAGGGGCGCCCTGGCACCACAGGGGCTGGAGTGGAGTCTGTG 5053



Qy 541 AGAATGAGCTCGACGGCAAGAAACGAGGCGGAGCTGCTGCGGAGAAAGTGAACTGC 600  
Db 5054 AGAATGAGCTCGACGGCAAGAAACGAGGCGGAGCTGCTGCGGAGAAAGTGAACTGC 5113  
Qy 601 TGGAGCAGGAGCTCGACGAGCTCGGCGCCAGGCGCCCTGGCCCGGACATGGGCGGC 660  
Db 5114 TGGAGCAGGAGCTCGACGAGCTCGGCGCCAGGCGCCCTGGCCCGGACATGGGCGGC 5173  
Qy 661 CCACCTTCCCGAGGACGTCTCCCTGCTGACGCGGAGCTGGAGCGGCTGGCGCCGAGC 720  
Db 5174 CCACCTTCCCGAGGACGTCTCCCTGCTGACGCGGAGCTGGAGCGGCTGGCGCCGAGC 5233  
Qy 721 TGGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
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Qy 781 TGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840  
Db 5294 TGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5353  
Qy 841 TGGCCATGTACACGCGGAAACGAGCGCTTGGAGAGGCGCTGACAGCAGCTGGCAGCTGGGG 900  
Db 5354 TGGCCATGTACACGCGGAAACGAGCGCTTGGAGAGGCGCTGACAGCAGCTGGCAGCTGGGG 5413  
Qy 901 ACAGCGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
Db 5414 ACAGCGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5473  
Qy 961 TCATAGCACTGACATCTGAGGGGCTGCTGGAGAGGCGAGCTGCGGAGCTGGCACTGG 1020  
Db 5474 TCATAGCACTGACATCTGAGGGGCTGCTGGAGAGGCGAGCTGCGGAGCTGGCACTGG 5533  
Qy 1021 GAGCAGGAGGCTCTCCCGTGATCCCGCTGCTGAGCAATTCAGACCCCTCTGAGAGAGC 1080  
Db 5534 GAGCAGGAGGCTCTCCCGTGATCCCGCTGCTGAGCAATTCAGACCCCTCTGAGAGAGC 5593  
Qy 1081 CACTCCCTGGGACACAGACCCAGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140  
Db 5594 CACTCCCTGGGACACAGACCCAGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5653  
Qy 1141 TCTGTAGTGTCCAGTGTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
Db 5654 TCTGTAGTGTCCAGTGTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5713  
Qy 1201 CTGCTCTTCCAGAGATGGTCCAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
Db 5714 CTGCTCTTCCAGAGATGGTCCAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5773  
Qy 1261 TTTGGCCTTTGTCGAAATAGATATCTCTCCCTCTCTCCAGGAGGAGGAGGAGGAGGAGG 1320  
Db 5774 TTTGGCCTTTGTCGAAATAGATATCTCTCCCTCTCTCCAGGAGGAGGAGGAGGAGGAGG 5833  
Qy 1321 AGACAGGGCTCCCTCCGCTCTCATCCCACTCTTTTCTCTCTGACACATTTGA 1380  
Db 5834 AGACAGGGCTCCCTCCGCTCTCATCCCACTCTTTTCTCTCTGACACATTTGA 5893  
Qy 1381 ATGCTTTGGAATAAGAAAGCCATATATGACAGAGCCCTTGGAAACCCAGCCCATCAG 1440  
Db 5894 ATGCTTTGGAATAAGAAAGCCATATATGACAGAGCCCTTGGAAACCCAGCCCATCAG 5953  
Qy 1441 AACCTGAGCTATTTTCTCTGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500  
Db 5954 AACCTGAGCTATTTTCTCTGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6013  
Qy 1501 TGGCTTTGAAACCTCAGGCTGCTCCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560  
Db 6014 TGGCTTTGAAACCTCAGGCTGCTCCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6073  
Qy 1561 AGGAGCCAGCAGCTGTGGAGACCTCTGACAGCCAGAGGAGGAGGAGGAGGAGGAGGAGG 1620  
Db 6074 AGGAGCCAGCAGCTGTGGAGACCTCTGACAGCCAGAGGAGGAGGAGGAGGAGGAGG 6133  
Qy 1621 GGGTTGAGAGCCAGTGGCGGAGTGTGTCAGCCCTCTGGGCGCCAGCCCTCTGTTACTGGT 1680

Db 6134 GGGTTGAGAGCCAGTGGCGGAGTGTGTCAGCCAGCCCTCTGGGCGCCAGCCCTGTTACTGGT 6193  
Qy 1681 TCTTTGCAAAATGGGAGCTGAGCAGCCTCTGGACAGCCAGTGCACCTTTTGCACCTCGGTGACCA 1740  
Db 6194 TCTTTGCAAAATGGGAGCTGAGCAGCCTCTGGACAGCCAGTGCACCTTTTGCACCTCGGTGACCA 6253  
Qy 1741 CTCTTTTAAAGCCATAGACCTGAGGCGCTGGGCTGGGCTGGGAAAGGAGGAGGTTGAA 1800  
Db 6254 CTCTTTTAAAGCCATAGACCTGAGGCGCTGGGCTGGGCTGGGAAAGGAGGAGGTTGAA 6313  
Qy 1801 ACCACCGTGAACAGAGAGGCTGCTTTCAGHKACCTCTCAGGAGGCTCTCCCATCTGTC 1860  
Db 6314 ACCACCGTGAACAGAGAGGCTGCTTTCAGHKACCTCTCAGGAGGCTCTCCCATCTGTC 6373  
Qy 1861 CAGCTGGGCGCAGAGGCTGGGAGTCCCTACCTCTTCCAGCTTGGCGGCGGCTACTCTGG 1920  
Db 6374 CAGCTGGGCGCAGAGGCTGGGAGTCCCTACCTCTTCCAGCTTGGCGGCGGCTACTCTGG 6433  
Qy 1921 AATGTTTTTCCCTCCCGAGAAATCAAGCTTTTGTGTCATCCAGAGAGCCCATATCACTAA 1980  
Db 6434 AATGTTTTTCCCTCCCGAGAAATCAAGCTTTTGTGTCATCCAGAGAGCCCATATCACTAA 6493  
Qy 1981 GATGGCATATATGTGATCTGGGCAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2040  
Db 6494 GATGGCATATATGTGATCTGGGCAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6553  
Qy 2041 ACCTTTCCCTCTTAGCACCTTTCAGGCGTGTGTTCTGGGTTTCTAGAGGTCTAGGACGCTC 2100  
Db 6554 ACCTTTCCCTCTTAGCACCTTTCAGGCGTGTGTTCTGGGTTTCTAGAGGTCTAGGACGCTC 6613  
Qy 2101 CTGAGAGCGCCAGAGAGCCAGAGCCCAAGCAGGACGAAAGAGGAGGATACACACAGCAG 2160  
Db 6614 CTGAGAGCGCCAGAGAGCCAGAGCCCAAGCAGGACGAAAGAGGAGGATACACACAGCAG 6673  
Qy 2161 TGTGAATAGCTGCGCACAGCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220  
Db 6674 TGTGAATAGCTGCGCACAGCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6733  
Qy 2221 CTAAAGGATCCAGAGAGCAGCTCCCTTCTCAGGAGCTTGGGAGGAGGAGGAGGAGGAGTCC 2280  
Db 6734 CTAAAGGATCCAGAGAGCAGCTCCCTTCTCAGGAGCTTGGGAGGAGGAGGAGGAGTCC 6793  
Qy 2281 AGGGTTTCTCTGAGATGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340  
Db 6794 AGGGTTTCTCTGAGATGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6853  
Qy 2341 TTTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTCT 2400  
Db 6854 TTTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTCT 6913  
Qy 2401 GTCC 2404  
Db 6914 GTCC 6917

RESULT 2  
AAA64508

ID AAA64508 standard; cDNA; 5492 BP.

XX AAA64508;

DT 02-JAN-2001 (first entry)

XX cDNA sequence of the wild type human FEZ1 gene.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;

KW tumour proliferation; tubulin; microtubule; protein EF1-gamma;

KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;

KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;

KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

XX WO200050565-A2.  
XX PN  
XX 31-AUG-2000.  
XX PF  
XX 25-FEB-2000; 2000WO-US04950.  
XX PR  
XX 25-FEB-1999; 99US-0121537.  
XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX PI Croce CM, Ishii H;  
XX WPI; 2000-558396/51.  
XX DR  
XX PT New polynucleotide homologous with a portion of one strand of the human  
XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
XX cancer -  
XX PS  
XX Example 2; Fig 5B; 255pp; English.  
XX  
CC The present sequence represents the cDNA sequence of the human FEZ1 gene.  
CC FEZ1 is a tumour suppressor gene, located at chromosome location 9p22.  
CC Decreased or no expression of FEZ1 is detected in a variety of cancer  
CC cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
CC also interacts with tubulin, with microtubules, and with protein  
CC EPI-gamma. Post-translational phosphorylation and dephosphorylation  
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
CC expression are useful for inducing cells to proliferate. Compounds  
CC which modulate FEZ1 association with tubulin are useful for alleviating  
CC tubulin hyper- or hypo- polymerisation disorders, such as those  
CC associated with aberrant initiation of mitosis, modulation of the  
CC initiation and rate of cell proliferation and cell growth, modulation of  
CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
CC DNA replication, intracellular distribution of organelles, metastatic  
CC potential of cell and cellular transformation from a non-cancerous to  
CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
CC phosphorylation are also useful for alleviating a disorder, such as  
CC tumorigenesis, tumour survival, growth and metastasis.  
XX  
SQ Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;

Query Match 81.8%; Score 1966; DB 21; Length 5492;  
Best Local Similarity 99.9%; Pred No. 0;  
Matches 2066; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 AGGTGTGCCAGAGTCAGCGAGATCTCCCTCTTGAAGCAGCAGCTGAAGAGTCCCAGA 396  
DB 1259 AGGTGTGCCAGAGTCAGCGAGATCTCCCTCTTGAAGCAGCAGCTGAAGAGTCCCAGA 1318  
QY 397 CGGAGGTGAACCCNAGGCTAGCGAGATCTCGGTCTCAAGGCACAGCTGAAGCAGCGC 456  
DB 1319 CGGAGGTGAACCCNAGGCTAGCGAGATCTCGGTCTCAAGGCACAGCTGAAGCAGCGC 1378  
QY 457 GGGGCAAGCTGGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 516  
DB 1379 GGGGCAAGCTGGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1438  
QY 517 AGGGCTTGGAGCTGGAGTCTGTGAGATAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 576  
DB 1439 AGGGCTTGGAGCTGGAGTCTGTGAGATAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1498  
QY 577 TGCTGCGGGAGAGGTGAACCTGTGAGAGAGGAGCTGAGAGCTGCGGGCCCGAGGCGCG 636  
DB 1499 TGCTGCGGGAGAGGTGAACCTGTGAGAGAGGAGCTGAGAGCTGCGGGCCCGAGGCGCG 1558  
QY 637 CCCTGGCCCGGACATGGGGCGGCCACCTTCCCGAGGAGCTCCCTGCCCTGAGCGGGG 696  
DB 1559 CCCTGGCCCGGACATGGGGCGGCCACCTTCCCGAGGAGCTCCCTGCCCTGAGCGGG 1618  
QY 697 AGCTGAGCGGCTGCGGGCCGAGCTGCGGGAGGAGCGGCAAGGCGCATGACAGATGTCT 756  
DB 1619 AGCTGAGCGGCTGCGGGCCGAGCTGCGGGAGGAGCGGCAAGGCGCATGACAGATGTCT 1678

QY 757 CGGGCTTCCAGCATGAGCGCTCGTGTGGAAGGAGGAGAGAGAGGTGATTTCAGTACC 816  
DB 1679 CGGGCTTCCAGCATGAGCGCTCGTGTGGAAGGAGGAGAGAGAGGTGATTTCAGTACC 1738  
QY 817 AGAAACAGCTGCAGCAGAGCTAGCTGGCCATGTACCAGCGGAACACAGCGCTTGAGAAGG 876  
DB 1739 AGAAACAGCTGCAGCAGAGCTAGCTGGCCATGTACCAGCGGAACACAGCGCTTGAGAAGG 1798  
QY 877 CCCTGAGCAGCTGGCAGCAGCGCGGGGAGCGCTTGGAGGTTGACCTGGAAG 936  
DB 1799 CCCTGAGCAGCTGGCAGCAGCGCGGGGAGCGCTTGGAGGTTGACCTGGAAG 1858  
QY 937 GGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCCTGGGAAG 996  
DB 1859 GGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCCTGGGAAG 1918  
QY 997 GCGAGTCTGGGGACCTGGCAGCTGGGAGCGAGGCTCTCCCGTGTGATCCCCCTCTGCAGC 1056  
DB 1919 GCGAGTCTGGGGACCTGGCAGCTGGGAGCGAGGCTCTCCCGTGTGATCCCCCTCTGCAGC 1978  
QY 1057 AATTGAGACCCCTCTGAGAGACGCCACTCCCTGGGACACAGACCCAGGAGCCCCGAGGGG 1116  
DB 1979 AATTGAGACCCCTCTGAGAGACGCCACTCCCTGGGACACAGACCCAGGAGCCCCGAGGGG 2038  
QY 1117 AGGCGAGGATGGCTTTCTTCCCTCTCTGATGTCCAGTGTCCACAGCCTCTGCAGCCC 1176  
DB 2039 AGGCGAGGATGGCTTTCTTCCCTCTCTGATGTCCAGTGTCCACAGCCTCTGCAGCCC 2098  
QY 1177 ACCAGAGCTGAGGCCCTGACTCTCTGGCTTTCCAGGAGATGGGTCCAGGGGTCTGTCT 1236  
DB 2099 ACCAGAGCTGAGGCCCTGACTCTCTGGCTTTCCAGGAGATGGGTCCAGGGGTCTGTCT 2158  
QY 1237 GCTTTGGTTAAGGGCTCCCTAAACTTTGGCTTTTGTTCGAAATAGATATCTCTCCCCCT 1296  
DB 2159 GCTTTGGTTAAGGGCTCCCTAAACTTTGGCTTTTGTTCGAAATAGATATCTCTCCCCCT 2218  
QY 1297 CTTCCAGGAGGTGGGCCACAGCAAGAACAGCGCTCCCTCCGCTTCTCATCCCAACCT 1356  
DB 2219 CTTCCAGGAGGTGGGCCACAGCAAGAACAGCGCTCCCTCCGCTTCTCATCCCAACCT 2278  
QY 1357 CTTTTTCTCTCTGACACATTGGAATGCTTGGAAATAGAAAGAGGCATATATGACCAG 1416  
DB 2279 CTTTTTCTCTCTGACACATTGGAATGCTTGGAAATAGAAAGAGGCATATATGACCAG 2338  
QY 1417 AAGCTTGGAAACAGCCCCCATCAGAACCTGAGCTATTTTCTCTGGCGCGCAGAGGTGTAG 1476  
DB 2339 AAGCTTGGAAACAGCCCCCATCAGAACCTGAGCTATTTTCTCTGGCGCGCAGAGGTGTAG 2398  
QY 1477 GGGTGAATGAGCGCGGGGAAAGCTGGCTTTGAAACCTCAGGGGCTGTCCAGCCCCGGCA 1536  
DB 2399 GGGTGAATGAGCGCGGGGAAAGCTGGCTTTGAAACCTCAGGGGCTGTCCAGCCCCGGCA 2458  
QY 1537 AGCCACAGGAGGAGGGGAGAGACAGGACGCCAGCAGTGTGGAGACCTTGCCACAGCCA 1596  
DB 2459 AGCCACAGGAGGAGGGGAGAGACAGGACGCCAGCAGTGTGGAGACCTTGCCACAGCCA 2518  
QY 1597 GAGGAGGCGCAGGGGAGAAATCCAGGGTTGAGAGCCAGTGGCGGTGTATGCGCAGCCCCCT 1656  
DB 2519 GAGGAGGCGCAGGGGAGAAATCCAGGGTTGAGAGCCAGTGGCGGTGTATGCGCAGCCCCCT 2578  
QY 1657 GGGGCCCAGGCCCTGTTTACTTGGTTCTTGAAATGGGAGCTGAGCAGCCTCTGGACAGCC 1716  
DB 2579 GGGGCCCAGGCCCTGTTTACTTGGTTCTTGAAATGGGAGCTGAGCAGCCTCTGGACAGCC 2638  
QY 1717 AGTGACCTTTGACCTCGGTGACCACTCTTTTAAGCCATAGACCTTGAGGCCCTGGGCT 1776  
DB 2639 AGTGACCTTTGACCTCGGTGACCACTCTTTTAAGCCATAGACCTTGAGGCCCTGGGCT 2698  
QY 1777 GGGTGTGGGAGGGAGGGTTGAAACCAACCGTGAACAGAGGGGTGTGGCTTTCAGGKAC 1836  
DB 2699 GGGTGTGGGAGGGAGGGTTGAAACCAACCGTGAACAGAGGGGTGTGGCTTTCAGGKAC 2758



QY 877 CCCTGCAGCAGCTGGGACAGCGCGGGAGCCCTTGGAGGTTGACCTGGAAG 936  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1688 CCCTGCAGCAGCTGGCAGTGGGACAGCGCGGGAGCCCTTGGAGGTTGACCTGGAAG 1747  
QY 937 GGGCTGACATCCCTTACGAGGACATCATAGCCACTGAGATCTGA 980  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1748 GGGCTGACATCCCTTACGAGGACATCATAGCCACTGAGATCTGA 1791

## RESULT 4

AAA64515  
ID AAA64515 standard; cDNA; 1722 BP.

AC AAA64515;

DT 02-JAN-2001 (first entry)

DE Nucleotide sequence of truncated FEZ1 transcript G3612.

QY Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.

OS Homo sapiens.

QY Key Location/Qualifiers  
FH 1..1722  
CDS /\*tag= a

FT /product= "truncated FEZ1"

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX P-PSDB; AAB08722.

XX New polynucleotide homologous with a portion of one strand of the human  
FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
cancer -

XX Disclosure; Fig 5H; 255pp; English.

XX The present sequence encodes a truncated human FEZ1 polypeptide. The  
CC encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour  
CC suppressor gene, located at chromosome location 8p22. Decreased  
CC or no expression of FEZ1 is detected in a variety of cancer cells.  
CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
CC also interacts with tubulin, with microtubules, and with protein  
CC Efi-gamma. Post-translational phosphorylation and dephosphorylation  
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
CC expression are useful for inducing cells to proliferate. Compounds  
CC which modulate FEZ1 association with tubulin are useful for alleviating  
CC tubulin hyper- or hypo- polymerisation disorders, such as those  
CC associated with aberrant initiation of mitosis, modulation of the  
CC initiation and rate of cell proliferation and cell growth, modulation of  
CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
CC DNA replication, intracellular distribution of organelles, metastatic  
CC potential of cell and cellular transformation from a non-cancerous to  
CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
CC phosphorylation are also useful for alleviating a disorder, such as  
CC tumorigenesis, tumour survival, growth and metastasis.

SQ Sequence 1722 BP; 381 A; 541 C; 563 G; 237 T; 0 other;  
Query Match 15.5%; Score 373; DB 21; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 5e-160;  
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGGTGTGCCAGAAAGTCAGGCGAGATCTCCCTCTCTGAAGCAGCAGCTGAAGGAGTCCCGA 396  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1148 AGGTGTGCCAGAAAGTCAGGCGAGATCTCCCTCTCTGAAGCAGCAGCTGAAGGAGTCCCGA 1207

QY 397 CGGAGGTGAACGCCCAAGGCTAGCGAGATCTTGGGTCTCAAGGCACACAGCTGAAGGACACGC 456  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1208 CGGAGGTGAACGCCCAAGGCTAGCGAGATCTTGGGTCTCAAGGCACACAGCTGAAGGACACGC 1267

QY 457 GGGGCAAGCTGGAGCGCCTGGAGCTCAGGACCCAGGACCTGGAGGGGGCCCTGGGCACCA 516  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1268 GGGGCAAGCTGGAGCGCCTGGAGCTCAGGACCCAGGACCTGGAGGGGGCCCTGGGCACCA 1327

QY 517 AGGGCTTGGAGCTGGAGGCTCTGTGAGATGAGCTGCAGCGCAAGAACGAGCGCGAGC 576  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1328 AGGGCTTGGAGCTGGAGGCTCTGTGAGATGAGCTGCAGCGCAAGAACGAGCGCGAGC 1387

QY 577 TGCTGGGGGAGAAAGGTGAACCTCTCTCGAGCAGGAGCTGCAGGAGCTGCGGGCCCGAGCCG 636  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1388 TGCTGGGGGAGAAAGGTGAACCTCTCTCGAGCAGGAGCTGCAGGAGCTGCGGGCCCGAGCCG 1447

QY 637 CCTGGCGCGGACATGGGGCCGCCACCTTCCCGAGGACGTCCTGCCCTGCAGCGGG 696  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
1448 CCTGGCGCGGACATGGGGCCGCCACCTTCCCGAGGACGTCCTGCCCTGCAGCGGG 1507

QY 697 AGCTGGAGCGGCT 709

Db 1508 AGCTGGAGCGGCT 1520

## RESULT 5

AAA64514

ID AAA64514 standard; cDNA; 1692 BP.

AC AAA64514;

DT 02-JAN-2001 (first entry)

DE Nucleotide sequence of truncated FEZ1 transcript G3611.

QY Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.

OS Homo sapiens.

QY Key Location/Qualifiers  
FH 1..1692  
CDS /\*tag= a

FT /product= "truncated FEZ1"

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX P-PSDB; AAB08721.



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ID XX AAA64510 standard; cDNA; 404 BP.
AC XX AAA64510;
XX XX
XX XX 02-JAN-2001 (first entry)
XX XX
XX XX Nucleotide sequence of truncated FEZ1 transcript E1678.
XX XX
XX XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
XX XX tumour proliferation; tubulin; microtubule; protein EFl-gamma;
XX XX tubulin polymerisation disorder; mitosis initiation; cell proliferation;
XX XX cell growth; cell shape; cell rigidity; cell motility; DNA replication;
XX XX tumorigenesis; tumour survival; metastasis; ss.
XX XX
XX XX Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX XX CDS 1..231
XX XX /*tag= a
XX XX /product= "truncated FEZ1"
XX XX
XX XX WO2000050565-A2.
XX XX
XX XX 31-AUG-2000.
XX XX
XX XX 25-FEB-2000; 2000WO-US04950.
XX XX
XX XX 25-FEB-1999; 99US-0121537.
XX XX
XX XX (UYJE-) UNIV JEFFERSON THOMAS.
XX XX
XX XX Croce CM, Ishii H;
XX XX
XX XX WPI; 2000-558396/51.
XX XX P-PSDB; AAB08717.
XX XX
XX XX New polynucleotide homologous with a portion of one strand of the human
XX XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as
XX XX cancer -
XX XX
XX XX Disclosure; Fig 5C; 255pp; English.
XX XX
XX XX The present sequence encodes a truncated human FEZ1 polypeptide. The
XX XX encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour
XX XX suppressor gene, located at chromosome location 8p22. Decreased
XX XX or no expression of FEZ1 is detected in a variety of cancer cells.
XX XX Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1
XX XX also interacts with tubulin, with microtubules, and with protein
XX XX EFl-gamma. Post-translational phosphorylation and dephosphorylation
XX XX modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene
XX XX expression are useful for inducing cells to proliferate. Compounds
XX XX which modulate FEZ1 association with tubulin are useful for alleviating
XX XX tubulin hyper- or hypo- polymerisation disorders, such as those
XX XX associated with aberrant initiation of mitosis, modulation of the
XX XX initiation and rate of cell proliferation and cell growth, modulation of
XX XX cell shape, cell rigidity, cell motility, rate and stage of cellular
XX XX DNA replication, intracellular distribution of organelles, metastatic
XX XX potential of cell and cellular transformation from a non-cancerous to
XX XX cancerous phenotype. Compounds which modulate FEZ1 binding and
XX XX phosphorylation are also useful for alleviating a disorder, such as
XX XX tumorigenesis, tumour survival, growth and metastasis.
XX XX
XX XX Sequence 404 BP; 92 A; 119 C; 127 G; 66 T; 0 other;
XX XX
XX XX Query Match 10.4%; Score 249; DB 21; Length 404;
XX XX Best Local Similarity 100.0%; Pred. No. 2.1e-103;
XX XX Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
Oy 732 CGGAGAGCCATGACATCTCTCGGCTTCAGATGAGCGGCTGTCGAGGAG 791
Db 156 CGGAAGCCCATGACATGTCCTCGGCTTCAGATGAGCGGCTGTCGAGGAG 215
Oy 792 GAGAAGGAGAGGTGATTTCAGTACCAAGAACAGCTGCAGAGAGCTACGTGGCCATGTAC 851

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Db 216 GAGAAGGAGAGGTGATTTCAGTACCAAGAACAGCTGCAGAGAGCTACGTGGCCATGTAC 275
Oy 852 CAGCGGAACAGCGCTCGAGAGAGGCGCTGCAGAGAGCTGCAGAGAGCTACGTGGGACAGCGCGGG 911
Db 276 CAGCGGAACAGCGCTCGAGAGAGGCGCTGCAGAGAGCTGCAGAGAGCTGCAGAGAGCTGCAGCGGG 335
Oy 912 GAGCCCTTGAGGTTGACCTGGAAGGGGCTGACATCCCTTACGAGGACATCATAGCCACT 971
Db 336 GAGCCCTTGAGGTTGACCTGGAAGGGGCTGACATCCCTTACGAGGACATCATAGCCACT 395
Oy 972 GAGATCTGA 980
Db 396 GAGATCTGA 404

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RESULT 8  
AAA64513  
ID AAA64513 standard; cDNA; 1512 BP.  
XX  
XX AAA64513;  
AC  
XX  
XX 02-JAN-2001 (first entry)  
XX  
XX Nucleotide sequence of truncated FEZ1 transcript D14.  
XX  
XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
XX XX tumour proliferation; tubulin; microtubule; protein EFl-gamma;  
XX XX tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
XX XX cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
XX XX tumorigenesis; tumour survival; metastasis; ss.  
XX XX  
XX XX Homo sapiens.  
XX XX  
XX XX Key Location/Qualifiers  
XX XX CDS 1..1512  
XX XX /\*tag= a  
XX XX /product= "truncated FEZ1"  
XX XX  
XX XX WO2000050565-A2.  
XX XX  
XX XX 31-AUG-2000.  
XX XX  
XX XX 25-FEB-2000; 2000WO-US04950.  
XX XX  
XX XX 25-FEB-1999; 99US-0121537.  
XX XX  
XX XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX XX  
XX XX Croce CM, Ishii H;  
XX XX  
XX XX WPI; 2000-558396/51.  
XX XX P-PSDB; AAB08720.  
XX XX  
XX XX New polynucleotide homologous with a portion of one strand of the human  
XX XX FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
XX XX cancer -  
XX XX  
XX XX Disclosure; Fig 5F; 255pp; English.  
XX XX  
XX XX The present sequence encodes a truncated human FEZ1 polypeptide. The  
XX XX encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour  
XX XX suppressor gene, located at chromosome location 8p22. Decreased  
XX XX or no expression of FEZ1 is detected in a variety of cancer cells.  
XX XX Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
XX XX also interacts with tubulin, with microtubules, and with protein  
XX XX EFl-gamma. Post-translational phosphorylation and dephosphorylation  
XX XX modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
XX XX expression are useful for inducing cells to proliferate. Compounds  
XX XX which modulate FEZ1 association with tubulin are useful for alleviating  
XX XX tubulin hyper- or hypo- polymerisation disorders, such as those  
XX XX associated with aberrant initiation of mitosis, modulation of the  
XX XX initiation and rate of cell proliferation and cell growth, modulation of  
XX XX cell shape, cell rigidity, cell motility, rate and stage of cellular  
XX XX DNA replication, intracellular distribution of organelles, metastatic  
XX XX potential of cell and cellular transformation from a non-cancerous to  
XX XX cancerous phenotype. Compounds which modulate FEZ1 binding and  
XX XX phosphorylation are also useful for alleviating a disorder, such as  
XX XX tumorigenesis, tumour survival, growth and metastasis.

CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
CC DNA replication, intracellular distribution of organelles, metastatic  
CC potential of cell and cellular transformation from a non-cancerous to  
CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
CC phosphorylation are also useful for alleviating a disorder, such as  
CC tumorigenesis, tumour survival, growth and metastasis.  
XX  
SQ Sequence 1512 BP; 335 A; 483 C; 481 G; 213 T; 0 other;  
Query Match 9.1%; Score 219; DB 21; Length 1512;  
Best Local Similarity 100.0%; Pred. No. 9.6e-30; Mismatches 0; Indels 0; Gaps 0;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 337 AGGTGTCAGAGTCCAGGAGATCTCCCTCTGAAGCAGCAGCTGAAGAGTCCAGCA 396  
DB 1148 AGGTGTCAGAGTCCAGGAGATCTCCCTCTGAAGCAGCAGCTGAAGAGTCCAGCA 1207  
QY 397 CGGAGGTGAACGCCAAGCTAGCGAGATCTGGTCTCAAGGCACAGCTGAAGACAGC 456  
DB 1208 CGGAGGTGAACGCCAAGCTAGCGAGATCTGGTCTCAAGGCACAGCTGAAGACAGC 1267  
QY 457 GGGCAAGCTGGAGGCTTGAGCTGAGGACCCAGGACCTGGAGGGCCCTGGCACCA 516  
DB 1268 GGGCAAGCTGGAGGCTTGAGCTGAGGACCCAGGACCTGGAGGGCCCTGGCACCA 1327  
QY 517 AGGCGCTGGAGCTGGAGGCTCTGTGAGATGAGCTGCAGC 555  
DB 1328 AGGCGCTGGAGCTGGAGGCTCTGTGAGATGAGCTGCAGC 1366  
RESULT 9  
AAAG4511  
ID AAA64511 standard; cDNA; 633 BP.  
XX  
AC AAA64511;  
XX  
DT 02-JAN-2001 (first entry)  
XX  
DE Nucleotide sequence of truncated FEZ1 transcript E264162.  
XX  
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein EPI-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..633  
FT /\*tag= a  
FT /product= "truncated FEZ1"  
XX  
PN WO200050565-A2.  
XX  
PD 31-AUG-2000.  
XX  
XX 25-FEB-2000; 2000WO-US04950.  
XX  
XX 25-FEB-1999; 99US-0121537.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Croce CM, Ishii H;  
XX  
XX WPI; 2000-558396/51.  
DR P-PSDB; AAB08718.  
XX  
XX New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -  
XX  
PS Disclosure; Fig 5D; 255pp; English.

XX The present sequence encodes a truncated human FEZ1 polypeptide. The  
CC encoding mRNA is transcribed by tumour cells. FEZ1 is a tumour  
CC suppressor gene, located at chromosome location 8p22. Decreased  
CC or no expression of FEZ1 is detected in a variety of cancer cells.  
CC Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
CC also interacts with tubulin, with microtubules, and with protein  
CC EPI-gamma. Post-translational phosphorylation and dephosphorylation  
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
CC expression are useful for inducing cells to proliferate. Compounds  
CC which modulate FEZ1 association with tubulin are useful for alleviating  
CC tubulin hyper- or hypo- polymerisation disorders, such as those  
CC associated with aberrant initiation of mitosis, modulation of the  
CC initiation and rate of cell proliferation and cell growth, modulation of  
CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
CC DNA replication, intracellular distribution of organelles, metastatic  
CC potential of cell and cellular transformation from a non-cancerous to  
CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
CC phosphorylation are also useful for alleviating a disorder, such as  
CC tumorigenesis, tumour survival, growth and metastasis.  
XX  
SQ Sequence 633 BP; 136 A; 217 C; 175 G; 105 T; 0 other;  
Query Match 3.3%; Score 80; DB 21; Length 633;  
Best Local Similarity 100.0%; Pred. No. 2.7e-26;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 901 ACAGCGCCGGGAGCCCTTGAGCTTGACCTGGAAGGGCTGACATCCCTACGAGCA 960  
DB 554 ACAGCGCCGGGAGCCCTTGAGCTTGACCTGGAAGGGCTGACATCCCTACGAGCA 613  
QY 961 TCATAGCCACTGAGATCTGA 980  
DB 614 TCATAGCCACTGAGATCTGA 633  
RESULT 10  
AAK88622/c  
ID AAK88622 standard; cDNA; 687 BP.  
XX  
AC AAK88622;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human digestive system antigen coding sequence SEQ ID NO: 938.  
XX  
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KW digestive system disorder; Meckel's diverticulum; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200155314-A2.  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01324.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.







Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGGGAGCGGAGGTTGCAGTGTAGGCAAGATCACGCCACT 42  
Db 309 GGGGAGCGGAGGTTGCAGTGTAGGCAAGATCACGCCACT 271

RESULT 11  
ABK83564  
ID ABK83564 standard; cDNA; 198161 BP.  
AC ABK83564;  
XX  
XX  
DT 14-AUG-2002 (first entry)  
XX  
XX Human cDNA differentially expressed in granulocytic cells #135.  
DE  
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX  
OS Homo sapiens.  
XX  
XX W0200228999-A2.  
XX  
XX 11-APR-2002.  
XX  
XX 03-OCT-2001; 2001WO-US30821.  
XX  
XX 03-OCT-2000; 2000US-237189P.  
XX  
XX (GENE-) GENE LOGIC INC.  
XX  
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX WPI; 2002-435328/46.  
XX  
XX Detecting granulocyte activation by detecting differential expression  
PT of genes associated with granulocyte activation, which serves as  
PT diagnostic markers that is useful for monitoring disease states and  
PT drug toxicity -  
XX  
XX Claim 1; SEQ ID No 135; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile  
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC periodontal disease; also bacterial infection, viral infection,  
CC parasitic infection, protozoal infection, fungal infection and M5 is  
CC useful for treating one of the above conditions. The present  
CC sequence represents a gene differentially expressed in granulocytes.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 198161 BP; 61561 A; 45946 C; 41360 G; 49294 T; 0 other;  
Query Match 1.6%; Score 39; DB 24; Length 198161;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGGGAGCGGAGGTTGCAGTGTAGGCAAGATCACGCCACT 42  
Db 150070 GGGGAGCGGAGGTTGCAGTGTAGGCAAGATCACGCCACT 150108

RESULT 12  
AAC04727/c  
ID AAC04727 standard; cDNA; 141 BP.  
XX  
XX AC AAC04727;  
XX  
XX DT 06-OCT-2000 (first entry)  
XX  
XX DE Human secreted protein 5' EST, SEQ ID NO: 8802.  
XX  
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN EP1033401-A2.  
XX  
XX PD 06-SEP-2000.  
XX  
XX PF 21-FEB-2000; 2000EP-0200610.  
XX  
XX PR 26-FEB-1999; 99US-0122487.  
XX  
XX PA (GEST) GENSET.  
XX  
XX Dumas Milne Edwards J, Duclert A, Giordano J;  
XX WPI; 2000-500381/45.  
XX  
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
XX PS Claim 1; SEQ ID 8802; 71pp + CD-ROM; English.  
XX  
XX CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNA or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design

```
CC expression and secretion vectors.
XX
SQ Sequence 141 BP; 20 A; 40 C; 37 G; 44 T; 0 other;
    Query Match 1.6%; Score 38; DB 21; Length 141;
    Best Local Similarity 100.0%; Pred. No. 4.3e-07;
    Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
    |||||
Db 106 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 69
    |||||

RESULT 13
AAI90310
ID AAI90310 standard; cDNA; 343 BP.
XX
AC AAI90310;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 10370.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
PD 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX P-PSDB; AAO10379.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX
XX Claim 1; SEQ ID NO 10370; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 343 BP; 122 A; 65 C; 68 G; 87 T; 1 other;
    Query Match 1.6%; Score 38; DB 22; Length 343;
    Best Local Similarity 100.0%; Pred. No. 4.2e-07;
    Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC expression and secretion vectors.
XX
SQ Sequence 141 BP; 20 A; 40 C; 37 G; 44 T; 0 other;
    Query Match 1.6%; Score 38; DB 24; Length 438;
    Best Local Similarity 100.0%; Pred. No. 4.1e-07;
    Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
    |||||
Db 88 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 51
    |||||

RESULT 14
ABL85949/c
ID ABL85949 standard; cDNA; 438 BP.
XX
XX ABL85949;
XX
DT 17-MAY-2002 (first entry)
XX
XX Human ovarian cancer related cDNA clone SEQ ID NO:8927.
XX
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200192581-A2.
XX
PD 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US17756.
XX
XX 26-MAY-2000; 2000US-207484P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Algate PA, Harlocker SL, Jones R;
XX
XX WPI; 2002-122075/16.
XX
XX Composition for therapy and diagnosis of ovarian cancer comprising
XX polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
XX polypeptide, antibody specific to polypeptide or T cell expressing
XX polypeptide -
XX
XX Claim 1; SEQ ID 8927; 489pp; English.
XX
XX The present invention describes a composition (I) comprising: carriers
XX and immunostimulants; and a polypeptide (II) of a ovarian tumour
XX polypeptide encoded by a polynucleotide (III) having a cDNA sequence
XX (S1) from the 10912 nucleotide sequences as given in ABL77023 to
XX ABL87934, (III) encoding (II) having a sequence (S2), a T cell
XX population of (III), or antigen presenting cells that express (II).
XX (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
XX (S1) can be used for detecting ovarian cancer in a patient's biological
XX sample preferably serum or ovarian tissue. The method comprises
XX contacting a biological sample from a patient with (IV), detecting the
XX amount of polynucleotide hybridising to (IV) and comparing the amount to
XX a predetermined cutoff value and thereby detecting ovarian cancer in the
XX patient, where the amount of polynucleotide hybridising to (IV) is
XX detected preferably by polymerase chain reaction (PCR). (I) comprising
XX (III) and/or (II) is useful for stimulating and/or expanding T cells
XX specific for an ovarian tumour protein comprising contacting T cells
XX with (III) or (II). (III) is useful in design and preparation of
XX ribozyme molecules for inhibiting expression of the tumour polypeptides
XX and proteins in tumour cells; and to isolate a full length gene from a
XX suitable library e.g., a tumour cDNA library using well known
XX techniques.
XX
XX Sequence 438 BP; 67 A; 133 C; 102 G; 131 T; 5 other;
    Query Match 1.6%; Score 38; DB 24; Length 438;
    Best Local Similarity 100.0%; Pred. No. 4.1e-07;
    Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
    |||||
Db 88 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 51
    |||||
```





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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	37	1.5	87543	4	US-09-751-211-3
C 3	37	1.5	99500	4	US-09-798-096-10
C 4	35	1.5	29629	4	US-09-729-995-3
C 5	35	1.5	162450	4	US-09-345-882-1
C 6	34	1.4	8517	3	US-08-827-208-1
C 7	34	1.4	8517	4	US-09-500-358-1
C 8	34	1.4	8517	4	US-09-498-809-1
C 9	32	1.3	62804	4	US-09-800-960-3
C 10	31	1.3	3286	4	US-09-211-417-2
C 11	31	1.3	4169	4	US-09-166-350-32
C 12	31	1.3	15652	4	US-09-422-916-60
C 13	31	1.3	17138	4	US-09-813-819-3
C 14	31	1.3	17138	4	US-09-920-048-3
C 15	31	1.3	38564	4	US-09-734-673-3
C 16	31	1.3	50000	4	US-09-146-053-4
C 17	31	1.3	72928	3	US-09-009-913-1
C 18	31	1.3	81001	4	US-09-750-580-1
C 19	31	1.3	152331	3	US-09-128-155-16
C 20	31	1.3	176373	3	US-09-128-155-17
C 21	31	1.3	246240	2	US-08-724-394A-20
C 22	31	1.3	246240	2	US-08-724-394A-21
C 23	31	1.3	246240	2	US-08-724-394A-22
C 24	30	1.2	73	3	US-09-056-762-8
C 25	30	1.2	1000	4	US-09-018-584A-33
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C 27	30	1.2	38844	4	US-09-734-675-3
C 28	30	1.2	40000	4	US-09-780-049-18
C 29	30	1.2	43950	4	US-09-735-934A-3
C 30	30	1.2	45546	4	US-09-146-053-6
C 31	30	1.2	59065	4	US-09-813-817-3
C 32	30	1.2	59065	4	US-09-978-197-3
C 33	30	1.2	84495	4	US-09-797-906-3
C 34	30	1.2	84495	4	US-09-797-906-3
C 35	29	1.2	683	4	US-09-740-235-19
C 36	29	1.2	1106	4	US-09-288-143-56
C 37	29	1.2	1232	4	US-09-345-293-1
C 38	29	1.2	2688	2	US-08-909-965C-1
C 39	29	1.2	3804	4	US-08-483-488-5
C 40	29	1.2	6060	5	PCT-US96-09430-7
C 41	29	1.2	6719	4	US-09-740-235-36
C 42	29	1.2	8021	4	US-09-740-235-2
C 43	29	1.2	13953	4	US-09-738-884-3
C 44	29	1.2	14581	4	US-08-520-373D-4
C 45	29	1.2	22481	4	US-08-367-841A-43
C 46	29	1.2	22481	5	PCT-US95-07201-43
C 47	29	1.2	22484	4	US-09-875-223-2
C 48	29	1.2	26664	4	US-09-564-805-28
C 49	29	1.2	35060	3	US-08-814-095-7
C 50	29	1.2	43950	4	US-09-735-934A-3
C 51	29	1.2	53526	3	US-08-658-136-2
C 52	29	1.2	53577	3	US-08-658-136-1
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C 61	29	1.2	72604	4	US-09-657-474-7
C 62	29	1.2	99500	4	US-09-798-096-10
C 63	28	1.2	418	4	US-09-490-818-5
C 64	28	1.2	1947	2	US-08-989-925-2
C 65	28	1.2	2115	1	US-08-395-800A-7
C 66	28	1.2	42571	4	US-09-810-347-3
C 67	28	1.2	44453	4	US-09-146-053-5
C 68	28	1.2	45716	4	US-08-965-048-5
C 69	28	1.2	45989	4	US-08-965-048-6
C 70	28	1.2	70000	4	US-09-851-896-3
C 71	28	1.2	162450	4	US-09-345-882-1
C 72	27	1.1	2839	4	US-09-061-702-1
C 73	27	1.1	3035	1	US-08-726-725-2
C 74	27	1.1	3373	1	US-08-273-411-2
C 75	27	1.1	8174	1	US-07-914-281-5
C 76	27	1.1	8174	1	US-08-393-246-5
C 77	27	1.1	8174	1	US-08-525-058A-5
C 78	27	1.1	8174	2	US-08-696-731-5
C 79	27	1.1	8174	4	US-09-042-531-5
C 80	27	1.1	8174	5	PCT-US91-00899-3
C 81	26	1.1	1901	4	US-09-338-907-181
C 82	26	1.1	1901	4	US-09-218-207-181
C 83	26	1.1	2509	2	US-09-014-969-1
C 84	26	1.1	31571	1	US-08-323-443B-1
C 85	26	1.1	53526	3	US-08-658-136-2
C 86	26	1.1	53577	3	US-08-658-136-1
C 87	26	1.1	56516	2	US-08-996-306-1
C 88	26	1.1	56516	4	US-09-338-907-1
C 89	26	1.1	56516	4	US-09-218-207-1
C 90	26	1.1	56520	4	US-09-338-907-179
C 91	26	1.1	56520	4	US-09-218-207-179
C 92	26	1.1	16998	4	US-09-676-6108-24
C 93	26	1.1	246240	2	US-08-724-394A-20
C 94	26	1.1	246240	2	US-08-724-394A-21
C 95	26	1.1	246240	2	US-08-724-394A-22
C 96	25	1.0	112	2	US-08-454-557C-27
C 97	25	1.0	112	2	US-08-340-426D-27
C 98	25	1.0	112	2	US-08-450-673C-27
C 99	25	1.0	112	5	PCT-US95-1711A-27
C 100	25	1.0	264	1	US-08-222-177A-10

c 101	25	1.0	531	4	US-09-404-879A-24	Sequence 24, Appl	174	24	1.0	11298	4	US-09-103-663-31	Sequence 31, Appl
102	25	1.0	1001	4	US-09-641-638-175	Sequence 175, App	c 175	24	1.0	11811	4	US-09-078-294-7	Sequence 7, Appl
103	25	1.0	2503	4	US-09-198-122-7	Sequence 7, Appl	c 176	24	1.0	12143	4	US-09-423-744A-1	Sequence 1, Appl
104	25	1.0	16063	4	US-08-801-052-3	Sequence 1, Appl	c 177	24	1.0	14636	4	US-09-173-914-6	Sequence 6, Appl
105	25	1.0	17041	1	US-08-076-011-1	Sequence 1, Appl	c 178	24	1.0	14636	4	US-09-173-914-6	Sequence 6, Appl
106	25	1.0	87350	3	US-08-781-891-79	Sequence 79, Appl	c 179	24	1.0	14796	4	US-08-975-080-35	Sequence 35, Appl
107	25	1.0	87543	4	US-09-791-211-3	Sequence 3, Appl	c 180	24	1.0	14796	4	US-09-630-706-10	Sequence 10, Appl
108	25	1.0	112132	4	US-09-741-150-3	Sequence 3, Appl	c 181	24	1.0	14796	4	US-09-496-694B-3	Sequence 3, Appl
109	24	1.0	565	4	US-09-328-111-267	Sequence 267, App	c 182	24	1.0	15328	2	US-08-888-497-33	Sequence 33, Appl
c 110	24	1.0	629	4	US-09-385-982-204	Sequence 204, App	c 183	24	1.0	15328	2	US-08-888-497-33	Sequence 33, Appl
111	24	1.0	652	4	US-09-328-111-717	Sequence 717, App	c 184	24	1.0	15328	5	PCT-US94-07926-33	Sequence 33, Appl
112	24	1.0	689	4	US-09-105-542A-14	Sequence 14, Appl	c 185	24	1.0	17327	1	US-07-906-871-15	Sequence 15, Appl
113	24	1.0	700	4	US-08-991-789A-174	Sequence 174, App	c 186	24	1.0	17606	4	US-08-943-731-4	Sequence 4, Appl
114	24	1.0	700	4	US-09-062-451-174	Sequence 174, App	c 187	24	1.0	19011	1	US-08-310-356-36	Sequence 36, Appl
115	24	1.0	700	4	US-09-588-326-174	Sequence 174, App	c 188	24	1.0	19557	5	PCT-US92-06300-1	Sequence 1, Appl
c 116	24	1.0	798	4	US-09-288-143-21	Sequence 21, Appl	c 189	24	1.0	19806	4	US-09-740-028A-3	Sequence 3, Appl
117	24	1.0	825	2	US-08-486-148B-1	Sequence 1, Appl	c 190	24	1.0	20303	1	US-08-370-975B-6	Sequence 6, Appl
118	24	1.0	1001	4	US-09-641-638-208	Sequence 208, App	c 191	24	1.0	26764	1	US-08-370-975B-1	Sequence 1, Appl
119	24	1.0	1363	1	US-08-776-088-21	Sequence 21, Appl	c 192	24	1.0	36651	4	US-09-738-894A-3	Sequence 3, Appl
120	24	1.0	1363	5	PCT-US95-09145A-21	Sequence 21, Appl	c 193	24	1.0	36741	4	US-09-301-665-3	Sequence 3, Appl
121	24	1.0	1491	4	US-08-913-014A-5	Sequence 5, Appl	c 194	24	1.0	45546	4	US-09-146-053-6	Sequence 6, Appl
122	24	1.0	1534	1	US-08-480-784-13	Sequence 13, Appl	c 195	24	1.0	50000	4	US-09-146-053-3	Sequence 3, Appl
123	24	1.0	1534	1	US-08-483-553-13	Sequence 13, Appl	c 196	24	1.0	50000	4	US-09-146-053-3	Sequence 3, Appl
124	24	1.0	1534	1	US-08-487-002-13	Sequence 13, Appl	c 197	24	1.0	59065	4	US-09-813-817-3	Sequence 3, Appl
125	24	1.0	1534	1	US-08-483-554B-13	Sequence 13, Appl	c 198	24	1.0	59065	4	US-09-978-197-3	Sequence 3, Appl
126	24	1.0	1534	1	US-08-488-011B-13	Sequence 13, Appl	c 199	24	1.0	70000	4	US-09-851-896-3	Sequence 3, Appl
127	24	1.0	1534	4	US-08-850-727-13	Sequence 13, Appl	c 200	24	1.0	72604	4	US-09-268-992-7	Sequence 7, Appl
128	24	1.0	1534	5	PCT-US95-10202-13	Sequence 13, Appl	c 201	24	1.0	72604	4	US-09-657-474-7	Sequence 7, Appl
129	24	1.0	1534	5	PCT-US95-10203-13	Sequence 13, Appl	c 202	24	1.0	80246	4	US-09-078-294-4	Sequence 4, Appl
130	24	1.0	1534	5	PCT-US95-10220-13	Sequence 13, Appl	c 203	24	1.0	80595	4	US-09-078-294-4	Sequence 4, Appl
c 131	24	1.0	1656	1	US-08-324-465-2	Sequence 2, Appl	c 204	24	1.0	90050	4	US-09-245-041-5	Sequence 5, Appl
132	24	1.0	1656	2	US-08-465-981-2	Sequence 2, Appl	c 205	23	1.0	330	3	US-09-157-177-114	Sequence 114, App
c 133	24	1.0	1656	5	PCT-US93-11915-2	Sequence 2, Appl	c 206	23	1.0	586	4	US-08-906-156A-20	Sequence 20, Appl
c 134	24	1.0	1690	1	US-08-943-731-166	Sequence 166, App	c 207	23	1.0	587	4	US-08-906-156A-68	Sequence 68, Appl
c 135	24	1.0	1725	1	US-08-324-465-5	Sequence 5, Appl	c 208	23	1.0	609	4	US-09-385-982-237	Sequence 237, App
c 136	24	1.0	1725	5	PCT-US93-11915-5	Sequence 5, Appl	c 209	23	1.0	737	2	US-08-257-963B-41	Sequence 41, Appl
c 137	24	1.0	1725	5	PCT-US93-11915-5	Sequence 5, Appl	c 210	23	1.0	737	4	US-08-367-841A-41	Sequence 41, Appl
c 138	24	1.0	1901	5	PCT-US93-05000-32	Sequence 32, Appl	c 211	23	1.0	737	5	PCT-US95-07201-41	Sequence 41, Appl
c 139	24	1.0	1924	1	US-08-480-784-14	Sequence 14, Appl	c 212	23	1.0	955	4	US-09-641-638-22	Sequence 22, Appl
140	24	1.0	1924	1	US-08-483-553-14	Sequence 14, Appl	c 213	23	1.0	956	4	US-09-641-638-35	Sequence 35, Appl
141	24	1.0	1924	1	US-08-487-002-14	Sequence 14, Appl	c 214	23	1.0	1001	4	US-09-641-638-40A	Sequence 40A, App
142	24	1.0	1924	1	US-08-483-554B-14	Sequence 14, Appl	c 215	23	1.0	1001	4	US-09-641-638-522	Sequence 522, App
143	24	1.0	1924	1	US-08-488-011B-14	Sequence 14, Appl	c 216	23	1.0	1116	4	US-09-177-325-1	Sequence 1, Appl
144	24	1.0	1924	4	US-08-850-727-14	Sequence 14, Appl	c 217	23	1.0	1116	4	US-09-411-812A-1	Sequence 1, Appl
145	24	1.0	1924	5	PCT-US95-10202-14	Sequence 14, Appl	c 218	23	1.0	1116	4	US-09-590-113-1	Sequence 1, Appl
146	24	1.0	1924	5	PCT-US95-10203-14	Sequence 14, Appl	c 219	23	1.0	1278	2	US-08-309-965C-4	Sequence 4, Appl
c 147	24	1.0	1924	5	PCT-US95-10220-14	Sequence 14, Appl	c 220	23	1.0	1295	4	US-09-254-465A-8	Sequence 8, Appl
c 148	24	1.0	2022	2	US-08-464-517-32	Sequence 32, Appl	c 221	23	1.0	1410	5	PCT-US95-15428-14	Sequence 14, Appl
c 149	24	1.0	2022	2	US-08-246-361A-32	Sequence 32, Appl	c 222	23	1.0	1804	1	US-08-306-691B-40	Sequence 40, Appl
c 150	24	1.0	2022	3	US-08-463-772-32	Sequence 32, Appl	c 223	23	1.0	1804	4	US-09-167-322-14	Sequence 14, Appl
c 151	24	1.0	2334	4	US-09-493-565-1	Sequence 1, Appl	c 224	23	1.0	1804	4	PCT-US93-06251-82	Sequence 82, Appl
c 152	24	1.0	2419	2	US-08-785-662-13	Sequence 13, Appl	c 225	23	1.0	1817	3	US-08-564-496C-14	Sequence 14, Appl
c 153	24	1.0	2419	5	PCT-US95-08745-13	Sequence 13, Appl	c 226	23	1.0	2255	4	US-08-871-572B-3	Sequence 3, Appl
c 154	24	1.0	2448	2	US-08-687-080-111	Sequence 111, App	c 227	23	1.0	2296	4	US-09-851-896-11	Sequence 11, Appl
c 155	24	1.0	2921	3	US-08-618-100B-4	Sequence 4, Appl	c 228	23	1.0	2329	4	US-08-927-219-80	Sequence 80, Appl
c 156	24	1.0	3507	1	US-08-832-883-67	Sequence 67, Appl	c 229	23	1.0	2426	4	US-09-605-785-470	Sequence 470, App
c 157	24	1.0	3507	2	US-08-832-877-67	Sequence 67, Appl	c 230	23	1.0	2426	4	US-09-439-313-470	Sequence 470, App
158	24	1.0	4183	4	US-09-460-145-1	Sequence 1, Appl	c 231	23	1.0	2426	4	US-09-352-616A-470	Sequence 470, App
159	24	1.0	4421	2	US-08-257-963B-9	Sequence 9, Appl	c 232	23	1.0	2886	2	US-08-687-080-55	Sequence 55, Appl
160	24	1.0	4421	4	US-08-367-841A-9	Sequence 9, Appl	c 233	23	1.0	4326	2	US-08-852-807-12	Sequence 12, Appl
161	24	1.0	4421	4	US-08-520-373D-6	Sequence 6, Appl	c 234	23	1.0	4326	2	US-08-852-807-12	Sequence 12, Appl
162	24	1.0	4421	5	PCT-US95-07201-9	Sequence 9, Appl	c 235	23	1.0	4421	2	US-08-257-963B-9	Sequence 9, Appl
c 163	24	1.0	4793	4	US-09-561-497-10	Sequence 10, Appl	c 236	23	1.0	4421	4	US-08-367-841A-9	Sequence 9, Appl
164	24	1.0	5375	3	US-08-757-223-7	Sequence 7, Appl	c 237	23	1.0	4421	4	US-08-520-373D-6	Sequence 6, Appl
c 165	24	1.0	6623	2	US-08-687-080-68	Sequence 68, Appl	c 238	23	1.0	4421	5	PCT-US95-07201-9	Sequence 9, Appl
166	24	1.0	7452	3	US-08-592-500-1	Sequence 1, Appl	c 239	23	1.0	4550	4	US-09-103-663-35	Sequence 35, Appl
167	24	1.0	7452	3	US-08-195-006-1	Sequence 1, Appl	c 240	23	1.0	5789	4	US-09-242-948-3	Sequence 3, Appl
168	24	1.0	7452	5	PCT-US94-07644A-1	Sequence 1, Appl	c 241	23	1.0	6340	1	US-08-187-785-3	Sequence 3, Appl
c 169	24	1.0	8453	4	US-09-167-681-45	Sequence 45, Appl	c 242	23	1.0	6709	4	US-09-285-601-3	Sequence 3, Appl
c 170	24	1.0	10504	4	US-09-423-744A-19	Sequence 19, Appl	c 243	23	1.0	7210	2	US-08-257-963B-10	Sequence 10, Appl
171	24	1.0	10684	3	US-08-618-100B-3	Sequence 3, Appl	c 244	23	1.0	7210	4	US-08-367-841A-10	Sequence 10, Appl
172	24	1.0	11298	1	US-07-869-933-31	Sequence 31, Appl	c 245	23	1.0	9837	1	PCT-US95-07201-10	Sequence 10, Appl
173	24	1.0	11298	1	US-08-201-879A-2	Sequence 2, Appl	c 246	23	1.0	9837	1	US-08-832-883-68	Sequence 68, Appl

C 247	23	1.0	9837	2	US-08-832-877-68	Sequence 68, Appl	C 320	22	0.9	619	4	US-09-385-982-358	Sequence 358, App
C 248	23	1.0	10380	4	US-09-077-354B-3	Sequence 3, Appli	C 321	22	0.9	764	4	US-09-288-143-57	Sequence 57, Appl
C 249	23	1.0	11298	1	US-07-869-933-31	Sequence 31, Appl	C 322	22	0.9	826	4	US-09-288-143-45	Sequence 45, Appl
C 250	23	1.0	11298	1	US-08-201-879A-2	Sequence 2, Appli	C 323	22	0.9	1045	5	US-08-599-252-92	Sequence 92, Appl
C 251	23	1.0	11298	1	US-08-103-663-31	Sequence 31, Appl	C 324	22	0.9	1045	5	PCT-US96-06352-92	Sequence 92, Appl
C 252	23	1.0	11613	1	US-08-484-044-10	Sequence 10, Appl	C 325	22	0.9	1045	5	PCT-US96-06583-92	Sequence 92, Appl
C 253	23	1.0	11811	4	US-09-078-294-7	Sequence 7, Appli	C 326	22	0.9	1182	4	US-09-469-242-1	Sequence 1, Appli
C 254	23	1.0	12394	4	US-09-488-856A-10	Sequence 10, Appl	C 327	22	0.9	1247	4	US-09-178-115-110	Sequence 110, App
C 255	23	1.0	12565	4	US-09-345-217-3	Sequence 3, Appli	C 328	22	0.9	1247	4	US-09-177-776-110	Sequence 110, App
C 256	23	1.0	12597	4	US-09-705-299-12	Sequence 12, Appl	C 329	22	0.9	1448	4	US-09-387-212-12	Sequence 12, App
C 257	23	1.0	13674	2	US-08-852-807-1	Sequence 1, Appli	C 330	22	0.9	1448	4	US-09-948-802-12	Sequence 12, Appl
C 258	23	1.0	13674	2	US-08-852-807-1	Sequence 1, Appli	C 331	22	0.9	1542	4	US-09-008-271A-13	Sequence 13, Appl
C 259	23	1.0	14581	4	US-08-520-373D-4	Sequence 4, Appli	C 332	22	0.9	2071	4	US-09-816-088-1	Sequence 1, Appli
C 260	23	1.0	15297	4	US-09-817-180-3	Sequence 3, Appli	C 333	22	0.9	2119	2	US-08-381-691-17	Sequence 17, Appl
C 261	23	1.0	17327	1	US-07-906-871-15	Sequence 15, Appl	C 334	22	0.9	2415	3	US-09-019-689-1	Sequence 1, Appli
C 262	23	1.0	18596	4	US-09-318-448-11	Sequence 11, Appl	C 335	22	0.9	2501	3	US-08-787-739-58	Sequence 58, Appl
C 263	23	1.0	20674	4	US-09-641-638-651	Sequence 651, App	C 336	22	0.9	2501	4	US-09-178-115-58	Sequence 58, Appl
C 264	23	1.0	20674	4	US-09-641-638-651	Sequence 651, App	C 337	22	0.9	2501	4	US-09-177-776-58	Sequence 58, Appl
C 265	23	1.0	22481	4	US-08-367-841A-43	Sequence 43, Appl	C 338	22	0.9	2721	3	US-08-921-195-1	Sequence 1, Appli
C 266	23	1.0	22481	5	PCT-US95-07201-43	Sequence 2, Appli	C 339	22	0.9	3095	1	US-08-119-773-1	Sequence 17, Appl
C 267	23	1.0	32484	4	US-09-875-223-2	Sequence 44, Appl	C 340	22	0.9	3214	1	US-08-484-105-17	Sequence 17, Appl
C 268	23	1.0	32042	4	US-09-245-281-44	Sequence 18, Appl	C 341	22	0.9	3214	1	US-08-484-106-17	Sequence 17, Appl
C 269	23	1.0	35100	1	US-08-306-691B-19	Sequence 19, Appl	C 342	22	0.9	3532	3	US-08-787-739-90	Sequence 90, Appl
C 270	23	1.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl	C 343	22	0.9	3532	4	US-09-178-115-90	Sequence 90, Appl
C 271	23	1.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl	C 344	22	0.9	3532	4	US-09-177-776-90	Sequence 90, Appl
C 272	23	1.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl	C 345	22	0.9	3885	1	US-08-688-145-1	Sequence 2, Appli
C 273	23	1.0	45716	4	US-08-965-048-5	Sequence 5, Appli	C 346	22	0.9	4136	4	US-09-103-875-2	Sequence 2, Appli
C 274	23	1.0	45989	4	US-08-965-048-6	Sequence 6, Appli	C 347	22	0.9	4233	4	US-09-056-105-27	Sequence 27, Appl
C 275	23	1.0	50000	4	US-09-146-053-4	Sequence 4, Appli	C 348	22	0.9	4285	4	US-09-040-774-1	Sequence 1, Appli
C 276	23	1.0	80246	4	US-09-078-294-4	Sequence 4, Appli	C 349	22	0.9	5037	4	US-09-705-299-13	Sequence 13, Appl
C 277	23	1.0	80595	4	US-09-078-294-3	Sequence 3, Appli	C 350	22	0.9	5137	5	PCT-US96-01314-39	Sequence 39, Appl
C 278	23	1.0	81001	4	US-09-750-580-1	Sequence 1, Appli	C 351	22	0.9	5138	2	US-08-476-062A-39	Sequence 39, Appl
C 279	23	1.0	98844	4	US-09-791-211-10	Sequence 10, Appl	C 352	22	0.9	5143	1	US-08-574-043A-7	Sequence 7, Appli
C 280	23	1.0	111282	4	US-09-754-250-3	Sequence 3, Appli	C 353	22	0.9	5143	2	US-08-795-015-7	Sequence 7, Appli
C 281	23	1.0	111282	4	US-09-754-250-3	Sequence 3, Appli	C 354	22	0.9	6235	4	US-09-305-384-5	Sequence 5, Appli
C 282	23	1.0	12132	4	US-09-741-150-3	Sequence 3, Appli	C 355	22	0.9	6678	3	US-08-816-617A-1	Sequence 1, Appli
C 283	23	1.0	168575	4	US-09-426-290-1	Sequence 1, Appli	C 356	22	0.9	6679	4	US-09-305-384-1	Sequence 1, Appli
C 284	23	1.0	176373	3	US-09-128-155-17	Sequence 17, Appl	C 357	22	0.9	6709	4	US-09-285-601-3	Sequence 3, Appli
C 285	22	0.9	68	4	US-09-358-972-253	Sequence 253, App	C 358	22	0.9	6769	1	US-08-784-20	Sequence 20, Appl
C 286	22	0.9	68	4	US-09-383-316-93	Sequence 93, Appl	C 359	22	0.9	6769	1	US-08-480-784-20	Sequence 20, Appl
C 287	22	0.9	257	1	US-08-741-402-3	Sequence 3, Appli	C 360	22	0.9	6769	1	US-08-483-553-20	Sequence 20, Appl
C 288	22	0.9	257	3	US-09-024-476-3	Sequence 3, Appli	C 361	22	0.9	6769	1	US-08-483-553-20	Sequence 20, Appl
C 289	22	0.9	262	2	US-08-481-658B-57	Sequence 57, Appl	C 362	22	0.9	6769	1	US-08-487-002-20	Sequence 20, Appl
C 290	22	0.9	262	2	US-08-481-658B-60	Sequence 60, Appl	C 363	22	0.9	6769	1	US-08-487-002-20	Sequence 20, Appl
C 291	22	0.9	262	2	US-08-477-504A-57	Sequence 57, Appl	C 364	22	0.9	6769	1	US-08-483-554B-20	Sequence 20, Appl
C 292	22	0.9	262	2	US-08-477-504A-60	Sequence 60, Appl	C 365	22	0.9	6769	1	US-08-483-554B-20	Sequence 20, Appl
C 293	22	0.9	262	2	US-08-486-756A-57	Sequence 57, Appl	C 366	22	0.9	6769	1	US-08-488-011B-20	Sequence 20, Appl
C 294	22	0.9	262	2	US-08-486-756A-60	Sequence 60, Appl	C 367	22	0.9	6769	1	US-08-488-011B-20	Sequence 20, Appl
C 295	22	0.9	262	2	US-08-485-862B-57	Sequence 57, Appl	C 368	22	0.9	6769	4	US-08-850-727-20	Sequence 20, Appl
C 296	22	0.9	262	2	US-08-485-862B-60	Sequence 60, Appl	C 369	22	0.9	6769	4	US-08-850-727-20	Sequence 20, Appl
C 297	22	0.9	262	3	US-08-787-739-57	Sequence 57, Appl	C 370	22	0.9	6769	5	PCT-US95-10202-20	Sequence 20, Appl
C 298	22	0.9	262	3	US-08-787-739-60	Sequence 60, Appl	C 371	22	0.9	6769	5	PCT-US95-10202-20	Sequence 20, Appl
C 299	22	0.9	262	3	US-08-487-077A-57	Sequence 57, Appl	C 372	22	0.9	6769	5	PCT-US95-10203-20	Sequence 20, Appl
C 300	22	0.9	262	3	US-08-487-077A-60	Sequence 60, Appl	C 373	22	0.9	6769	5	PCT-US95-10203-20	Sequence 20, Appl
C 301	22	0.9	262	3	US-08-485-863A-57	Sequence 57, Appl	C 374	22	0.9	6769	5	PCT-US95-10220-20	Sequence 20, Appl
C 302	22	0.9	262	3	US-08-485-863A-60	Sequence 60, Appl	C 375	22	0.9	6769	5	PCT-US95-10220-20	Sequence 20, Appl
C 303	22	0.9	262	4	US-08-485-049D-60	Sequence 60, Appl	C 376	22	0.9	7228	2	US-08-850-049-128	Sequence 128, App
C 304	22	0.9	262	4	US-09-178-115-57	Sequence 57, Appl	C 377	22	0.9	7228	2	US-08-850-049-128	Sequence 128, App
C 305	22	0.9	262	4	US-08-178-115-60	Sequence 60, Appl	C 378	22	0.9	7228	2	US-08-050-478-128	Sequence 128, App
C 306	22	0.9	262	4	US-09-177-776-57	Sequence 57, Appl	C 379	22	0.9	7228	2	US-08-050-478-128	Sequence 128, App
C 307	22	0.9	262	4	US-09-177-776-60	Sequence 60, Appl	C 380	22	0.9	7228	4	US-09-414-117-129	Sequence 129, App
C 308	22	0.9	423	4	US-08-943-731-131	Sequence 131, App	C 381	22	0.9	7228	4	US-09-414-117-129	Sequence 129, App
C 309	22	0.9	489	4	US-09-370-838-109	Sequence 109, App	C 382	22	0.9	7228	4	US-09-678-437-128	Sequence 128, App
C 310	22	0.9	498	4	US-09-078-294-29	Sequence 29, Appl	C 383	22	0.9	7228	4	US-09-678-437-129	Sequence 129, App
C 311	22	0.9	517	1	US-08-480-784-33	Sequence 33, Appl	C 384	22	0.9	7301	4	US-09-816-088-3	Sequence 3, Appli
C 312	22	0.9	517	1	US-08-483-553-33	Sequence 33, Appl	C 385	22	0.9	7379	4	US-09-341-587-5	Sequence 5, Appli
C 313	22	0.9	517	1	US-08-487-002-33	Sequence 33, Appl	C 386	22	0.9	7676	1	US-08-451-777A-7	Sequence 7, Appli
C 314	22	0.9	517	1	US-08-483-554B-33	Sequence 33, Appl	C 387	22	0.9	7676	2	US-08-451-778A-7	Sequence 7, Appli
C 315	22	0.9	517	1	US-08-488-011B-33	Sequence 33, Appl	C 388	22	0.9	7676	2	US-08-998-208-7	Sequence 7, Appli
C 316	22	0.9	517	1	US-08-850-727-33	Sequence 33, Appl	C 389	22	0.9	7676	5	PCT-US95-05743-7	Sequence 7, Appli
C 317	22	0.9	517	5	PCT-US95-10202-33	Sequence 33, Appl	C 390	22	0.9	9365	4	US-09-608-285A-8	Sequence 8, Appli
C 318	22	0.9	517	5	PCT-US95-10203-33	Sequence 33, Appl	C 391	22	0.9	9365	4	US-09-350-836B-8	Sequence 8, Appli
C 319	22	0.9	517	5	PCT-US95-10220-33	Sequence 33, Appl	C 392	22	0.9	9365	4	US-09-370-265-8	Sequence 8, Appli

393	22	0.9	10898	2	US-08-481-658B-5	Sequence 5, Appli	c 466	21	0.9	5261	1	US-08-366-051B-3	Sequence 3, Appli
394	22	0.9	10898	2	US-08-477-504A-5	Sequence 5, Appli	c 467	21	0.9	5543	2	US-08-687-080-101	Sequence 101, App
395	22	0.9	10898	2	US-08-486-156A-1	Sequence 5, Appli	c 468	21	0.9	5581	4	US-08-973-544-1	Sequence 1, Appli
396	22	0.9	10898	2	US-08-485-862B-5	Sequence 5, Appli	c 469	21	0.9	5668	4	US-09-112-096-14	Sequence 14, Appli
397	22	0.9	10898	3	US-08-787-739-5	Sequence 5, Appli	c 470	21	0.9	5668	4	US-09-112-096-14	Sequence 777, App
398	22	0.9	10898	3	US-08-487-077A-5	Sequence 5, Appli	c 471	21	0.9	6063	1	US-08-195-744-4	Sequence 4, Appli
399	22	0.9	10898	3	US-08-485-863A-5	Sequence 5, Appli	c 472	21	0.9	6063	2	US-08-788-279-4	Sequence 4, Appli
400	22	0.9	10898	4	US-08-485-049D-5	Sequence 5, Appli	c 473	21	0.9	7622	4	US-09-305-639-1	Sequence 1, Appli
401	22	0.9	10898	4	US-09-178-115-5	Sequence 5, Appli	c 474	21	0.9	8353	3	US-08-611-587-1	Sequence 1, Appli
402	22	0.9	10898	4	US-09-177-776-5	Sequence 5, Appli	c 475	21	0.9	8392	1	US-08-080-255-6	Sequence 6, Appli
403	22	0.9	14747	4	US-09-608-285A-42	Sequence 42, Appl	c 476	21	0.9	8392	3	US-08-465-713-6	Sequence 6, Appli
404	22	0.9	15581	3	US-08-646-538-35	Sequence 35, Appl	c 477	21	0.9	8392	5	PCT-US93-05857-6	Sequence 6, Appli
405	22	0.9	15581	4	US-09-503-222-35	Sequence 35, Appl	c 478	21	0.9	9301	4	US-09-449-218D-18	Sequence 18, Appl
406	22	0.9	15977	4	US-08-608-285A-59	Sequence 59, Appl	c 479	21	0.9	10825	3	US-08-652-265-1	Sequence 1, Appli
407	22	0.9	16389	4	US-09-741-154-3	Sequence 3, Appli	c 480	21	0.9	10825	3	US-08-652-265-3	Sequence 3, Appli
408	22	0.9	16389	4	US-09-741-154-3	Sequence 3, Appli	c 481	21	0.9	10825	3	US-08-652-265-5	Sequence 5, Appli
409	22	0.9	18443	4	US-09-078-294-6	Sequence 6, Appli	c 482	21	0.9	10825	3	US-08-652-265-7	Sequence 7, Appli
410	22	0.9	18596	4	US-09-318-448-11	Sequence 11, Appl	c 483	21	0.9	10825	3	US-08-834-497A-1	Sequence 1, Appli
411	22	0.9	19736	4	US-09-740-035-3	Sequence 3, Appli	c 484	21	0.9	10825	3	US-08-834-497A-3	Sequence 3, Appli
412	22	0.9	19736	4	US-09-740-035-3	Sequence 3, Appli	c 485	21	0.9	10825	3	US-08-834-497A-5	Sequence 5, Appli
413	22	0.9	21835	4	US-08-943-731-3	Sequence 3, Appli	c 486	21	0.9	10825	3	US-08-834-497A-7	Sequence 7, Appli
414	22	0.9	32042	4	US-09-245-281-44	Sequence 44, Appl	c 487	21	0.9	10825	4	US-09-503-444A-1	Sequence 1, Appli
415	22	0.9	36741	4	US-09-301-665-3	Sequence 3, Appli	c 488	21	0.9	10825	4	US-09-503-444A-3	Sequence 3, Appli
416	22	0.9	40000	4	US-09-780-049-18	Sequence 18, Appl	c 489	21	0.9	10825	4	US-09-503-444A-5	Sequence 5, Appli
417	22	0.9	40352	3	US-08-846-111D-15	Sequence 15, Appl	c 490	21	0.9	10825	4	US-09-503-444A-7	Sequence 7, Appli
418	22	0.9	40352	4	US-09-443-077-15	Sequence 15, Appl	c 491	21	0.9	11288	4	US-08-646-301A-1	Sequence 1, Appli
419	22	0.9	42571	4	US-08-810-347-3	Sequence 3, Appli	c 492	21	0.9	11288	4	US-08-481-968A-4	Sequence 4, Appli
420	22	0.9	49136	4	US-09-422-869-1	Sequence 1, Appli	c 493	21	0.9	11288	4	US-08-154-712B-4	Sequence 4, Appli
421	22	0.9	169998	4	US-09-676-610B-24	Sequence 24, Appl	c 494	21	0.9	12146	4	US-09-277-457-27	Sequence 27, Appl
422	21	0.9	60	2	US-08-454-557C-66	Sequence 66, Appl	c 495	21	0.9	14796	4	US-08-975-080-35	Sequence 35, Appl
423	21	0.9	60	2	US-08-340-426D-66	Sequence 66, Appl	c 496	21	0.9	14796	4	US-09-630-706-10	Sequence 10, Appl
424	21	0.9	60	2	US-08-450-673C-66	Sequence 66, Appl	c 497	21	0.9	14796	4	US-09-496-694B-3	Sequence 3, Appli
425	21	0.9	60	5	PCT-US95-17111A-66	Sequence 66, Appl	c 498	21	0.9	26684	4	US-09-564-805-28	Sequence 28, Appl
426	21	0.9	377	2	US-08-454-557C-37	Sequence 37, Appl	c 499	21	0.9	31571	1	US-08-323-443B-1	Sequence 1, Appli
427	21	0.9	377	2	US-08-340-426D-37	Sequence 37, Appl	c 500	21	0.9	36159	4	US-09-749-588-3	Sequence 3, Appli
428	21	0.9	377	2	US-08-450-673C-37	Sequence 37, Appl	c 501	21	0.9	38564	4	US-09-734-673-3	Sequence 3, Appli
429	21	0.9	377	5	PCT-US95-17111A-37	Sequence 37, Appl	c 502	21	0.9	65042	4	US-09-784-316-3	Sequence 3, Appli
430	21	0.9	379	3	US-09-157-177-134	Sequence 134, App	c 503	21	0.9	152331	3	US-09-128-155-16	Sequence 16, Appl
431	21	0.9	542	4	US-09-305-639-5	Sequence 5, Appli	c 504	20	0.8	57	3	US-09-056-762-9	Sequence 9, Appli
432	21	0.9	561	4	US-09-404-879A-50	Sequence 50, Appl	c 505	20	0.8	75	3	US-09-056-762-7	Sequence 7, Appli
433	21	0.9	569	4	US-08-943-731-144	Sequence 144, App	c 506	20	0.8	674	4	US-09-328-111-76	Sequence 76, Appl
434	21	0.9	591	4	US-09-385-982-406	Sequence 406, App	c 507	20	0.8	788	4	US-09-288-143-27	Sequence 27, Appl
435	21	0.9	618	4	US-09-328-111-215	Sequence 215, App	c 508	20	0.8	1052	4	US-09-442-143A-9	Sequence 9, Appli
436	21	0.9	951	4	US-09-605-785-570	Sequence 570, App	c 509	20	0.8	1534	2	US-08-370-975B-10	Sequence 10, Appl
437	21	0.9	999	4	US-08-641-638-290	Sequence 290, App	c 510	20	0.8	1589	1	US-07-971-092-1	Sequence 1, Appli
438	21	0.9	1000	2	US-08-718-538-1	Sequence 1, Appli	c 511	20	0.8	1611	6	5198342-1	Patent No. 5198342
439	21	0.9	1381	2	US-08-454-557C-49	Sequence 49, Appl	c 512	20	0.8	1624	2	US-08-852-807-10	Sequence 10, Appl
440	21	0.9	1381	2	US-08-340-426D-49	Sequence 49, Appl	c 513	20	0.8	1773	4	US-08-943-731-215	Sequence 215, App
441	21	0.9	1381	2	US-08-450-673C-49	Sequence 49, Appl	c 514	20	0.8	2372	1	US-07-903-103-1	Sequence 1, Appli
442	21	0.9	1386	5	PCT-US95-17111A-49	Sequence 49, Appl	c 515	20	0.8	2372	1	US-08-044-619A-1	Sequence 1, Appli
443	21	0.9	1386	2	US-08-687-080-76	Sequence 76, Appl	c 516	20	0.8	2372	1	US-08-283-911-1	Sequence 1, Appli
444	21	0.9	1418	5	PCT-US95-17111A-120	Sequence 120, App	c 517	20	0.8	2372	1	US-08-245-500A-2	Sequence 2, Appli
445	21	0.9	1442	2	US-08-454-557C-120	Sequence 120, App	c 518	20	0.8	2372	1	US-08-390-546-2	Sequence 2, Appli
446	21	0.9	1442	2	US-08-340-426D-120	Sequence 120, App	c 519	20	0.8	2372	1	US-08-390-479A-2	Sequence 2, Appli
447	21	0.9	1442	2	US-08-450-673C-120	Sequence 120, App	c 520	20	0.8	2372	1	US-08-557-393-2	Sequence 2, Appli
448	21	0.9	1480	2	US-08-454-557C-38	Sequence 38, Appl	c 521	20	0.8	2372	1	US-08-390-516C-2	Sequence 2, Appli
449	21	0.9	1480	2	US-08-340-426D-38	Sequence 38, Appl	c 522	20	0.8	2372	1	US-08-390-517A-2	Sequence 2, Appli
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451	21	0.9	2127	1	US-08-832-883-54	Sequence 54, Appl	c 524	20	0.8	2372	2	US-08-801-718-2	Sequence 2, Appli
452	21	0.9	2127	2	US-08-832-883-54	Sequence 54, Appl	c 525	20	0.8	2372	4	US-09-073-567-1	Sequence 1, Appli
453	21	0.9	2542	1	US-08-441-370-1	Sequence 1, Appli	c 526	20	0.8	2372	4	US-09-280-805-1	Sequence 1, Appli
454	21	0.9	2542	2	US-08-886-152-4	Sequence 4, Appli	c 527	20	0.8	2372	4	US-09-048-810-1	Sequence 1, Appli
455	21	0.9	2559	2	US-08-196-222-4	Sequence 4, Appli	c 528	20	0.8	2372	4	US-09-170-159A-2	Sequence 2, Appli
456	21	0.9	2559	4	US-08-965-729A-2	Sequence 2, Appli	c 529	20	0.8	2372	4	US-09-480-718-43	Sequence 43, Appl
457	21	0.9	3424	4	US-09-632-098-1	Sequence 1, Appli	c 530	20	0.8	2950	5	PCT-US93-08386-7	Sequence 7, Appli
458	21	0.9	3431	4	US-09-632-098-1	Sequence 1, Appli	c 531	20	0.8	2957	2	US-08-394-152A-48	Sequence 48, Appl
459	21	0.9	3468	4	US-09-632-098-3	Sequence 3, Appli	c 532	20	0.8	2968	5	PCT-US93-08386-1	Sequence 1, Appli
460	21	0.9	3848	4	US-09-112-096-28	Sequence 28, Appl	c 533	20	0.8	3017	2	US-08-394-152A-39	Sequence 39, Appl
461	21	0.9	4576	1	US-08-832-883-49	Sequence 49, Appl	c 534	20	0.8	3441	4	US-09-026-033-17	Sequence 17, Appl
462	21	0.9	4576	2	US-08-832-883-49	Sequence 49, Appl	c 535	20	0.8	4630	4	US-09-442-143A-1	Sequence 1, Appli
463	21	0.9	4803	4	US-09-197-636-1	Sequence 1, Appli	c 536	20	0.8	5232	3	US-09-212-971-3	Sequence 3, Appli
464	21	0.9	4803	4	US-09-197-636-3	Sequence 3, Appli	c 537	20	0.8	5232	3	US-08-800-929A-3	Sequence 3, Appli
465	21	0.9	5261	1	US-08-045-806-3	Sequence 3, Appli	c 538	20	0.8	5232	4	US-09-617-053A-3	Sequence 3, Appli



539	20	0.8	6246	4	US-08-943-731-640	Sequence 640, App	612	19	0.8	18073	4	US-09-078-294-12	Sequence 12, Appl
c 540	20	0.8	6464	2	US-08-400-159-5	Sequence 5, Appli	c 613	19	0.8	35060	3	US-08-814-095-7	Sequence 7, Appli
c 541	20	0.8	6464	2	US-08-611-729A-5	Sequence 5, Appli	c 614	19	0.8	72928	3	US-09-009-913-1	Sequence 1, Appli
c 542	20	0.8	7610	4	US-09-659-975B-12	Sequence 12, Appl	615	18	0.7	20	4	US-09-280-805-245	Sequence 245, App
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c 544	20	0.8	29629	4	US-09-729-995-3	Sequence 3, Appli	c 617	18	0.7	149	2	US-08-340-426D-89	Sequence 89, Appl
c 545	20	0.8	44453	4	US-09-146-053-5	Sequence 5, Appli	c 618	18	0.7	149	2	US-08-450-673C-89	Sequence 89, Appl
c 546	20	0.8	49136	4	US-09-422-869-1	Sequence 1, Appli	c 619	18	0.7	149	2	PCT-US95-1711A-89	Sequence 89, Appl
c 547	20	0.8	51259	3	US-08-781-891-209	Sequence 209, App	620	18	0.7	165	1	US-08-209-747-9	Sequence 9, Appli
c 548	20	0.8	168575	4	US-09-426-290-1	Sequence 1, Appli	621	18	0.7	165	1	US-08-458-298-9	Sequence 9, Appli
c 549	19	0.8	320	3	US-08-157-177-131	Sequence 131, App	622	18	0.7	300	4	US-09-199-637A-198	Sequence 198, App
c 550	19	0.8	434	2	US-08-332-766A-10	Sequence 10, App	623	18	0.7	325	2	US-08-940-332-3	Sequence 3, Appli
c 551	19	0.8	462	4	US-09-328-111-79	Sequence 79, Appl	c 624	18	0.7	345	4	US-09-385-982-164	Sequence 164, App
c 552	19	0.8	523	4	US-09-286-132-8	Sequence 8, Appli	c 625	18	0.7	372	4	US-09-018-584A-13	Sequence 13, Appl
c 553	19	0.8	523	4	US-09-836-941-8	Sequence 8, Appli	626	18	0.7	378	4	US-09-199-637A-197	Sequence 197, App
c 554	19	0.8	542	4	US-09-461-697-136	Sequence 136, App	627	18	0.7	396	4	US-09-199-637A-262	Sequence 262, App
c 555	19	0.8	588	4	US-09-385-982-128	Sequence 128, App	628	18	0.7	411	4	US-09-385-982-5	Sequence 5, Appli
c 556	19	0.8	597	4	US-08-286-132-7	Sequence 7, Appli	629	18	0.7	423	4	US-09-199-637A-196	Sequence 196, App
c 557	19	0.8	597	4	US-09-836-941-7	Sequence 7, Appli	c 630	18	0.7	461	4	US-09-404-879A-1	Sequence 1, Appli
c 558	19	0.8	738	4	US-09-662-250A-23	Sequence 23, Appl	c 631	18	0.7	461	4	US-09-404-879A-3	Sequence 3, Appli
c 559	19	0.8	1000	4	US-09-018-584A-40	Sequence 40, Appl	c 632	18	0.7	489	4	US-09-199-637A-260	Sequence 260, App
c 560	19	0.8	1001	4	US-09-641-638-397	Sequence 397, App	c 633	18	0.7	624	1	US-08-776-088-7	Sequence 7, Appli
c 561	19	0.8	1320	1	US-08-599-252-84	Sequence 84, Appl	634	18	0.7	624	5	PCT-US95-09145A-7	Sequence 7, Appli
c 562	19	0.8	1320	1	US-08-436-074-57	Sequence 57, Appl	635	18	0.7	670	4	US-09-605-785-680	Sequence 680, App
c 563	19	0.8	1320	5	PCT-US96-06352-84	Sequence 84, Appl	636	18	0.7	687	4	US-09-199-637A-195	Sequence 195, App
c 564	19	0.8	1320	5	PCT-US96-06583-84	Sequence 84, Appl	637	18	0.7	690	4	US-09-199-637A-194	Sequence 194, App
c 565	19	0.8	1366	4	US-09-265-630-10	Sequence 10, Appl	c 638	18	0.7	690	4	US-09-199-637A-264	Sequence 264, App
c 566	19	0.8	1509	4	US-09-265-630-12	Sequence 12, Appl	c 639	18	0.7	957	4	US-09-199-637A-193	Sequence 193, App
c 567	19	0.8	1725	4	US-09-082-440-3	Sequence 3, Appli	640	18	0.7	1001	4	US-09-641-638-521	Sequence 521, App
c 568	19	0.8	1725	4	US-09-712-495-3	Sequence 3, Appli	c 641	18	0.7	1001	4	US-09-641-638-521	Sequence 521, App
c 569	19	0.8	1762	4	US-09-443-184-35	Sequence 35, Appl	c 642	18	0.7	1275	2	US-08-958-642-1	Sequence 1, Appli
c 570	19	0.8	1798	4	US-09-345-214-16	Sequence 16, Appl	c 643	18	0.7	1275	3	US-08-778-394-3	Sequence 3, Appli
c 571	19	0.8	2019	4	US-09-345-214-15	Sequence 15, Appl	c 644	18	0.7	1275	3	US-08-778-423A-1	Sequence 1, Appli
c 572	19	0.8	2053	4	US-09-227-357-45	Sequence 45, Appl	c 645	18	0.7	1288	4	US-08-047-041A-24	Sequence 24, Appl
c 573	19	0.8	2248	4	US-09-345-214-20	Sequence 20, Appl	c 646	18	0.7	1288	4	US-09-417-278A-1	Sequence 1, Appli
c 574	19	0.8	2262	4	US-09-286-132-1	Sequence 1, Appli	c 647	18	0.7	1316	1	US-08-047-041A-11	Sequence 11, Appl
c 575	19	0.8	2262	4	US-09-836-941-1	Sequence 1, Appli	c 648	18	0.7	1316	2	US-08-795-006A-31	Sequence 31, Appl
c 576	19	0.8	2387	4	US-09-375-318-38	Sequence 38, Appl	c 649	18	0.7	1316	4	US-09-184-073-31	Sequence 31, Appl
c 577	19	0.8	2589	2	US-08-482-728A-3	Sequence 3, Appli	c 650	18	0.7	1558	4	US-09-123-030-7	Sequence 7, Appli
c 578	19	0.8	2743	1	US-08-317-707-1	Sequence 1, Appli	651	18	0.7	1624	4	US-08-430-225A-19	Sequence 19, Appl
c 579	19	0.8	3760	2	US-08-724-354D-1	Sequence 1, Appli	652	18	0.7	1643	2	US-08-933-750C-68	Sequence 68, Appl
c 580	19	0.8	3760	3	US-09-270-994D-1	Sequence 1, Appli	653	18	0.7	1643	3	US-09-234-613-68	Sequence 68, Appl
c 581	19	0.8	4041	1	US-08-147-812-4	Sequence 4, Appli	654	18	0.7	1653	4	US-09-199-637A-192	Sequence 192, App
c 582	19	0.8	4110	3	US-09-123-708-1	Sequence 1, Appli	655	18	0.7	1827	4	US-09-199-637A-191	Sequence 191, App
c 583	19	0.8	4110	3	US-09-123-624-1	Sequence 1, Appli	656	18	0.7	1844	1	US-07-872-644-26	Sequence 26, Appl
c 584	19	0.8	4165	1	US-08-147-812-6	Sequence 6, Appli	657	18	0.7	1844	1	US-08-297-494-26	Sequence 26, Appl
c 585	19	0.8	4265	4	US-09-651-011A-3	Sequence 3, Appli	658	18	0.7	1844	1	US-08-297-510-26	Sequence 26, Appl
c 586	19	0.8	4441	4	US-09-641-999-2	Sequence 2, Appli	659	18	0.7	1844	1	US-08-479-532-26	Sequence 26, Appl
c 587	19	0.8	4543	2	US-08-519-547A-5	Sequence 5, Appli	660	18	0.7	1844	1	US-08-455-526-26	Sequence 26, Appl
c 588	19	0.8	5037	4	US-09-705-299-13	Sequence 13, Appl	661	18	0.7	1844	1	US-08-455-525-26	Sequence 26, Appl
c 589	19	0.8	6038	4	US-09-305-639-4	Sequence 4, Appli	662	18	0.7	1844	1	US-09-139-491-26	Sequence 26, Appl
c 590	19	0.8	7152	4	US-09-167-681-29	Sequence 29, Appl	663	18	0.7	1844	5	PCT-US92-03222-26	Sequence 26, Appl
c 591	19	0.8	7210	2	US-08-237-963B-10	Sequence 10, Appl	664	18	0.7	1920	4	US-09-199-637A-190	Sequence 190, App
c 592	19	0.8	7210	4	US-08-367-841A-10	Sequence 10, Appl	665	18	0.7	1932	4	US-09-199-637A-189	Sequence 189, App
c 593	19	0.8	7210	5	PCT-US95-07201-10	Sequence 10, Appl	666	18	0.7	1938	4	US-09-199-637A-252	Sequence 252, App
c 594	19	0.8	7622	4	US-09-305-639-1	Sequence 1, Appli	667	18	0.7	1999	4	US-09-167-109-4	Sequence 4, Appli
c 595	19	0.8	8367	2	US-08-583-562B-7	Sequence 7, Appli	668	18	0.7	2004	2	US-08-691-814B-1	Sequence 1, Appli
c 596	19	0.8	8367	2	US-08-779-113-7	Sequence 7, Appli	669	18	0.7	2101	4	US-09-199-637A-102	Sequence 102, App
c 597	19	0.8	8396	4	US-09-328-174A-1	Sequence 1, Appli	670	18	0.7	2285	2	US-08-940-332-1	Sequence 1, Appli
c 598	19	0.8	8409	1	US-09-167-681-37	Sequence 37, Appl	c 671	18	0.7	2336	1	US-08-247-946A-1	Sequence 1, Appli
c 599	19	0.8	9103	1	US-08-466-033-182	Sequence 182, App	c 672	18	0.7	2336	5	PCT-US95-06420-1	Sequence 1, Appli
c 600	19	0.8	9103	2	US-08-444-733-182	Sequence 182, App	673	18	0.7	2373	4	US-08-975-762-45	Sequence 45, Appl
c 601	19	0.8	9103	2	US-08-464-134-182	Sequence 182, App	674	18	0.7	2373	4	US-09-295-028-45	Sequence 45, Appl
c 602	19	0.8	9103	2	US-08-461-361-182	Sequence 182, App	675	18	0.7	2373	4	US-09-106-582-45	Sequence 45, Appl
c 603	19	0.8	9103	2	US-08-485-910-182	Sequence 182, App	676	18	0.7	2539	3	US-09-000-016-3	Sequence 3, Appli
c 604	19	0.8	9103	5	PCT-US95-06266-156	Sequence 156, App	677	18	0.7	2539	4	US-09-514-340-3	Sequence 3, Appli
c 605	19	0.8	9388	4	US-08-991-789A-141	Sequence 141, App	678	18	0.7	2679	1	US-08-479-328-1	Sequence 1, Appli
c 606	19	0.8	9388	4	US-09-062-451-141	Sequence 141, App	679	18	0.7	2679	1	US-08-761-119-1	Sequence 1, Appli
c 607	19	0.8	9388	4	US-09-598-326-141	Sequence 141, App	680	18	0.7	2679	2	US-08-668-128B-1	Sequence 1, Appli
c 608	19	0.8	12394	4	US-09-488-856A-10	Sequence 10, Appl	681	18	0.7	2679	2	US-08-805-445-1	Sequence 1, Appli
c 609	19	0.8	13875	2	US-08-734-344-1	Sequence 1, Appli	682	18	0.7	2679	3	US-08-959-625-1	Sequence 1, Appli
c 610	19	0.8	14747	4	US-09-608-285A-42	Sequence 42, Appl	683	18	0.7	2679	3	US-09-008-466-1	Sequence 1, Appli
c 611	19	0.8	15977	4	US-09-608-285A-59	Sequence 59, Appl	684	18	0.7	2679	3	US-08-580-980A-1	Sequence 1, Appli

685	18	0.7	2679	3	US-09-053-453-1	Sequence 1, Appli	758	17	0.7	841	5	PCT-US93-06251-80	Sequence 80, Appl
686	18	0.7	2679	3	US-08-644-116A-1	Sequence 1, Appli	759	17	0.7	841	5	PCT-US93-06251-81	Sequence 81, Appl
687	18	0.7	2793	1	US-08-209-747-1	Sequence 1, Appli	760	17	0.7	882	4	US-09-134-001C-1530	Sequence 1530, Ap
688	18	0.7	2793	1	US-08-458-298-1	Sequence 1, Appli	761	17	0.7	882	4	US-09-288-143-55	Sequence 55, Appl
689	18	0.7	2809	3	US-09-000-016-1	Sequence 1, Appli	762	17	0.7	895	4	US-09-247-155-141	Sequence 141, Appl
690	18	0.7	2809	3	US-09-514-340-1	Sequence 1, Appli	763	17	0.7	895	4	US-08-961-083-23	Sequence 23, Appl
691	18	0.7	2885	3	US-08-948-705-2	Sequence 2, Appli	764	17	0.7	1000	4	US-09-641-638-636	Sequence 636, App
692	18	0.7	2884	4	US-08-605-785-335	Sequence 335, App	765	17	0.7	1000	4	US-09-641-638-637	Sequence 637, App
693	18	0.7	2984	4	US-08-439-313-335	Sequence 335, App	766	17	0.7	1001	4	US-09-641-638-86	Sequence 86, Appl
694	18	0.7	2984	4	US-09-352-616A-335	Sequence 335, App	767	17	0.7	1001	4	US-09-641-638-121	Sequence 121, App
695	18	0.7	2984	4	US-09-232-149A-335	Sequence 335, App	768	17	0.7	1002	4	US-09-641-638-578	Sequence 578, App
696	18	0.7	3011	1	US-07-821-716-1	Sequence 1, Appli	769	17	0.7	1082	2	US-08-909-965C-12	Sequence 12, Appl
697	18	0.7	3047	1	US-08-280-690-1	Sequence 1, Appli	770	17	0.7	1082	2	US-09-195-666A-11	Sequence 11, Appl
698	18	0.7	3568	1	US-08-218-363-3	Sequence 3, Appli	771	17	0.7	1095	3	US-09-195-666A-12	Sequence 12, Appl
699	18	0.7	3590	1	US-08-587-889-1	Sequence 1, Appli	772	17	0.7	1095	3	US-09-195-666A-13	Sequence 13, Appl
700	18	0.7	3590	5	PCT-US96-09193-1	Sequence 1, Appli	773	17	0.7	1095	3	US-09-195-666A-14	Sequence 14, Appl
701	18	0.7	3748	2	US-08-958-840-1	Sequence 9, Appli	774	17	0.7	1095	4	US-09-635-705-11	Sequence 11, Appl
702	18	0.7	4517	4	US-09-140-804-9	Sequence 9, Appli	775	17	0.7	1095	4	US-09-635-705-12	Sequence 12, Appl
703	18	0.7	4704	2	US-08-476-062A-52	Sequence 52, Appl	776	17	0.7	1095	4	US-09-635-705-13	Sequence 13, Appl
704	18	0.7	5035	2	US-08-616-392C-3	Sequence 3, Appli	777	17	0.7	1095	4	US-09-635-705-14	Sequence 14, Appl
705	18	0.7	5044	4	US-08-735-935-3	Sequence 3, Appli	778	17	0.7	1095	4	US-09-634-858A-11	Sequence 11, Appl
706	18	0.7	5095	1	US-08-092-817-3	Sequence 3, Appli	779	17	0.7	1095	4	US-09-634-858A-12	Sequence 12, Appl
707	18	0.7	5095	4	US-08-485-128-3	Sequence 3, Appli	780	17	0.7	1095	4	US-09-634-858A-13	Sequence 13, Appl
708	18	0.7	8779	2	US-08-750-703-4	Sequence 4, Appli	781	17	0.7	1095	4	US-09-634-858A-14	Sequence 14, Appl
709	18	0.7	15202	3	US-08-922-635-21	Sequence 21, Appl	782	17	0.7	1174	2	US-08-481-658B-39	Sequence 39, Appl
710	18	0.7	15602	4	US-08-844-634-17	Sequence 17, Appl	783	17	0.7	1174	2	US-08-477-504A-39	Sequence 39, Appl
711	18	0.7	17949	4	US-08-087-465-3	Sequence 3, Appli	784	17	0.7	1174	2	US-08-486-756A-39	Sequence 39, Appl
712	18	0.7	21234	4	US-09-810-671-3	Sequence 3, Appli	785	17	0.7	1174	2	US-08-485-862B-39	Sequence 39, Appl
713	18	0.7	29598	4	US-09-341-587-6	Sequence 6, Appli	786	17	0.7	1174	3	US-08-787-739-39	Sequence 39, Appl
714	18	0.7	40328	3	US-08-742-185-102	Sequence 102, App	787	17	0.7	1174	3	US-08-487-077A-39	Sequence 39, Appl
715	18	0.7	42235	4	US-09-199-637A-1	Sequence 1, Appli	788	17	0.7	1174	3	US-08-485-863A-39	Sequence 39, Appl
716	18	0.7	43795	3	US-08-742-185-101	Sequence 101, App	789	17	0.7	1174	4	US-08-485-049D-39	Sequence 39, Appl
717	17	0.7	20	1	US-07-922-723A-35	Sequence 35, Appl	790	17	0.7	1174	4	US-09-178-115-39	Sequence 39, Appl
718	17	0.7	20	1	US-07-799-828C-35	Sequence 35, Appl	791	17	0.7	1174	4	US-09-177-776-39	Sequence 39, Appl
719	17	0.7	25	2	US-07-952-277A-35	Sequence 35, Appl	792	17	0.7	1200	4	US-09-018-584A-37	Sequence 37, Appl
720	17	0.7	69	4	US-09-358-972-254	Sequence 94, App	793	17	0.7	1233	4	US-09-015-188-4	Sequence 4, Appli
721	17	0.7	69	4	US-09-383-316-94	Sequence 94, Appl	794	17	0.7	1237	4	US-09-535-008-56	Sequence 56, Appl
722	17	0.7	144	1	US-08-209-747-13	Sequence 13, Appl	795	17	0.7	1255	1	US-08-097-938-3	Sequence 3, Appli
723	17	0.7	144	1	US-08-458-298-13	Sequence 13, Appl	796	17	0.7	1255	1	US-08-476-000-3	Sequence 3, Appli
724	17	0.7	165	1	US-08-209-747-5	Sequence 5, Appli	797	17	0.7	1255	1	US-08-476-840-3	Sequence 3, Appli
725	17	0.7	165	1	US-08-458-298-5	Sequence 5, Appli	798	17	0.7	1255	3	US-08-476-976-3	Sequence 3, Appli
726	17	0.7	239	2	US-08-687-080-93	Sequence 93, Appl	799	17	0.7	1255	3	US-08-474-410-3	Sequence 3, Appli
727	17	0.7	260	4	US-09-030-607-216	Sequence 216, App	800	17	0.7	1255	4	US-08-486-673B-3	Sequence 2, Appli
728	17	0.7	260	4	US-09-605-785-216	Sequence 216, App	801	17	0.7	1276	4	US-09-177-325-2	Sequence 2, Appli
729	17	0.7	260	4	US-09-439-313-216	Sequence 216, App	802	17	0.7	1276	4	US-08-411-812A-2	Sequence 2, Appli
730	17	0.7	260	4	US-08-352-616A-216	Sequence 216, App	803	17	0.7	1276	4	US-09-590-113-2	Sequence 2, Appli
731	17	0.7	260	4	US-09-232-149A-216	Sequence 216, App	804	17	0.7	1373	2	US-08-907-674-2	Sequence 2, Appli
732	17	0.7	265	2	US-08-849-701-1	Sequence 1, Appli	805	17	0.7	1373	2	US-09-215-087-2	Sequence 2, Appli
733	17	0.7	294	2	US-08-481-658B-61	Sequence 61, Appl	806	17	0.7	1373	3	US-09-391-959-2	Sequence 2, Appli
734	17	0.7	294	2	US-08-477-504A-61	Sequence 61, Appl	807	17	0.7	1401	2	US-08-481-658B-49	Sequence 49, Appl
735	17	0.7	294	2	US-08-486-756A-61	Sequence 61, Appl	808	17	0.7	1401	2	US-08-477-504A-49	Sequence 49, Appl
736	17	0.7	294	2	US-08-485-862B-61	Sequence 61, Appl	809	17	0.7	1401	2	US-08-486-756A-49	Sequence 49, Appl
737	17	0.7	294	3	US-08-787-739-61	Sequence 61, Appl	810	17	0.7	1401	2	US-08-485-862B-49	Sequence 49, Appl
738	17	0.7	294	3	US-08-487-077A-61	Sequence 61, Appl	811	17	0.7	1401	2	US-08-787-739-49	Sequence 49, Appl
739	17	0.7	294	3	US-08-485-863A-61	Sequence 61, Appl	812	17	0.7	1401	3	US-08-487-077A-49	Sequence 49, Appl
740	17	0.7	294	4	US-08-485-049D-61	Sequence 61, Appl	813	17	0.7	1401	3	US-08-485-863A-49	Sequence 49, Appl
741	17	0.7	294	4	US-08-178-115-61	Sequence 61, Appl	814	17	0.7	1401	4	US-08-485-049D-49	Sequence 49, Appl
742	17	0.7	294	4	US-09-177-776-61	Sequence 61, Appl	815	17	0.7	1401	4	US-09-178-115-49	Sequence 49, Appl
743	17	0.7	410	4	US-08-221-298-63	Sequence 63, Appl	816	17	0.7	1401	4	US-09-177-776-49	Sequence 49, Appl
744	17	0.7	516	4	US-09-018-584A-24	Sequence 24, Appl	817	17	0.7	1402	4	US-09-196-520-5	Sequence 5, Appli
745	17	0.7	592	4	US-09-276-531-115	Sequence 115, App	818	17	0.7	1441	4	US-09-122-1710-4	Sequence 4, Appli
746	17	0.7	614	4	US-09-844-525A-12	Sequence 12, Appl	819	17	0.7	1491	2	US-08-941-647A-4	Sequence 1, Appli
747	17	0.7	618	4	US-08-385-982-218	Sequence 218, App	820	17	0.7	1505	4	US-09-142-481-1	Sequence 1, Appli
748	17	0.7	619	4	US-08-998-416-708	Sequence 708, App	821	17	0.7	1613	3	US-08-938-830-28	Sequence 28, Appl
749	17	0.7	640	4	US-09-385-982-2	Sequence 2, Appli	822	17	0.7	1662	3	US-08-807-342B-3	Sequence 3, Appli
750	17	0.7	653	4	US-09-328-111-614	Sequence 614, App	823	17	0.7	1719	3	US-09-008-481A-4	Sequence 4, Appli
751	17	0.7	665	4	US-08-896-164-43	Sequence 43, Appl	824	17	0.7	1719	3	US-09-195-666A-18	Sequence 18, Appl
752	17	0.7	675	4	US-08-896-164-41	Sequence 41, Appl	825	17	0.7	1719	4	US-09-309-592-4	Sequence 4, Appli
753	17	0.7	696	4	US-09-740-235-16	Sequence 16, Appl	826	17	0.7	1719	4	US-08-635-705-18	Sequence 18, Appl
754	17	0.7	789	1	US-08-039-778B-14	Sequence 14, Appl	827	17	0.7	1776	2	US-09-634-858A-18	Sequence 18, Appl
755	17	0.7	807	2	US-08-394-152A-42	Sequence 42, Appl	828	17	0.7	1776	2	US-08-531-927B-1	Sequence 1, Appli
756	17	0.7	807	2	US-08-531-927B-9	Sequence 9, Appli	829	17	0.7	1776	4	US-09-041-886-12	Sequence 12, Appl
757	17	0.7	821	4	US-09-342-691C-7	Sequence 7, Appli	830	17	0.7	1803	4	US-09-006-428A-18	Sequence 18, Appl

831	17	0.7	1829	2	US-08-687-080-57	Sequence 57, Appl	c 904	17	0.7	3463	4	US-09-533-220A-1	Sequence 1, Appl
832	17	0.7	1853	4	US-09-605-785-369	Sequence 369, App	905	17	0.7	3500	4	US-09-197-636-7	Sequence 7, Appl
833	17	0.7	1853	4	US-09-439-313-369	Sequence 369, App	906	17	0.7	3564	4	US-09-347-878-15	Sequence 15, Appl
834	17	0.7	1853	4	US-09-062-451-295	Sequence 295, App	c 907	17	0.7	3621	2	US-09-019-201A-1	Sequence 1, Appl
835	17	0.7	1853	4	US-09-352-616A-369	Sequence 369, App	c 908	17	0.7	3653	4	US-08-973-334-1	Sequence 1, Appl
836	17	0.7	1858	4	US-09-006-428A-16	Sequence 16, Appl	c 909	17	0.7	3653	4	US-09-563-869A-1	Sequence 1, Appl
837	17	0.7	1875	2	US-08-683-743-3	Sequence 3, Appl	c 910	17	0.7	3653	4	US-08-549-489-1	Sequence 1, Appl
838	17	0.7	1875	4	US-09-750-580-2	Sequence 2, Appl	c 911	17	0.7	3663	4	US-09-499-884-11	Sequence 11, Appl
839	17	0.7	1901	4	US-09-338-907-181	Sequence 181, App	c 912	17	0.7	3729	1	US-08-554-612C-25	Sequence 25, Appl
840	17	0.7	1901	4	US-09-218-207-181	Sequence 181, App	c 913	17	0.7	4129	2	US-08-370-319C-12	Sequence 12, Appl
841	17	0.7	1960	2	US-08-533-306A-1	Sequence 1, Appl	914	17	0.7	4129	4	US-09-224-834-12	Sequence 12, Appl
842	17	0.7	1960	2	US-08-742-923A-1	Sequence 1, Appl	c 915	17	0.7	4136	4	US-09-103-875-2	Sequence 2, Appl
843	17	0.7	1988	2	US-08-257-963B-11	Sequence 11, Appl	916	17	0.7	4284	4	US-09-662-250A-3	Sequence 3, Appl
844	17	0.7	1988	4	US-08-367-841A-11	Sequence 11, Appl	c 917	17	0.7	4460	4	US-09-103-875-4	Sequence 4, Appl
845	17	0.7	1988	5	PCT-US95-07201-11	Sequence 11, Appl	c 918	17	0.7	4543	4	US-09-221-017B-1103	Sequence 1103, Ap
846	17	0.7	2023	4	US-09-491-522-6	Sequence 6, Appl	919	17	0.7	4803	4	US-09-197-636-3	Sequence 3, Appl
847	17	0.7	2086	3	US-08-589-028-9	Sequence 9, Appl	920	17	0.7	4803	4	US-09-197-636-3	Sequence 3, Appl
848	17	0.7	2086	3	US-08-784-582-9	Sequence 9, Appl	921	17	0.7	5009	3	US-08-978-741-7	Sequence 7, Appl
849	17	0.7	2086	4	US-08-785-271-9	Sequence 9, Appl	c 922	17	0.7	5009	4	US-09-333-729A-8	Sequence 8, Appl
850	17	0.7	2096	3	US-09-008-481A-10	Sequence 10, Appl	c 923	17	0.7	5192	2	US-08-619-198-8	Sequence 8, Appl
851	17	0.7	2096	3	US-09-195-666A-16	Sequence 16, Appl	c 924	17	0.7	5198	2	US-08-619-198-1	Sequence 1, Appl
852	17	0.7	2096	4	US-09-309-592-10	Sequence 10, Appl	c 925	17	0.7	5262	4	US-08-520-373D-5	Sequence 5, Appl
853	17	0.7	2096	4	US-09-635-705-16	Sequence 16, Appl	926	17	0.7	5381	4	US-09-750-580-4	Sequence 4, Appl
854	17	0.7	2096	4	US-09-634-858A-16	Sequence 16, Appl	927	17	0.7	5408	1	US-08-471-058-20	Sequence 20, Appl
855	17	0.7	2100	3	US-08-938-850-2	Sequence 2, Appl	928	17	0.7	5408	3	US-08-471-057-20	Sequence 20, Appl
856	17	0.7	2100	3	US-09-020-222-2	Sequence 2, Appl	c 929	17	0.7	5581	4	US-08-973-544-1	Sequence 1, Appl
857	17	0.7	2140	3	US-09-058-389A-6	Sequence 6, Appl	c 930	17	0.7	5615	4	US-09-302-769-47	Sequence 47, Appl
858	17	0.7	2140	4	US-09-611-781-6	Sequence 6, Appl	c 931	17	0.7	5843	1	US-08-554-612C-2	Sequence 2, Appl
859	17	0.7	2184	4	US-09-605-785-370	Sequence 370, App	932	17	0.7	6614	4	US-09-150-460B-3	Sequence 3, Appl
860	17	0.7	2184	4	US-09-439-313-370	Sequence 370, App	c 933	17	0.7	7886	2	US-08-751-189-2	Sequence 2, Appl
861	17	0.7	2184	4	US-09-062-451-296	Sequence 296, App	c 934	17	0.7	7886	2	US-09-060-836-2	Sequence 2, Appl
862	17	0.7	2184	4	US-09-352-616A-370	Sequence 370, App	c 935	17	0.7	7886	2	US-09-184-445-2	Sequence 2, Appl
863	17	0.7	2382	4	US-09-641-741-1	Sequence 1, Appl	c 936	17	0.7	8021	3	US-09-740-235-2	Sequence 2, Appl
864	17	0.7	2461	1	US-08-832-883-3	Sequence 3, Appl	937	17	0.7	8342	3	US-08-545-860D-63	Sequence 63, Appl
865	17	0.7	2461	2	US-08-832-877-113	Sequence 113, App	c 938	17	0.7	8342	3	US-08-545-860D-63	Sequence 63, Appl
866	17	0.7	2504	4	US-09-218-363-7	Sequence 7, Appl	c 939	17	0.7	8342	5	PCT-US94-04496-63	Sequence 63, Appl
867	17	0.7	2531	2	US-08-818-514-4	Sequence 4, Appl	c 940	17	0.7	8342	5	PCT-US94-04496-63	Sequence 63, Appl
868	17	0.7	2531	2	US-08-818-514-5	Sequence 5, Appl	c 941	17	0.7	8392	1	US-08-080-255-6	Sequence 6, Appl
869	17	0.7	2531	3	US-09-115-934A-4	Sequence 4, Appl	c 942	17	0.7	8392	3	US-08-465-713-6	Sequence 6, Appl
870	17	0.7	2531	3	US-09-115-934A-5	Sequence 5, Appl	c 943	17	0.7	8392	5	PCT-US93-05857-6	Sequence 6, Appl
871	17	0.7	2531	4	US-09-844-525A-3	Sequence 3, Appl	944	17	0.7	8722	4	US-09-221-017B-263	Sequence 263, App
872	17	0.7	2562	2	US-08-436-771-8	Sequence 8, Appl	945	17	0.7	8835	3	US-08-884-324-10	Sequence 10, Appl
873	17	0.7	2562	2	US-08-434-998-8	Sequence 8, Appl	c 946	17	0.7	9306	4	US-09-453-702B-231	Sequence 231, App
874	17	0.7	2562	2	US-08-487-797-8	Sequence 8, Appl	947	17	0.7	9620	4	US-08-952-127-11	Sequence 11, Appl
875	17	0.7	2562	5	PCT-US95-02058-8	Sequence 8, Appl	c 948	17	0.7	9707	2	US-08-961-527-164	Sequence 164, App
876	17	0.7	2628	1	US-08-143-219-1	Sequence 1, Appl	c 949	17	0.7	10079	2	US-08-476-866-20	Sequence 20, Appl
877	17	0.7	2630	3	US-08-669-286-6	Sequence 6, Appl	c 950	17	0.7	10684	3	US-08-618-100B-3	Sequence 3, Appl
878	17	0.7	2630	4	US-08-469-233-6	Sequence 6, Appl	c 951	17	0.7	10898	2	US-08-481-658B-5	Sequence 5, Appl
879	17	0.7	2630	4	US-08-642-146-6	Sequence 6, Appl	c 952	17	0.7	10898	2	US-08-477-504A-5	Sequence 5, Appl
880	17	0.7	2680	2	US-08-533-306A-5	Sequence 5, Appl	c 953	17	0.7	10898	2	US-08-486-756A-5	Sequence 5, Appl
881	17	0.7	2680	2	US-08-742-923A-5	Sequence 5, Appl	c 954	17	0.7	10898	2	US-08-485-862B-5	Sequence 5, Appl
882	17	0.7	2682	4	US-09-020-465-1	Sequence 1, Appl	c 955	17	0.7	10898	3	US-08-787-739-5	Sequence 5, Appl
883	17	0.7	2719	3	US-08-706-216-1	Sequence 1, Appl	c 956	17	0.7	10898	3	US-08-487-077A-5	Sequence 5, Appl
884	17	0.7	2768	1	US-08-321-478-1	Sequence 1, Appl	c 957	17	0.7	10898	3	US-08-485-863A-5	Sequence 5, Appl
885	17	0.7	2768	1	US-08-321-478-3	Sequence 3, Appl	c 958	17	0.7	10898	4	US-08-485-049D-5	Sequence 5, Appl
886	17	0.7	2768	1	US-08-321-478-5	Sequence 5, Appl	c 959	17	0.7	10898	4	US-09-178-115-5	Sequence 5, Appl
887	17	0.7	2771	1	US-08-273-411-5	Sequence 5, Appl	c 960	17	0.7	11098	4	US-09-177-776-5	Sequence 5, Appl
888	17	0.7	2784	1	US-08-471-454-1	Sequence 1, Appl	c 961	17	0.7	11220	4	US-09-105-537-32	Sequence 32, Appl
889	17	0.7	2784	2	US-08-466-974-1	Sequence 1, Appl	962	17	0.7	11531	1	US-08-068-945A-1	Sequence 1, Appl
890	17	0.7	2784	2	US-08-471-453-1	Sequence 1, Appl	963	17	0.7	11531	1	US-08-442-806-1	Sequence 1, Appl
891	17	0.7	2813	4	US-09-689-255C-3	Sequence 3, Appl	964	17	0.7	12565	4	US-09-345-217-3	Sequence 3, Appl
892	17	0.7	2887	2	US-08-533-306A-3	Sequence 3, Appl	c 965	17	0.7	12847	1	US-08-550-715-1	Sequence 1, Appl
893	17	0.7	2887	2	US-08-742-923A-3	Sequence 3, Appl	966	17	0.7	14753	4	US-09-821-736-3	Sequence 3, Appl
894	17	0.7	2929	4	US-09-705-299-10	Sequence 10, Appl	c 967	17	0.7	16063	4	US-09-801-052-3	Sequence 3, Appl
895	17	0.7	3090	4	US-09-276-531-78	Sequence 78, Appl	968	17	0.7	16595	4	US-09-146-053-7	Sequence 7, Appl
896	17	0.7	3158	2	US-08-464-517-36	Sequence 36, Appl	c 969	17	0.7	18073	4	US-09-078-294-12	Sequence 12, Appl
897	17	0.7	3158	2	US-08-246-361A-36	Sequence 36, Appl	970	17	0.7	20598	4	US-09-593-995-10	Sequence 10, Appl
898	17	0.7	3158	3	US-08-463-772-36	Sequence 36, Appl	c 971	17	0.7	22846	2	US-08-469-461-3	Sequence 3, Appl
899	17	0.7	3195	2	US-08-951-648-5	Sequence 5, Appl	c 972	17	0.7	22846	3	US-07-890-609-3	Sequence 3, Appl
900	17	0.7	3195	3	US-09-174-437-5	Sequence 5, Appl	973	17	0.7	28994	3	US-08-884-324-14	Sequence 14, Appl
901	17	0.7	3267	2	US-08-257-963B-12	Sequence 12, Appl	c 974	17	0.7	36651	4	US-09-738-894A-3	Sequence 3, Appl
902	17	0.7	3267	4	US-08-367-841A-12	Sequence 12, Appl	c 975	17	0.7	36778	4	US-09-105-537-5	Sequence 5, Appl
903	17	0.7	3267	5	PCT-US95-07201-12	Sequence 12, Appl	c 976	17	0.7	38506	3	US-09-320-878-19	Sequence 19, Appl

c 977 17 0.7 38844 4 US-09-734-675-3  
c 978 17 0.7 51259 3 US-08-781-891-209  
c 979 17 0.7 55827 4 US-09-813-133A-3  
980 17 0.7 65042 4 US-08-784-316-3  
981 17 0.7 80161 3 US-09-036-987A-1  
982 17 0.7 80161 4 US-09-370-700-1  
983 17 0.7 98844 4 US-08-791-211-10  
c 984 17 0.7 4403765 4 US-09-103-840A-2  
c 985 17 0.7 4411529 4 US-09-103-840A-1  
986 16 0.7 19 1 US-08-487-759-1  
987 16 0.7 19 2 US-08-807-104-1  
988 16 0.7 19 2 US-08-807-104-4  
989 16 0.7 19 2 US-08-807-104-6  
990 16 0.7 19 2 US-08-807-104-7  
991 16 0.7 19 2 US-08-807-104-8  
992 16 0.7 19 2 US-08-807-104-9  
993 16 0.7 19 2 US-08-807-104-10  
994 16 0.7 19 2 US-08-807-104-13  
995 16 0.7 19 2 US-08-807-104-14  
996 16 0.7 19 2 US-08-807-104-15  
997 16 0.7 19 2 US-08-807-104-16  
998 16 0.7 19 3 US-08-973-139-1  
999 16 0.7 19 3 US-08-480-068-1  
1000 16 0.7 19 3 US-08-480-068-4

## ALIGNMENTS

RESULT 1  
US-08-781-891-79/c  
; Sequence 79, Application US/08781891  
; Patent No. 6090620  
; GENERAL INFORMATION:  
; APPLICANT: Fu, Ying-Hui  
; APPLICANT: Yu, Chang-En  
; APPLICANT: Oshima, Junko  
; APPLICANT: Mulligan, John T.  
; APPLICANT: Schellenberg, Gerald D.  
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO  
; TITLE OF INVENTION: WERNER'S SYNDROME  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781.891  
; FILING DATE: 27-DEC-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6090620tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 240052.419  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87350 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-781-891-79

Query Match 1.5%; Score 37; DB 3; Length 87350;  
Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGAGGGGAGGTTGCAGTGCAGCAAGATCAGCCACT 42  
Db 77833 GGAGGGGAGGTTGCAGTGCAGCAAGATCAGCCACT 77797

RESULT 2  
US-09-791-211-3/c  
; Sequence 3, Application US/09791211  
; Patent No. 6448080  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION  
; FILE REFERENCE: RTS-0205  
; CURRENT APPLICATION NUMBER: US/09/791.211  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 3  
; LENGTH: 87543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 7421  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
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; LOCATION: 33095

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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; LOCATION: 68733
; OTHER INFORMATION: unknown

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; NAME/KEY: unsure
; LOCATION: 68739
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; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-3

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Query Match      1.5%; Score 37; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      6 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
Db      78026 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 77990

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RESULT 3
US-09-798-096-10
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

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Query Match      1.5%; Score 37; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      6 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 42
Db      55180 GGAGGGGAGGTTGCAGTGAGCCCAAGATCAGCCCACT 55216

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RESULT 4
US-09-729-995-3/c
; Sequence 3, Application US/09729995
; Patent No. 6428206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human

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## US-09-729-995-3

Query Match 1.5%; Score 35; DB 4; Length 29629;  
Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGAGGTTGCAGTGGCCGAAGATCAGCCACTACAC 46  
|||||

Db 2123 GGAGGTTGCAGTGGCCGAAGATCAGCCACTACAC 2089  
|||||

## RESULT 5

## US-09-345-982-1

; Sequence 1, Application US/09345882

; Patent No. 6399373

; GENERAL INFORMATION:

; APPLICANT: Bougueleret, Lydie

; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)

; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

; FILE REFERENCE: GENSET.031A

; CURRENT APPLICATION NUMBER: US/09/345.882

; CURRENT FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: US 60/091,315

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/111,909

; PRIOR FILING DATE: 1998-12-10

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: Patent.pm

; SEQ ID NO 1

; LENGTH: 162450

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 72794

; OTHER INFORMATION: 5-124-273 : polymorphic base A or G

; FEATURE:

; NAME/KEY: allele

; LOCATION: 88073

; OTHER INFORMATION: 5-127-261 : polymorphic base A or C

; FEATURE:

; NAME/KEY: allele

; LOCATION: 90842

; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G

; FEATURE:

; NAME/KEY: allele

; LOCATION: 93714

; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT

; FEATURE:

; NAME/KEY: allele

; LOCATION: 97122

; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T

; FEATURE:

; NAME/KEY: allele

; LOCATION: 97152

; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T

; FEATURE:

; NAME/KEY: allele

; LOCATION: 99098

; OTHER INFORMATION: 5-130-257 : polymorphic base A or G

; FEATURE:

; NAME/KEY: allele

; LOCATION: 99117

; OTHER INFORMATION: 5-130-276 : polymorphic base A or G

; FEATURE:

; NAME/KEY: allele

; LOCATION: 103806

; OTHER INFORMATION: 5-131-395 : polymorphic base A or T

; FEATURE:

; NAME/KEY: allele

; LOCATION: 106940

; OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A

; FEATURE:

; NAME/KEY: allele  
; LOCATION: 108106  
; OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A  
; FEATURE:  
; LOCATION: 108149  
; OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 108308  
; OTHER INFORMATION: 5-135-357 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 108471  
; OTHER INFORMATION: 5-136-174 : polymorphic base C or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 134134  
; OTHER INFORMATION: 5-140-120 : polymorphic base C or T  
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; NAME/KEY: allele  
; LOCATION: 134362  
; OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A  
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; NAME/KEY: allele  
; LOCATION: 134374  
; OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 146328  
; OTHER INFORMATION: 5-143-84 : polymorphic base A or G  
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; NAME/KEY: allele  
; LOCATION: 146345  
; OTHER INFORMATION: 5-143-101 : polymorphic base A or C  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 150329  
; OTHER INFORMATION: 5-145-24 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 160031  
; OTHER INFORMATION: 5-148-352 : polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 72771..72817  
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 72771..72817  
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51  
; FEATURE:  
; NAME/KEY: allele  
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; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52  
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; NAME/KEY: allele  
; LOCATION: 90819..90865  
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70  
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; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32  
; FEATURE:  
; NAME/KEY: allele

LOCATION: 93690..93736  
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NAME/KEY: allele  
LOCATION: 97099..97145  
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50  
FEATURE:  
NAME/KEY: allele  
LOCATION: 97099..97145  
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71  
FEATURE:  
NAME/KEY: allele  
LOCATION: 97130..97177  
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33  
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OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54  
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OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34  
FEATURE:  
NAME/KEY: allele  
LOCATION: 99075..99121  
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55  
FEATURE:  
NAME/KEY: allele  
LOCATION: 99094..99140  
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35  
FEATURE:  
NAME/KEY: allele  
LOCATION: 99094..99140  
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56  
FEATURE:  
NAME/KEY: allele  
LOCATION: 103783..103828  
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36  
FEATURE:  
NAME/KEY: allele  
LOCATION: 103783..103828  
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57  
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NAME/KEY: allele  
LOCATION: 106918..106966  
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37  
FEATURE:  
NAME/KEY: allele  
LOCATION: 106918..106966  
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108084..108130  
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108084..108130  
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108127..108177  
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108127..108177  
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60  
FEATURE:

Query Match 1.5%; Score 35; DB 4; Length 162450;  
Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 6 GGAGCGGAGGTTGCAGTGAGCCAAGATCACGCCA 40

Db 29125 GGAGCGGAGGTTGCAGTGAGCCAAGATCACGCCA 29159  
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RESULT 6  
US-08-827-208-1/c  
; Sequence 1, Application US/08827208  
; Patent No. 6025178  
; GENERAL INFORMATION:  
; APPLICANT: Chiou, Xue-Chiou C.  
; APPLICANT: Kramer, Ruth M.  
; APPLICANT: Pickard, Richard T.  
; APPLICANT: Sharp, John D.  
; APPLICANT: Striffler, Beth A.  
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; APPLICATION NUMBER: US/08/827,208  
; FILING DATE: 28-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/014,608  
; FILING DATE: 29-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/041,264  
; FILING DATE: 19-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-10610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8517 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 1611..2063  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 5315..6045  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 6143..6758  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 7075..7317  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 7473..8499  
; US-08-827-208-1

Query Match 1.4%; Score 34; DB 3; Length 8517;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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; LOCATION: 7473..8499
US-09-498-809-1
Query Match      1.4%; Score 34; DB 4; Length 8517;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCGGAGGTTGTCAGTGAGCCCAAGATCACGCCCA 40
Db 6091 GAGCGGAGGTTGTCAGTGAGCCCAAGATCACGCCCA 6058

RESULT 9
US-09-900-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: THEREOF
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01158
; CURRENT APPLICATION NUMBER: US/09/800,960
; EARLIER FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match      1.3%; Score 32; DB 4; Length 62804;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 36
Db 43316 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 43285

RESULT 10
US-09-211-417-2/c
; Sequence 2, Application US/09211417A
; Patent No. 6177254
; GENERAL INFORMATION:
; APPLICANT: Rattner, Jerome B
; APPLICANT: Whitehead, Clark M
; TITLE OF INVENTION: NUCLEOLUS AUTOANTIGENIC MARKER FOR SYSTEMIC LUPUS
; TITLE OF INVENTION: ERHYMATOSUS
; TITLE OF INVENTION: GenBank
; FILE REFERENCE: UCC1
; CURRENT APPLICATION NUMBER: US/09/211,417A
; EARLIER FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Sequence of ASE-1
; Patent No. 6177254
US-09-211-417-2

Query Match      1.3%; Score 31; DB 4; Length 3286;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 6 GGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 36
Db 2795 GGAGCGGAGGTTGTCAGTGAGCCCAAGATCAC 2765

RESULT 11
US-09-166-350-32
; Sequence 32, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: Uses Therefor
; TITLE OF INVENTION: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 4169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-32

Query Match      1.3%; Score 31; DB 4; Length 4169;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCA 35
Db 3831 GGGAGCGGAGGTTGTCAGTGAGCCCAAGATCA 3861

RESULT 12
US-09-422-936-60/c
; Sequence 60, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 15652
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(15652)
; OTHER INFORMATION: n = A, T, G, or C
; NAME/KEY: misc_feature
; LOCATION: (1)...(15652)
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OTHER INFORMATION: r = G or A; y = T/U or C; m = A or C;  
OTHER INFORMATION: k = G or T/U; s = G or C; w = A or T/U;  
OTHER INFORMATION: b = A, C, or T/U; d = A, G, or T/U;  
OTHER INFORMATION: h = A, C, or T/U; v = A, G, or C

NAME/KEY: exon

LOCATION: (3419)...(3444)

NAME/KEY: intron

LOCATION: (3445)...(3908)

NAME/KEY: exon

LOCATION: (3909)...(3993)

NAME/KEY: intron

LOCATION: (3994)...(4694)

NAME/KEY: exon

LOCATION: (4695)...(4898)

NAME/KEY: intron

LOCATION: (4899)...(5652)

NAME/KEY: exon

LOCATION: (5653)...(5838)

NAME/KEY: intron

LOCATION: (5839)...(7184)

NAME/KEY: exon

LOCATION: (7185)...(7205)

NAME/KEY: intron

LOCATION: (7206)...(8310)

NAME/KEY: exon

LOCATION: (8311)...(8806)

NAME/KEY: intron

LOCATION: (8807)...(12271)

NAME/KEY: exon

LOCATION: (12272)...(12406)

NAME/KEY: intron

LOCATION: (12407)...(12820)

NAME/KEY: exon

LOCATION: (12821)...(12991)

NAME/KEY: intron

LOCATION: (12992)...(14089)

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LOCATION: (14192)...(14477)

NAME/KEY: exon

LOCATION: (14478)...(14543)

NAME/KEY: intron

LOCATION: (14544)...(15002)

NAME/KEY: exon

LOCATION: (15003)...(15194)

NAME/KEY: intron

LOCATION: (15195)...(15652)

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LOCATION: (15653)...(15652)

NAME/KEY: exon

LOCATION: (15653)...(15652)

SEQ ID NO 3

LENGTH: 17138

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(17138)

OTHER INFORMATION: n = A, T, C or G

US-09-813-819-3

Query Match 1.3%; Score 31; DB 4; Length 17138;

Best Local Similarity 100.0%; Pred. No. 4.3e-05;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGAGTTGCAGTGAGCCCAAGATCAGCCCACT 42

Db 189 GGAGTTGCAGTGAGCCCAAGATCAGCCCACT 159

RESULT 14

US-09-920-048-3/c

Sequence 3, Application US/09920048

Patent No. 6344352

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001177DIV

CURRENT APPLICATION NUMBER: US/09/920,048

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/813,819

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 17138

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(17138)

OTHER INFORMATION: n = A, T, C or G

Query Match 1.3%; Score 31; DB 4; Length 17138;

Best Local Similarity 100.0%; Pred. No. 4.3e-05;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGAGTTGCAGTGAGCCCAAGATCAGCCCACT 42

Db 189 GGAGTTGCAGTGAGCCCAAGATCAGCCCACT 159

RESULT 15

US-09-734-673-3/c

Sequence 3, Application US/09734673

Patent No. 6410294

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001020

CURRENT APPLICATION NUMBER: US/09/734,673

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 38564

TYPE: DNA

ORGANISM: Human

FEATURE:

OTHER INFORMATION: r = G or A; y = T/U or C; m = A or C;  
OTHER INFORMATION: k = G or T/U; s = G or C; w = A or T/U;  
OTHER INFORMATION: b = A, C, or T/U; d = A, G, or T/U;  
OTHER INFORMATION: h = A, C, or T/U; v = A, G, or C

NAME/KEY: exon

LOCATION: (3419)...(3444)

NAME/KEY: intron

LOCATION: (3445)...(3908)

NAME/KEY: exon

LOCATION: (3909)...(3993)

NAME/KEY: intron

LOCATION: (3994)...(4694)

NAME/KEY: exon

LOCATION: (4695)...(4898)

NAME/KEY: intron

LOCATION: (4899)...(5652)

NAME/KEY: exon

LOCATION: (5653)...(5838)

NAME/KEY: intron

LOCATION: (5839)...(7184)

NAME/KEY: exon

LOCATION: (7185)...(7205)

NAME/KEY: intron

LOCATION: (7206)...(8310)

NAME/KEY: exon

LOCATION: (8311)...(8806)

NAME/KEY: intron

LOCATION: (8807)...(12271)

NAME/KEY: exon

LOCATION: (12272)...(12406)

NAME/KEY: intron

LOCATION: (12407)...(12820)

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LOCATION: (12992)...(14089)

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LOCATION: (15195)...(15652)

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NAME/KEY: exon

LOCATION: (15653)...(15652)

NAME/KEY: intron

LOCATION: (15653)...(15652)

NAME/KEY: exon

LOCATION: (15653)...(15652)

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; NAME/KEY: misc_feature
; LOCATION: (1)...(38564)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3

Query Match      1.3%; Score 31; DB 4; Length 38564;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      32975 GGGAGGGGGAGGTTGCAGTGAGCCCAAGATCA 32945
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Job time : 119.105 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 254.144 Seconds  
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13697.491 Million cell updates/sec

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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	193	8.0	475	9	US-09-918-995-29121
2	39	1.6	30350	9	US-10-118-328-3
3	39	1.6	397658	10	US-09-813-320-3
4	38	1.6	438	10	US-09-867-701-8927
5	38	1.6	449	10	US-09-867-701-4634
6	38	1.6	455	9	US-09-918-995-24949
7	38	1.6	9883	9	US-10-016-157A-71
8	38	1.6	15857	10	US-09-764-864-1704
9	38	1.6	16225	9	US-10-079-854-370
10	38	1.6	16225	9	US-09-764-891-9432
11	38	1.6	16225	10	US-09-764-878-370
12	38	1.6	18657	9	US-10-074-045-70
13	38	1.6	32195	9	US-09-764-891-8668
14	38	1.6	45839	12	US-10-025-187-3
15	38	1.6	62944	10	US-09-954-456-2257
16	38	1.6	175561	9	US-10-017-721-3
17	38	1.6	397658	10	US-09-813-320-3
18	37	1.5	89	9	US-09-764-891-9583
19	37	1.5	245	9	US-10-040-739-1286

20	37	1.5	248	9	US-10-092-154-1741	Sequence 1741, Ap
21	37	1.5	248	10	US-09-764-847-1741	Sequence 1741, Ap
22	37	1.5	563	9	US-09-918-995-11202	Sequence 11202, A
23	37	1.5	2147	9	US-10-092-154-1738	Sequence 1738, Ap
24	37	1.5	2147	10	US-09-764-847-1738	Sequence 1738, Ap
25	37	1.5	2854	9	US-09-764-891-8205	Sequence 8205, Ap
26	37	1.5	3271	9	US-09-764-891-8206	Sequence 8206, Ap
27	37	1.5	11991	9	US-09-764-891-9893	Sequence 9893, Ap
28	37	1.5	11991	10	US-09-764-877-2942	Sequence 2942, Ap
29	37	1.5	15366	9	US-10-074-095-1057	Sequence 1057, Ap
30	37	1.5	15366	10	US-09-764-860-1057	Sequence 1057, Ap
31	37	1.5	28690	9	US-10-010-802-1	Sequence 1, Appli
32	37	1.5	30350	9	US-10-118-328-3	Sequence 3, Appli
33	36	1.5	493	9	US-09-764-891-1697	Sequence 1697, Ap
34	36	1.5	506	9	US-10-092-154-1626	Sequence 1626, Ap
35	36	1.5	506	10	US-09-764-847-1626	Sequence 1626, Ap
36	36	1.5	692	9	US-09-764-891-2627	Sequence 2627, Ap
37	36	1.5	1351	9	US-09-764-891-8391	Sequence 8391, Ap
38	36	1.5	1430	9	US-09-764-891-10178	Sequence 10178, A
39	36	1.5	1655	10	US-09-764-877-2361	Sequence 2361, Ap
40	35	1.5	318	10	US-09-867-701-3011	Sequence 3011, Ap
41	35	1.5	477	9	US-09-918-995-11218	Sequence 11218, A
42	35	1.5	488	9	US-09-918-995-11210	Sequence 11210, A
43	35	1.5	620	9	US-10-198-846-5084	Sequence 5084, Ap
44	35	1.5	5257	9	US-10-171-581-63	Sequence 63, Appli
45	35	1.5	8911	10	US-09-764-853-895	Sequence 895, Appli
46	35	1.5	29629	12	US-10-135-689-3	Sequence 3, Appli
47	35	1.5	32082	9	US-09-764-891-9679	Sequence 9679, Ap
48	35	1.5	32184	9	US-09-764-891-8538	Sequence 8538, Ap
49	35	1.5	32204	9	US-09-764-891-8537	Sequence 8537, Ap
50	35	1.5	106344	9	US-09-910-185-10	Sequence 10, Appli
51	34	1.4	5629	9	US-10-092-154-1162	Sequence 1162, Ap
52	34	1.4	6265	9	US-10-092-154-1161	Sequence 1161, Ap
53	34	1.4	6265	10	US-09-764-847-1161	Sequence 1161, Ap
54	34	1.4	48841	9	US-09-844-653-32	Sequence 32, Appli
55	34	1.4	170834	10	US-09-835-232-7	Sequence 7, Appli
56	34	1.4	302250	10	US-09-962-832-154	Sequence 154, App
57	34	1.4	15295	10	US-09-764-877-3404	Sequence 3404, Ap
58	33	1.4	15295	10	US-09-967-768A-314	Sequence 314, App
59	33	1.4	17424	10	US-09-867-701-9905	Sequence 9905, Ap
60	32	1.3	338	10	US-09-867-701-8173	Sequence 8173, Ap
61	32	1.3	414	10	US-09-867-701-8173	Sequence 8173, Ap
62	32	1.3	449	10	US-09-867-701-8942	Sequence 8942, Ap
63	32	1.3	455	10	US-09-867-701-6589	Sequence 6589, Ap
64	32	1.3	485	9	US-09-918-995-2090	Sequence 2090, Ap
65	32	1.3	1669	9	US-09-892-877-24	Sequence 24, Appli
66	32	1.3	1669	9	US-09-948-783-25	Sequence 25, Appli
67	32	1.3	2571	10	US-09-764-877-2215	Sequence 2215, Ap
68	32	1.3	2571	10	US-09-764-877-2216	Sequence 2216, Ap
69	32	1.3	2571	10	US-09-764-877-2217	Sequence 2217, Ap
70	32	1.3	2892	9	US-10-079-854-197	Sequence 197, App
71	32	1.3	2892	9	US-09-764-878-197	Sequence 197, App
72	32	1.3	3351	9	US-10-092-154-1138	Sequence 1138, Ap
73	32	1.3	3351	10	US-09-764-847-1138	Sequence 1138, Ap
74	32	1.3	5632	9	US-09-764-891-7395	Sequence 7395, Ap
75	32	1.3	6295	9	US-10-163-866-9	Sequence 8, Appli
76	32	1.3	6296	9	US-10-163-866-9	Sequence 9, Appli
77	32	1.3	13315	9	US-10-079-854-328	Sequence 328, App
78	32	1.3	13315	10	US-09-764-878-328	Sequence 328, App
79	32	1.3	13409	9	US-09-764-891-9601	Sequence 9601, App
80	32	1.3	14718	9	US-09-764-891-5981	Sequence 5981, Ap
81	32	1.3	16062	9	US-09-764-891-8047	Sequence 8047, Ap
82	32	1.3	19696	9	US-10-091-572-874	Sequence 874, App
83	32	1.3	19696	9	US-09-764-891-9327	Sequence 9327, App
84	32	1.3	20261	9	US-10-079-854-325	Sequence 325, App
85	32	1.3	20261	10	US-09-764-878-325	Sequence 325, App
86	32	1.3	27154	9	US-09-764-891-8396	Sequence 8396, Ap
87	32	1.3	31168	9	US-09-764-868-1464	Sequence 1464, Ap
88	32	1.3	31813	9	US-09-764-891-9685	Sequence 9685, Ap
89	32	1.3	53000	9	US-09-953-611-10	Sequence 10, Appli
90	32	1.3	60153	9	US-10-222-334-7	Sequence 7, Appli
91	32	1.3	62804	12	US-10-096-960-3	Sequence 3, Appli
92	32	1.3	143306	10	US-09-729-920-3	Sequence 3, Appli

c 93	32	1.3	167343	10	US-09-962-436-281	Sequence 281, App	c 166	31	1.3	46718	10	US-09-816-093-3	Sequence 3, Appli
c 94	32	1.3	167343	10	US-09-964-824A-273	Sequence 273, App	167	31	1.3	53542	10	US-09-801-574-61	Sequence 61, Appl
c 95	32	1.3	174566	9	US-10-020-141-1	Sequence 1, Appli	168	31	1.3	62944	10	US-09-954-456-2257	Sequence 2257, Ap
c 96	32	1.3	368004	10	US-09-949-654-3	Sequence 3, Appli	169	31	1.3	75270	9	US-09-790-852-1	Sequence 1, Appli
c 97	32	1.3	402850	9	US-09-844-653-5	Sequence 5, Appli	c 170	31	1.3	81001	10	US-09-842-364-1	Sequence 1, Appli
c 98	31	1.3	114	9	US-10-125-540-610	Sequence 610, App	c 171	31	1.3	81001	10	US-09-751-877-1	Sequence 1542, Ap
c 99	31	1.3	114	10	US-09-764-870-610	Sequence 610, App	c 172	31	1.3	110096	10	US-09-880-107-1542	Sequence 3, Appli
c 100	31	1.3	146	10	US-10-091-504-1389	Sequence 1389, App	c 173	31	1.3	116592	10	US-09-818-512-3	Sequence 3, Appli
c 101	31	1.3	146	10	US-09-764-869-1389	Sequence 1389, App	c 174	31	1.3	116840	9	US-10-020-141-3	Sequence 11, Appl
c 102	31	1.3	159	9	US-09-764-872-544	Sequence 544, App	c 175	31	1.3	139257	9	US-09-920-671-11	Sequence 79, Appl
c 103	31	1.3	410	9	US-09-918-995-13769	Sequence 13769, A	c 176	31	1.3	145831	10	US-09-969-708-79	Sequence 2116, Ap
c 104	31	1.3	436	10	US-09-867-701-429	Sequence 429, App	c 177	31	1.3	145831	10	US-09-954-456-2116	Sequence 16, Appl
c 105	31	1.3	456	9	US-09-918-995-28012	Sequence 28012, A	c 178	31	1.3	152331	9	US-10-095-407-16	Sequence 7, Appli
c 106	31	1.3	510	9	US-10-138-846-13421	Sequence 13421, A	c 179	31	1.3	170834	10	US-09-835-232-7	Sequence 3, Appli
c 107	31	1.3	525	9	US-09-918-995-31520	Sequence 31520, A	c 180	31	1.3	174493	9	US-10-238-709-3	Sequence 3, Appli
c 108	31	1.3	528	9	US-09-918-995-31523	Sequence 31523, A	c 181	31	1.3	174493	10	US-09-804-471A-3	Sequence 3, Appli
c 109	31	1.3	860	9	US-10-138-846-6751	Sequence 6751, App	c 182	31	1.3	176373	9	US-10-095-407-17	Sequence 17, Appl
c 110	31	1.3	2194	9	US-09-764-891-7481	Sequence 7481, App	c 183	31	1.3	203654	10	US-09-820-905-3	Sequence 3, Appli
c 111	31	1.3	2195	9	US-09-764-891-7482	Sequence 7482, App	c 184	31	1.3	235033	9	US-10-301-844-1	Sequence 1, Appli
c 112	31	1.3	2197	9	US-09-764-891-7483	Sequence 7483, App	c 185	31	1.3	237326	9	US-10-301-844-2	Sequence 2, Appli
c 113	31	1.3	3045	10	US-09-354-456-218	Sequence 218, App	c 186	31	1.3	465237	10	US-09-933-267A-1	Sequence 1, Appli
c 114	31	1.3	3045	10	US-09-880-107-2319	Sequence 2319, App	c 187	31	1.3	1503841	9	US-09-946-807-1	Sequence 1, Appli
c 115	31	1.3	3593	9	US-09-764-891-10220	Sequence 10220, A	c 188	31	1.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 116	31	1.3	4025	10	US-09-764-877-2340	Sequence 2340, App	c 189	31	1.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 117	31	1.3	4025	10	US-09-764-877-2343	Sequence 2343, App	c 190	30	1.2	107	9	US-09-764-891-7423	Sequence 7423, Ap
c 118	31	1.3	4025	10	US-09-764-877-2345	Sequence 2345, App	c 191	30	1.2	107	9	US-09-764-891-7426	Sequence 7426, Ap
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c 127	31	1.3	12149	10	US-09-764-869-2258	Sequence 2258, App	c 200	30	1.2	351	9	US-09-803-719-715	Sequence 715, App
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c 134	31	1.3	15531	9	US-10-125-540-600	Sequence 600, App	c 207	30	1.2	482	10	US-09-867-701-8803	Sequence 8803, Ap
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c 138	31	1.3	19125	10	US-09-764-877-2805	Sequence 2805, App	c 211	30	1.2	574	10	US-09-954-456-1482	Sequence 1482, Ap
c 139	31	1.3	19740	9	US-10-142-356-3	Sequence 3, Appli	c 212	30	1.2	586	9	US-10-091-504-2281	Sequence 2281, Ap
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c 141	31	1.3	21358	9	US-09-764-872-816	Sequence 816, App	c 214	30	1.2	593	9	US-10-091-504-2278	Sequence 2278, Ap
c 142	31	1.3	21358	9	US-09-764-872-816	Sequence 816, App	c 215	30	1.2	593	9	US-10-091-504-2280	Sequence 2280, Ap
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c 147	31	1.3	23645	9	US-09-860-670-264	Sequence 264, App	c 220	30	1.2	1002	9	US-09-764-891-9626	Sequence 9626, Ap
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c 151	31	1.3	26995	9	US-10-079-854-227	Sequence 227, App	c 224	30	1.2	1432	9	US-09-764-891-9623	Sequence 9623, Ap
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c 157	31	1.3	31871	10	US-09-764-847-1403	Sequence 255, App	c 230	30	1.2	1946	9	US-10-037-270-462	Sequence 462, App
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c 159	31	1.3	32195	10	US-10-091-504-2017	Sequence 2017, App	c 232	30	1.2	2109	9	US-10-072-349-325	Sequence 325, App
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c 163	31	1.3	32249	9	US-09-860-670-260	Sequence 260, App	c 236	30	1.2	3270	10	US-09-764-864-1691	Sequence 1691, Ap
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c 165	31	1.3	46718	9	US-10-274-873-3	Sequence 3, Appli	c 238	30	1.2	4837	10	US-09-764-877-2839	Sequence 2839, Ap

239	30	1.2	4963	9	US-10-135-540-606	Sequence 606, App	312	30	1.2	32193	10	US-09-764-878-200	Sequence 200, App
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c 247	30	1.2	6040	10	US-09-764-860-1029	Sequence 1029, Ap	c 320	30	1.2	52216	9	US-09-747-810-1	Sequence 1, Appli
c 248	30	1.2	6284	10	US-09-764-877-3643	Sequence 3643, Ap	c 321	30	1.2	64467	9	US-10-274-409-3	Sequence 3, Appli
c 249	30	1.2	6461	9	US-10-125-540-546	Sequence 546, App	c 322	30	1.2	65608	9	US-09-954-531-180	Sequence 180, App
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c 264	30	1.2	11337	10	US-09-764-877-2651	Sequence 2651, Ap	c 337	30	1.2	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 265	30	1.2	11618	9	US-09-764-891-9890	Sequence 9890, Ap	c 338	30	1.2	1503841	10	US-09-795-668-1	Sequence 1, Appli
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c 269	30	1.2	12452	10	US-09-764-877-3989	Sequence 3989, Ap	c 342	29	1.2	143	10	US-09-764-847-1676	Sequence 1676, Ap
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c 274	30	1.2	13824	10	US-09-764-877-3492	Sequence 3492, Ap	c 347	29	1.2	167	9	US-09-764-891-6593	Sequence 6593, Ap
c 275	30	1.2	14040	9	US-09-764-891-5478	Sequence 5478, Ap	c 348	29	1.2	167	9	US-09-764-891-6594	Sequence 6594, Ap
c 276	30	1.2	14040	9	US-09-764-891-10205	Sequence 10205, A	c 349	29	1.2	201	12	US-10-033-528-1856	Sequence 1856, Ap
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c 284	30	1.2	15843	9	US-10-091-504-2396	Sequence 2396, Ap	c 357	29	1.2	388	10	US-09-925-302-360	Sequence 360, App
c 285	30	1.2	15843	10	US-09-764-869-2396	Sequence 2396, Ap	c 358	29	1.2	401	9	US-09-946-807-121	Sequence 121, App
c 286	30	1.2	16057	9	US-10-091-504-1435	Sequence 1435, Ap	c 359	29	1.2	401	9	US-09-946-807-1471	Sequence 1471, Ap
c 287	30	1.2	16057	10	US-09-764-869-1435	Sequence 1435, Ap	c 360	29	1.2	401	10	US-09-795-668-121	Sequence 121, App
c 288	30	1.2	16086	10	US-09-764-877-2385	Sequence 2385, Ap	c 361	29	1.2	401	10	US-09-795-668-1471	Sequence 1471, Ap
c 289	30	1.2	16181	9	US-10-092-154-1426	Sequence 1426, Ap	c 362	29	1.2	401	10	US-09-795-686-121	Sequence 121, App
c 290	30	1.2	16181	9	US-09-764-891-6956	Sequence 6956, Ap	c 363	29	1.2	401	10	US-09-795-686-1471	Sequence 1471, Ap
c 291	30	1.2	16181	10	US-09-764-847-1426	Sequence 1426, Ap	c 364	29	1.2	403	9	US-09-946-807-1470	Sequence 1470, Ap
c 292	30	1.2	16774	9	US-10-091-504-2395	Sequence 2395, Ap	c 365	29	1.2	403	9	US-09-946-807-1472	Sequence 1472, Ap
c 293	30	1.2	16774	10	US-10-091-504-2398	Sequence 2398, Ap	c 366	29	1.2	403	10	US-09-795-668-1470	Sequence 1470, Ap
c 294	30	1.2	16774	10	US-09-764-869-2395	Sequence 2395, Ap	c 367	29	1.2	403	10	US-09-795-668-1472	Sequence 1472, Ap
c 295	30	1.2	16774	10	US-09-764-869-2398	Sequence 2398, Ap	c 368	29	1.2	403	10	US-09-795-686-1470	Sequence 1470, Ap
c 296	30	1.2	17000	9	US-10-073-961-467	Sequence 467, App	c 369	29	1.2	403	10	US-09-795-686-1472	Sequence 1472, Ap
c 297	30	1.2	17000	10	US-09-764-887-467	Sequence 467, App	c 370	29	1.2	438	9	US-10-198-846-2733	Sequence 2733, Ap
c 298	30	1.2	17286	10	US-09-764-877-3234	Sequence 3234, Ap	c 371	29	1.2	442	9	US-09-764-891-8331	Sequence 8331, Ap
c 299	30	1.2	17538	10	US-09-893-348-9	Sequence 9, Appli	c 372	29	1.2	443	9	US-09-764-891-8332	Sequence 8332, Ap
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c 302	30	1.2	30568	10	US-09-764-877-3851	Sequence 3851, Ap	c 375	29	1.2	463	9	US-10-198-846-10846	Sequence 10846, A
c 303	30	1.2	31814	10	US-09-817-182-3	Sequence 3, Appli	c 376	29	1.2	470	9	US-09-764-891-8941	Sequence 8941, Ap
c 304	30	1.2	32167	9	US-09-764-891-8197	Sequence 8197, Ap	c 377	29	1.2	617	9	US-10-060-031-2606	Sequence 2606, Ap
c 305	30	1.2	32188	9	US-10-074-095-799	Sequence 799, App	c 378	29	1.2	683	9	US-10-232-803-19	Sequence 19, Appl
c 306	30	1.2	32188	10	US-09-764-860-799	Sequence 799, App	c 379	29	1.2	761	9	US-09-986-480-101	Sequence 101, App
c 307	30	1.2	32190	9	US-10-079-854-201	Sequence 201, App	c 380	29	1.2	818	9	US-10-198-846-6587	Sequence 6587, Ap
c 308	30	1.2	32190	10	US-09-764-878-201	Sequence 201, App	c 381	29	1.2	830	9	US-10-198-846-4206	Sequence 4206, Ap
c 309	30	1.2	32192	9	US-09-764-891-9791	Sequence 9791, Ap	c 382	29	1.2	837	9	US-10-198-846-6650	Sequence 6650, Ap
c 310	30	1.2	32192	10	US-09-764-877-3657	Sequence 3657, Ap	c 383	29	1.2	879	10	US-09-764-853-13	Sequence 13, Appl
c 311	30	1.2	32193	9	US-10-079-854-200	Sequence 200, App	c 384	29	1.2	884	9	US-10-198-846-4038	Sequence 4038, Ap

c 385	29	1.2	886	9	US-10-198-846-1423	Sequence 1423, Ap	458	29	1.2	2336	9	US-10-123-909-383	Sequence 383, App
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c 387	29	1.2	889	9	US-10-198-846-12070	Sequence 12070, A	460	29	1.2	2336	9	US-10-124-813-383	Sequence 383, App
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c 391	29	1.2	1180	10	US-09-764-860-809	Sequence 809, App	464	29	1.2	2336	9	US-10-125-924-383	Sequence 383, App
c 392	29	1.2	1257	9	US-10-074-095-996	Sequence 996, App	465	29	1.2	2336	9	US-10-127-825A-383	Sequence 383, App
c 393	29	1.2	1257	10	US-09-764-860-996	Sequence 996, App	466	29	1.2	2336	9	US-10-127-829A-383	Sequence 383, App
c 394	29	1.2	1848	9	US-09-989-920-111	Sequence 111, App	467	29	1.2	2336	9	US-10-127-835A-383	Sequence 383, App
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c 396	29	1.2	1990	10	US-09-764-847-1675	Sequence 1675, Ap	469	29	1.2	2336	9	US-10-127-901A-383	Sequence 383, App
c 397	29	1.2	2169	9	US-10-098-841-266	Sequence 266, App	470	29	1.2	2336	9	US-10-128-693A-383	Sequence 383, App
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c 401	29	1.2	2336	9	US-09-978-192A-144	Sequence 144, App	474	29	1.2	2336	9	US-10-131-824A-383	Sequence 383, App
c 402	29	1.2	2336	9	US-09-999-832A-144	Sequence 144, App	475	29	1.2	2336	9	US-10-131-830A-383	Sequence 383, App
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c 410	29	1.2	2336	9	US-10-176-918-383	Sequence 383, App	483	29	1.2	2336	9	US-10-147-517-383	Sequence 383, App
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558	29	1.2	2336	9	US-10-158-785-383	Sequence 383, App	c 631	29	1.2	16100	10	US-09-764-877-3698	Sequence 3698, Ap
559	29	1.2	2336	9	US-09-978-187B-144	Sequence 144, App	c 632	29	1.2	16825	9	US-10-092-154-1495	Sequence 1495, Ap
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561	29	1.2	2336	9	US-10-123-812-383	Sequence 383, App	c 634	29	1.2	17431	9	US-10-072-349-247	Sequence 247, App
562	29	1.2	2336	9	US-09-978-643A-144	Sequence 144, App	c 635	29	1.2	17431	10	US-09-764-855-247	Sequence 247, App
563	29	1.2	2336	9	US-10-166-709A-144	Sequence 144, App	c 636	29	1.2	17538	10	US-09-893-348-9	Sequence 9, Appli
564	29	1.2	2336	9	US-10-192-007-383	Sequence 383, App	c 637	29	1.2	17601	9	US-09-764-891-7111	Sequence 7111, Ap
565	29	1.2	2336	9	US-10-194-359-383	Sequence 383, App	c 638	29	1.2	17787	9	US-09-764-868-1285	Sequence 1285, Ap
566	29	1.2	2338	9	US-10-037-270-411	Sequence 411, App	c 639	29	1.2	17787	9	US-09-764-868-1285	Sequence 1285, Ap
567	29	1.2	2584	9	US-10-198-846-13670	Sequence 13670, A	c 640	29	1.2	17787	9	US-09-764-891-5648	Sequence 5648, Ap
568	29	1.2	2916	9	US-09-822-846-249	Sequence 249, App	c 641	29	1.2	17787	9	US-09-764-891-5648	Sequence 5648, Ap
569	29	1.2	3144	9	US-10-163-866-31	Sequence 31, Appl	c 642	29	1.2	17787	9	US-09-764-891-6051	Sequence 6051, Ap
570	29	1.2	3895	9	US-10-011-585A-76	Sequence 76, Appl	c 643	29	1.2	17787	9	US-09-764-891-6051	Sequence 6051, Ap
571	29	1.2	4108	10	US-09-883-096-1	Sequence 1, Appli	c 644	29	1.2	17792	9	US-10-091-504-1599	Sequence 1599, Ap
572	29	1.2	4242	12	US-10-044-090-190	Sequence 190, App	c 645	29	1.2	17792	10	US-09-764-869-1599	Sequence 1599, Ap
573	29	1.2	4440	9	US-09-981-353-132	Sequence 132, App	c 646	29	1.2	18820	9	US-09-764-891-6452	Sequence 6452, Ap
574	29	1.2	4660	9	US-10-091-504-1572	Sequence 1572, App	c 647	29	1.2	18981	9	US-09-764-891-7649	Sequence 7649, Ap
575	29	1.2	4660	10	US-09-764-869-1572	Sequence 1572, Ap	c 648	29	1.2	19553	9	US-10-092-154-1425	Sequence 1425, Ap
576	29	1.2	4963	10	US-09-764-877-2903	Sequence 2903, Ap	c 649	29	1.2	19553	10	US-09-764-847-1425	Sequence 1425, Ap
577	29	1.2	5156	10	US-09-764-877-3945	Sequence 3945, Ap	c 650	29	1.2	21724	10	US-09-764-864-1603	Sequence 1603, Ap
578	29	1.2	5881	9	US-09-764-891-9918	Sequence 9918, Ap	c 651	29	1.2	21727	10	US-09-764-864-1604	Sequence 1604, Ap
579	29	1.2	6153	9	US-09-764-891-5720	Sequence 5720, Ap	c 652	29	1.2	21833	10	US-09-764-877-2275	Sequence 2275, Ap
580	29	1.2	6153	10	US-09-764-877-3077	Sequence 3077, Ap	c 653	29	1.2	22073	9	US-09-764-891-7351	Sequence 7351, Ap
581	29	1.2	6465	10	US-09-954-456-193	Sequence 193, App	c 654	29	1.2	22484	10	US-09-875-114-2	Sequence 2, Appli
582	29	1.2	6719	9	US-10-232-803-36	Sequence 36, Appl	c 655	29	1.2	22484	9	US-09-880-107-3341	Sequence 3341, Ap
583	29	1.2	6834	9	US-09-764-891-8002	Sequence 8002, Ap	c 656	29	1.2	22645	9	US-09-764-891-7673	Sequence 7673, Ap
584	29	1.2	8021	9	US-10-091-438-263	Sequence 263, App	c 657	29	1.2	22645	9	US-09-764-891-8183	Sequence 8183, Ap
585	29	1.2	8021	9	US-10-232-803-2	Sequence 2, Appli	c 658	29	1.2	23309	10	US-09-764-877-2455	Sequence 2455, Ap
586	29	1.2	8095	9	US-09-989-920-73	Sequence 73, Appl	c 659	29	1.2	23309	9	US-10-291-737-3	Sequence 3, Appli
587	29	1.2	8194	9	US-09-799-629-15	Sequence 15, Appl	c 660	29	1.2	26591	10	US-09-764-869-1997	Sequence 2678, Ap
588	29	1.2	8194	9	US-10-035-045-15	Sequence 15, Appl	c 661	29	1.2	26591	10	US-09-764-877-2678	Sequence 2678, Ap
589	29	1.2	8746	9	US-10-074-095-1022	Sequence 1022, Ap	c 662	29	1.2	26664	9	US-09-988-626-28	Sequence 28, Appl
590	29	1.2	8746	10	US-09-764-860-1022	Sequence 1022, Ap	c 663	29	1.2	26664	9	US-09-988-687-28	Sequence 28, Appl
591	29	1.2	8835	9	US-09-764-891-5494	Sequence 5494, Ap	c 664	29	1.2	27332	10	US-09-764-847-1555	Sequence 1555, Ap
592	29	1.2	8894	10	US-09-764-864-1692	Sequence 1692, Ap	c 665	29	1.2	27332	10	US-09-764-847-1555	Sequence 1555, Ap
593	29	1.2	8894	10	US-09-764-877-3063	Sequence 3063, Ap	c 666	29	1.2	27681	9	US-10-091-504-1997	Sequence 1997, Ap
594	29	1.2	9519	9	US-10-092-154-1056	Sequence 1056, Ap	c 667	29	1.2	27681	10	US-09-764-869-1997	Sequence 1997, Ap
595	29	1.2	9519	10	US-09-764-847-1056	Sequence 1056, Ap	c 668	29	1.2	27681	10	US-09-764-869-1997	Sequence 1997, Ap
596	29	1.2	9519	10	US-09-764-877-3534	Sequence 3534, Ap	c 669	29	1.2	28818	10	US-09-764-869-1998	Sequence 1998, Ap
597	29	1.2	9620	9	US-09-764-891-8895	Sequence 8895, Ap	c 670	29	1.2	29695	10	US-09-752-820A-3	Sequence 3, Appli
598	29	1.2	9877	10	US-09-764-877-3944	Sequence 3944, Ap	c 671	29	1.2	29695	10	US-09-813-319A-3	Sequence 3, Appli
599	29	1.2	9970	10	US-09-764-877-2277	Sequence 2277, Ap	c 672	29	1.2	31132	10	US-09-764-864-1690	Sequence 1690, Ap
600	29	1.2	10195	10	US-09-764-864-1600	Sequence 1600, Ap	c 673	29	1.2	31132	10	US-09-764-877-3062	Sequence 3062, Ap
601	29	1.2	10198	9	US-09-764-891-8743	Sequence 8743, Ap	c 674	29	1.2	31766	9	US-10-288-478-5	Sequence 5, Appli
602	29	1.2	10198	9	US-09-764-891-8743	Sequence 8743, Ap	c 675	29	1.2	31766	10	US-09-765-344-5	Sequence 5, Appli
603	29	1.2	10248	9	US-10-092-154-1238	Sequence 1238, Ap	c 676	29	1.2	32170	9	US-10-074-095-1108	Sequence 1108, Ap

677	29	1.2	32170	10	US-09-764-860-1108	Sequence 1108, Ap	750	28	1.2	2275	9	US-09-764-891-9061	Sequence 9061, Ap
678	29	1.2	32184	9	US-09-764-891-7300	Sequence 7300, Ap	751	28	1.2	2275	9	US-09-764-891-9062	Sequence 9062, Ap
679	29	1.2	32190	9	US-10-091-504-2209	Sequence 2209, Ap	752	28	1.2	2517	9	US-10-198-846-11008	Sequence 11008, A
680	29	1.2	32190	10	US-09-764-869-2209	Sequence 2209, Ap	c 753	28	1.2	2503	10	US-09-822-830A-221	Sequence 221, App
681	29	1.2	32191	9	US-09-764-891-6454	Sequence 6454, Ap	754	28	1.2	3088	10	US-09-954-456-45	Sequence 45, Appl
682	29	1.2	32194	9	US-09-764-891-7028	Sequence 7028, Ap	755	28	1.2	3088	10	US-09-954-456-1621	Sequence 1621, Ap
683	29	1.2	32195	9	US-10-102-672-92	Sequence 92, Appl	756	28	1.2	3088	10	US-09-969-347-234	Sequence 234, App
684	29	1.2	32203	9	US-10-091-504-1849	Sequence 1849, Ap	c 757	28	1.2	3805	9	US-09-764-891-7518	Sequence 7518, Ap
685	29	1.2	32203	10	US-09-764-869-1849	Sequence 1849, Ap	c 758	28	1.2	3846	9	US-10-245-103-55	Sequence 55, Appl
686	29	1.2	32249	9	US-09-764-891-7364	Sequence 7364, Ap	c 759	28	1.2	3846	9	US-10-245-103-55	Sequence 55, Appl
687	29	1.2	32249	9	US-09-764-891-7619	Sequence 7619, Ap	c 760	28	1.2	3846	9	US-10-245-143-55	Sequence 55, Appl
688	29	1.2	33795	10	US-09-880-107-2184	Sequence 2184, Ap	c 761	28	1.2	3846	9	US-10-245-771-55	Sequence 55, Appl
689	29	1.2	35465	9	US-10-161-572-6	Sequence 6, Appli	c 762	28	1.2	3846	9	US-10-245-851-55	Sequence 55, Appl
690	29	1.2	36991	9	US-10-161-572-8	Sequence 8, Appli	c 763	28	1.2	3846	9	US-10-245-883-55	Sequence 55, Appl
691	29	1.2	38374	10	US-09-880-107-3463	Sequence 3463, Ap	c 764	28	1.2	3846	9	US-10-237-535-55	Sequence 55, Appl
692	29	1.2	42999	10	US-09-740-029-3	Sequence 3, Appli	c 765	28	1.2	3846	9	US-10-238-183-55	Sequence 55, Appl
693	29	1.2	43058	10	US-09-954-456-292	Sequence 292, App	c 766	28	1.2	3846	9	US-10-238-283-55	Sequence 55, Appl
694	29	1.2	43058	10	US-09-954-456-292	Sequence 292, App	c 767	28	1.2	3846	9	US-10-238-370-55	Sequence 55, Appl
695	29	1.2	43058	10	US-09-954-456-529	Sequence 529, App	c 768	28	1.2	3846	9	US-10-245-055-55	Sequence 55, Appl
696	29	1.2	43058	10	US-09-954-456-529	Sequence 529, App	c 769	28	1.2	3846	9	US-10-245-147-55	Sequence 55, Appl
697	29	1.2	43058	10	US-09-880-107-3950	Sequence 3950, App	c 770	28	1.2	3846	9	US-10-245-730-55	Sequence 55, Appl
698	29	1.2	43058	10	US-09-880-107-3950	Sequence 3950, App	c 771	28	1.2	3846	9	US-10-245-739-55	Sequence 55, Appl
699	29	1.2	43950	12	US-10-060-332-3	Sequence 3, Appli	c 772	28	1.2	3846	9	US-10-246-210-55	Sequence 55, Appl
700	29	1.2	49984	10	US-09-739-457-5	Sequence 5, Appli	c 773	28	1.2	3846	9	US-10-239-196-55	Sequence 55, Appl
701	29	1.2	53522	9	US-09-904-968A-1	Sequence 1, Appli	c 774	28	1.2	3846	9	US-10-243-024-55	Sequence 55, Appl
702	29	1.2	56516	9	US-09-853-526-1	Sequence 1, Appli	c 775	28	1.2	3846	9	US-10-243-409-55	Sequence 55, Appl
703	29	1.2	56516	10	US-09-901-484A-1	Sequence 1, Appli	c 776	28	1.2	3846	9	US-10-245-033-55	Sequence 55, Appl
704	29	1.2	56520	9	US-09-853-526-179	Sequence 179, App	c 777	28	1.2	3846	9	US-10-245-621-55	Sequence 55, Appl
705	29	1.2	56520	10	US-09-901-484A-179	Sequence 179, App	c 778	28	1.2	3846	9	US-10-245-880-55	Sequence 55, Appl
706	29	1.2	57130	10	US-09-835-081-3	Sequence 3, Appli	c 779	28	1.2	3846	9	US-10-243-095-55	Sequence 55, Appl
707	29	1.2	58837	10	US-09-982-091A-5	Sequence 5, Appli	c 780	28	1.2	3846	9	US-10-245-185-55	Sequence 55, Appl
708	29	1.2	62804	12	US-10-096-960-3	Sequence 3, Appli	c 781	28	1.2	3846	9	US-10-245-427-55	Sequence 55, Appl
709	29	1.2	65359	10	US-09-804-472-3	Sequence 3, Appli	c 782	28	1.2	3846	9	US-10-245-473-55	Sequence 55, Appl
710	29	1.2	65464	9	US-09-859-888-3	Sequence 3, Appli	c 783	28	1.2	3846	9	US-10-245-770-55	Sequence 55, Appl
711	29	1.2	73308	10	US-09-954-456-2276	Sequence 2276, Ap	c 784	28	1.2	3846	9	US-10-245-877-55	Sequence 55, Appl
712	29	1.2	90541	10	US-09-759-359A-3	Sequence 3, Appli	c 785	28	1.2	3846	9	US-10-246-976-55	Sequence 55, Appl
713	29	1.2	96649	9	US-09-956-712-10	Sequence 10, Appl	c 786	28	1.2	3846	9	US-10-243-320-55	Sequence 55, Appl
714	29	1.2	118951	9	US-10-161-572-11	Sequence 11, Appl	c 787	28	1.2	3846	9	US-10-242-743-55	Sequence 55, Appl
715	29	1.2	132762	9	US-09-954-556-17	Sequence 17, Appl	c 788	28	1.2	3846	9	US-10-242-845-55	Sequence 55, Appl
716	29	1.2	145831	10	US-09-969-708-79	Sequence 79, Appl	c 789	28	1.2	3846	9	US-10-237-636-55	Sequence 55, Appl
717	29	1.2	145831	10	US-09-954-456-2116	Sequence 2116, Ap	c 790	28	1.2	3846	9	US-10-238-325-55	Sequence 55, Appl
718	29	1.2	180216	10	US-09-835-232-6	Sequence 6, Appli	c 791	28	1.2	3846	9	US-10-238-346-55	Sequence 55, Appl
719	29	1.2	402850	9	US-09-844-653-5	Sequence 5, Appli	c 792	28	1.2	3846	9	US-10-238-411-55	Sequence 55, Appl
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721	28	1.2	198	9	US-10-066-543-2824	Sequence 2824, Ap	c 794	28	1.2	3846	9	US-10-243-425-55	Sequence 55, Appl
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723	28	1.2	290	10	US-09-764-869-1466	Sequence 1466, Ap	c 796	28	1.2	3846	9	US-10-245-874-55	Sequence 1703, Ap
724	28	1.2	315	10	US-09-964-824A-523	Sequence 523, Ap	c 797	28	1.2	3901	10	US-09-764-864-1703	Sequence 1703, Ap
725	28	1.2	315	10	US-09-964-824A-523	Sequence 523, Ap	c 798	28	1.2	5281	9	US-09-764-891-6949	Sequence 6949, Ap
726	28	1.2	347	9	US-09-918-995-18604	Sequence 18604, A	c 799	28	1.2	5281	9	US-10-079-854-409	Sequence 409, App
727	28	1.2	371	10	US-09-867-701-4466	Sequence 4466, Ap	c 800	28	1.2	5299	10	US-09-764-878-409	Sequence 409, App
728	28	1.2	391	10	US-09-867-701-6668	Sequence 6668, Ap	c 801	28	1.2	5299	10	US-09-764-878-409	Sequence 409, App
729	28	1.2	418	9	US-10-165-835-5	Sequence 5, Appli	c 802	28	1.2	5530	9	US-10-091-548-112	Sequence 112, App
730	28	1.2	451	9	US-09-918-995-8988	Sequence 8988, Ap	c 803	28	1.2	5530	9	US-10-091-548-112	Sequence 112, App
731	28	1.2	451	10	US-09-764-877-3554	Sequence 3554, Ap	c 804	28	1.2	5530	10	US-10-074-095-1167	Sequence 1167, Ap
732	28	1.2	455	9	US-10-198-846-1579	Sequence 1579, Ap	c 805	28	1.2	5530	10	US-09-764-860-1167	Sequence 1167, Ap
733	28	1.2	465	9	US-09-918-995-15943	Sequence 15943, A	c 806	28	1.2	5793	9	US-09-764-891-7965	Sequence 7966, Ap
734	28	1.2	472	10	US-09-880-107-1468	Sequence 1468, Ap	c 807	28	1.2	6637	9	US-09-764-891-9887	Sequence 9887, Ap
735	28	1.2	485	10	US-09-880-107-1468	Sequence 1468, Ap	c 808	28	1.2	6637	9	US-09-764-868-1357	Sequence 1357, Ap
736	28	1.2	521	10	US-09-880-107-3960	Sequence 3960, App	c 809	28	1.2	8210	10	US-09-764-878-406	Sequence 406, App
737	28	1.2	543	10	US-09-867-701-2460	Sequence 2460, Ap	c 810	28	1.2	8210	10	US-09-764-878-406	Sequence 406, App
738	28	1.2	549	10	US-09-998-598-1277	Sequence 1277, Ap	c 811	28	1.2	8553	9	US-09-764-891-7456	Sequence 7456, Ap
739	28	1.2	558	9	US-10-198-846-11656	Sequence 11656, A	c 812	28	1.2	8895	9	US-10-091-438-250	Sequence 250, App
740	28	1.2	573	9	US-10-198-846-11923	Sequence 11923, A	c 813	28	1.2	8895	9	US-10-091-438-256	Sequence 256, App
741	28	1.2	633	9	US-10-198-846-3496	Sequence 3496, Ap	c 814	28	1.2	8895	10	US-09-764-853-887	Sequence 887, App
742	28	1.2	662	9	US-10-198-846-7374	Sequence 7374, Ap	c 815	28	1.2	8895	10	US-09-764-853-937	Sequence 937, App
743	28	1.2	11652	10	US-09-764-877-3957	Sequence 3957, Ap	c 816	28	1.2	9656	9	US-10-091-438-246	Sequence 246, App
744	28	1.2	1452	9	US-10-091-572-856	Sequence 856, App	c 817	28	1.2	9656	9	US-10-091-438-255	Sequence 255, App
745	28	1.2	1452	9	US-09-764-891-9295	Sequence 9295, Ap	c 818	28	1.2	9656	10	US-09-764-853-886	Sequence 886, App
746	28	1.2	1647	10	US-09-764-877-2360	Sequence 2360, Ap	c 819	28	1.2	9656	10	US-09-764-853-933	Sequence 933, App
747	28	1.2	1742	9	US-10-097-065-100	Sequence 100, App	c 820	28	1.2	10680	9	US-09-764-891-8367	Sequence 8367, Ap
748	28	1.2	1956	10	US-09-822-830A-190	Sequence 190, App	c 821	28	1.2	11538	9	US-10-091-504-1598	Sequence 1598, Ap
749	28	1.2	2112	9	US-10-198-846-12649	Sequence 12649, A	c 822	28	1.2	11538	10	US-09-764-865-1598	Sequence 1598, Ap

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c 824	28	1.2	11990	10	US-09-969-708-569	Sequence 569, Ap	897	27	1.1	89	9	US-10-092-154-1924	Sequence 1924, Ap
825	28	1.2	12988	9	US-10-091-504-2285	Sequence 2285, Ap	898	27	1.1	89	10	US-09-764-847-1922	Sequence 1922, Ap
826	28	1.2	12988	10	US-09-764-869-2285	Sequence 2285, Ap	899	27	1.1	89	10	US-09-764-847-1924	Sequence 1924, Ap
827	28	1.2	13026	9	US-09-764-891-10217	Sequence 10217, A	900	27	1.1	104	10	US-09-764-877-2686	Sequence 2686, Ap
c 828	28	1.2	17904	9	US-09-764-891-6418	Sequence 6418, Ap	901	27	1.1	123	10	US-09-764-877-2684	Sequence 2684, Ap
829	28	1.2	18036	9	US-10-091-504-2287	Sequence 2287, Ap	c 902	27	1.1	128	9	US-09-764-891-8156	Sequence 8156, Ap
830	28	1.2	18036	10	US-09-764-869-2287	Sequence 2287, Ap	c 903	27	1.1	135	10	US-09-867-701-9896	Sequence 9896, Ap
831	28	1.2	19206	9	US-10-091-504-1258	Sequence 1258, Ap	904	27	1.1	345	10	US-09-867-701-9896	Sequence 9896, Ap
832	28	1.2	19206	10	US-09-764-869-1258	Sequence 1258, Ap	905	27	1.1	353	10	US-09-867-701-9896	Sequence 9896, Ap
833	28	1.2	19274	9	US-10-091-504-1254	Sequence 1254, Ap	906	27	1.1	466	9	US-09-918-995-17792	Sequence 17792, A
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c 835	28	1.2	20020	9	US-10-091-483-325	Sequence 325, Ap	908	27	1.1	529	9	US-09-918-995-9685	Sequence 9685, Ap
836	28	1.2	20020	10	US-09-764-891-8223	Sequence 8223, Ap	c 909	27	1.1	684	9	US-09-918-995-9212	Sequence 9212, Ap
c 837	28	1.2	20020	10	US-09-764-846-325	Sequence 325, Ap	c 910	27	1.1	957	9	US-10-198-846-6471	Sequence 6471, Ap
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839	28	1.2	20966	9	US-10-231-814-7	Sequence 7, Appl	c 912	27	1.1	1264	9	US-10-198-846-13301	Sequence 13301, A
840	28	1.2	20966	10	US-09-776-976-7	Sequence 7, Appl	c 913	27	1.1	1882	9	US-10-062-831-32	Sequence 32, Appl
841	28	1.2	20966	10	US-09-758-055-7	Sequence 7, Appl	c 914	27	1.1	1882	9	US-09-892-877-76	Sequence 76, Appl
842	28	1.2	20966	10	US-09-909-547-7	Sequence 7, Appl	c 915	27	1.1	2290	10	US-09-948-783-75	Sequence 75, Appl
c 843	28	1.2	21358	9	US-09-764-872-816	Sequence 816, Ap	c 916	27	1.1	2468	9	US-09-822-849A-152	Sequence 152, App
c 844	28	1.2	21358	9	US-09-764-891-9107	Sequence 9107, Ap	c 917	27	1.1	2839	10	US-10-153-668-355	Sequence 355, Appl
845	28	1.2	21458	9	US-09-764-891-8810	Sequence 8810, Ap	c 918	27	1.1	3373	9	US-09-748-451-1	Sequence 1, Appl
c 846	28	1.2	21608	9	US-10-091-504-1733	Sequence 1733, Ap	c 919	27	1.1	3566	10	US-10-105-963-9	Sequence 9, Appl
c 847	28	1.2	21608	10	US-09-764-869-1733	Sequence 1733, Ap	c 920	27	1.1	3566	10	US-10-074-095-1105	Sequence 1105, Ap
c 848	28	1.2	21676	9	US-09-764-872-815	Sequence 815, Ap	c 921	27	1.1	4618	9	US-09-764-860-1105	Sequence 1105, Ap
c 849	28	1.2	21676	9	US-09-764-891-9106	Sequence 9106, Ap	c 922	27	1.1	4618	10	US-10-092-154-1491	Sequence 1491, Ap
c 850	28	1.2	23544	9	US-09-764-891-8517	Sequence 8517, Ap	c 923	27	1.1	5935	10	US-09-764-847-1491	Sequence 1491, Ap
c 851	28	1.2	23603	9	US-09-860-670-264	Sequence 264, Ap	c 924	27	1.1	6133	10	US-09-754-949-8	Sequence 8, Appl
c 852	28	1.2	23613	9	US-09-860-670-258	Sequence 258, Ap	c 925	27	1.1	6133	10	US-09-764-891-5720	Sequence 5720, Ap
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c 858	28	1.2	25574	9	US-09-764-891-8307	Sequence 8307, Ap	c 931	27	1.1	8191	10	US-09-764-891-9520	Sequence 9520, Ap
c 859	28	1.2	25576	9	US-09-764-891-8306	Sequence 8306, Ap	c 932	27	1.1	12167	10	US-09-764-847-1920	Sequence 1920, Ap
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c 861	28	1.2	31140	9	US-09-764-891-9479	Sequence 9479, Ap	c 934	27	1.1	12194	10	US-10-091-438-283	Sequence 283, Ap
862	28	1.2	31348	9	US-10-091-504-1259	Sequence 1259, Ap	c 935	27	1.1	15843	10	US-09-764-853-897	Sequence 897, App
863	28	1.2	31348	10	US-09-764-869-1259	Sequence 1259, Ap	c 936	27	1.1	15843	10	US-10-091-504-2396	Sequence 2396, Ap
c 864	28	1.2	31730	10	US-09-764-877-3810	Sequence 3810, Ap	c 937	27	1.1	16774	9	US-09-764-869-2396	Sequence 2396, Ap
c 865	28	1.2	32169	9	US-09-764-891-8605	Sequence 8605, Ap	c 938	27	1.1	16774	9	US-10-091-504-2398	Sequence 2398, Ap
c 866	28	1.2	32189	9	US-10-079-854-379	Sequence 379, App	c 939	27	1.1	16774	10	US-09-764-869-2395	Sequence 2395, Ap
c 867	28	1.2	32189	10	US-09-764-891-8604	Sequence 8604, Ap	c 940	27	1.1	16774	10	US-09-764-869-2398	Sequence 2398, Ap
c 868	28	1.2	32189	9	US-09-764-878-379	Sequence 379, App	c 941	27	1.1	17946	10	US-09-764-869-2312	Sequence 2312, Ap
c 869	28	1.2	32190	9	US-09-860-670-255	Sequence 255, App	c 942	27	1.1	17946	10	US-09-764-869-2312	Sequence 2312, Ap
c 870	28	1.2	32193	10	US-09-764-877-2147	Sequence 2147, Ap	c 943	27	1.1	18636	9	US-09-764-862-17	Sequence 17, Appl
c 871	28	1.2	32193	10	US-09-764-877-2623	Sequence 2623, Ap	c 944	27	1.1	30573	9	US-09-764-891-6869	Sequence 6869, Ap
c 872	28	1.2	32195	9	US-10-091-504-1605	Sequence 1605, Ap	c 945	27	1.1	32152	9	US-09-764-872-518	Sequence 518, App
c 873	28	1.2	32195	9	US-10-125-540-611	Sequence 611, App	c 946	27	1.1	32152	9	US-10-072-349-328	Sequence 328, App
c 874	28	1.2	32195	9	US-10-125-540-617	Sequence 617, App	c 947	27	1.1	32152	10	US-09-764-853-328	Sequence 328, App
c 875	28	1.2	32195	10	US-09-764-870-611	Sequence 611, App	c 948	27	1.1	32152	9	US-10-092-154-1963	Sequence 1963, App
c 876	28	1.2	32195	10	US-09-764-870-617	Sequence 617, App	c 949	27	1.1	32152	9	US-09-764-847-1963	Sequence 1963, Ap
c 877	28	1.2	32195	10	US-09-764-869-1605	Sequence 1605, Ap	c 950	27	1.1	32170	10	US-10-074-095-1108	Sequence 1108, Ap
c 878	28	1.2	32199	9	US-10-072-349-210	Sequence 210, App	c 951	27	1.1	32170	10	US-09-764-860-1108	Sequence 1108, Ap
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c 882	28	1.2	32221	9	US-10-079-854-377	Sequence 377, App	c 955	27	1.1	32192	10	US-09-764-891-8319	Sequence 8319, Ap
c 883	28	1.2	32221	10	US-09-764-878-377	Sequence 377, App	c 956	27	1.1	32192	10	US-09-764-847-1416	Sequence 1416, Ap
c 884	28	1.2	32249	9	US-09-860-670-260	Sequence 260, App	c 957	27	1.1	32204	9	US-09-764-872-517	Sequence 517, App
c 885	28	1.2	42571	9	US-10-224-413-3	Sequence 3, Appl	c 958	27	1.1	32204	9	US-10-072-349-327	Sequence 327, App
c 886	28	1.2	53000	9	US-09-953-611-10	Sequence 10, Appl	c 959	27	1.1	32204	10	US-09-764-855-327	Sequence 327, App
c 887	28	1.2	68004	10	US-09-780-172-18	Sequence 18, Appl	c 960	27	1.1	33239	10	US-09-814-950-3	Sequence 3, Appl
c 888	28	1.2	75270	9	US-09-740-041-3	Sequence 3, Appl	c 961	27	1.1	48841	9	US-09-844-653-32	Sequence 32, Appl
c 889	28	1.2	88191	10	US-09-799-799-3	Sequence 3, Appl	c 962	27	1.1	51552	10	US-09-733-294A-30	Sequence 30, Appl
c 890	28	1.2	98829	9	US-10-017-724-3	Sequence 3, Appl	c 963	27	1.1	119596	9	US-10-270-336-3	Sequence 3, Appl
c 891	28	1.2	133893	9	US-10-161-510-1	Sequence 1, Appl	c 964	27	1.1	132762	9	US-09-954-556-17	Sequence 17, Appl
c 892	28	1.2	172637	10	US-09-805-458A-3	Sequence 3, Appl	c 965	26	1.1	245	10	US-09-764-864-1662	Sequence 1662, Ap
c 893	28	1.2	202001	9	US-10-274-990-3	Sequence 3, Appl	c 966	26	1.1	250	9	US-10-092-154-1703	Sequence 1703, Ap
c 894	28	1.2	202001	10	US-09-734-674-3	Sequence 3, Appl	c 967	26	1.1	258	10	US-09-764-847-1703	Sequence 1703, Ap
c 895	28	1.2	202001	10	US-09-734-674-3	Sequence 3, Appl	c 968	26	1.1	258	10	US-09-867-701-8975	Sequence 8975, Ap

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969 26 1.1 273 9 US-09-764-891-7564 Sequence 7564, Ap
970 26 1.1 276 9 US-09-764-891-7561 Sequence 7561, Ap
971 26 1.1 307 9 US-09-764-891-6081 Sequence 6081, Ap
c 972 26 1.1 362 9 US-09-918-995-18419 Sequence 18419, A
973 26 1.1 402 9 US-10-198-846-1750 Sequence 1750, A
c 974 26 1.1 408 9 US-10-060-036-774 Sequence 774, App
975 26 1.1 460 9 US-10-046-935-394 Sequence 394, App
976 26 1.1 460 9 US-09-878-178-394 Sequence 394, App
977 26 1.1 460 9 US-10-146-502-394 Sequence 394, App
978 26 1.1 468 9 US-09-918-995-14317 Sequence 14317, A
979 26 1.1 499 9 US-09-918-995-20762 Sequence 20762, A
980 26 1.1 685 9 US-09-986-480-66 Sequence 66, App1
981 26 1.1 848 9 US-10-198-846-10677 Sequence 10677, A
982 26 1.1 859 9 US-10-198-846-7208 Sequence 7208, App
c 983 26 1.1 875 9 US-10-074-095-171 Sequence 171, App
984 26 1.1 875 10 US-09-764-860-171 Sequence 171, App
985 26 1.1 964 9 US-09-984-130-91 Sequence 91, App1
986 26 1.1 1035 9 US-09-764-891-2666 Sequence 2666, App
c 987 26 1.1 1039 9 US-09-764-891-1988 Sequence 1988, App
988 26 1.1 1086 10 US-09-529-063-6 Sequence 6, App1
989 26 1.1 1445 10 US-09-822-830A-344 Sequence 344, App
990 26 1.1 1766 9 US-09-764-891-7393 Sequence 7393, App
991 26 1.1 1901 9 US-09-853-526-181 Sequence 181, App
992 26 1.1 1901 10 US-09-901-484A-181 Sequence 181, App
993 26 1.1 2764 9 US-09-978-295A-258 Sequence 258, App
994 26 1.1 2764 9 US-09-978-597-258 Sequence 258, App
995 26 1.1 2764 9 US-09-978-192A-258 Sequence 258, App
996 26 1.1 2764 9 US-09-999-832A-258 Sequence 258, App
997 26 1.1 2764 9 US-09-978-189-258 Sequence 258, App
998 26 1.1 2764 9 US-10-174-590-117 Sequence 117, App
999 26 1.1 2764 9 US-10-176-758-117 Sequence 117, App
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## ALIGNMENTS

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RESULT 1
US-09-918-995-29121
; Sequence 29121, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIORITY APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29121
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(475)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29121

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Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2024 GCCAGTTTACGGCAACCTTTCCCTTACGACCTTCAGGCTGAGTTCTGGTTTCT 2083
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Qy 2084 AGAGTCAGACGGCTCTCTCAGCGCCAGGAGCCAGAGCCCAAGCAGCAAAAG 2143
Db 102 AGAGTCAGACGGCTCTCTCAGCGCCAGGAGCCAGAGCCCAAGCAGCAAAAG 161

RESULT 2
US-10-118-328-3/c
; Sequence 3, Application US/10118328
; Patent No. US20020169289A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001220
; CURRENT APPLICATION NUMBER: US/10/118,328
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,460
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-328-3

Query Match 1.6%; Score 39; DB 9; Length 30350;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTAC 44
Db 11147 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTAC 11109

RESULT 3
US-09-813-320-3/c
; Sequence 3, Application US/09813320
; Patent No. US20020142378A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Hongyu et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001172
; CURRENT APPLICATION NUMBER: US/09/813,320
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 397658
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(397658)
; OTHER INFORMATION: n = A,T,C or G
US-09-813-320-3

Query Match 1.6%; Score 39; DB 10; Length 397658;
Best Local Similarity 100.0%; Pred. No. 9.8e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAGGGGAGGTTGCAGTGAGCCAGCAAGATCAGCCACTA 43
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## RESULT 4

US-09-867-701-8927/c  
; Sequence 8927, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8927  
; LENGTH: 438  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(438)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-867-701-8927

Query Match 1.6%; Score 38; DB 10; Length 438;

Best Local Similarity 100.0%; Pred. No. 3.6e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 42

Db 88 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 51

## RESULT 5

US-09-867-701-4634/c  
; Sequence 4634, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4634  
; LENGTH: 449  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-4634

Query Match 1.6%; Score 38; DB 10; Length 449;

Best Local Similarity 100.0%; Pred. No. 3.5e-09; Mismatches 0; Indels 0; Gaps 0;

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Db 91 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 54

## RESULT 6

US-09-918-995-24949  
; Sequence 24949, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24949  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(456)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-24949

Query Match 1.6%; Score 38; DB 9; Length 456;

Best Local Similarity 100.0%; Pred. No. 3.5e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 42

Db 99 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 136

## RESULT 7

US-10-016-157A-71  
; Sequence 71, Application US/10016157A  
; Publication No. US20020192220A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Yongming  
; APPLICANT: Recipon, Herve  
; APPLICANT: Ghosh, Malavika  
; APPLICANT: Liu, Chenchua  
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro  
; FILE REFERENCE: DEX-0253  
; CURRENT APPLICATION NUMBER: US/10/016,157A  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: US 60/244,717  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 250  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 71  
; LENGTH: 9883  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7153)..(7153)  
; OTHER INFORMATION: n=a, c, g or t  
US-10-016-157A-71

Query Match 1.6%; Score 38; DB 9; Length 9883;

Best Local Similarity 100.0%; Pred. No. 3.4e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 42

Db 6724 GGGAGCGGAGGTTGCAGTGAGCCCAAGATCAGCCACT 6761

## RESULT 8

US-09-764-864-1704/c  
; Sequence 1704, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper

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; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 15857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1704

Query Match          1.6%; Score 38; DB 10; Length 15857;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      14952 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 14915

RESULT 9
US-10-079-854-370/c
; Sequence 370, Application US/10079854
; Publication No. US20030054368A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121C1
; CURRENT APPLICATION NUMBER: US/10/079,854
; CURRENT FILING DATE: 2002-02-22
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 370
; LENGTH: 16225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-854-370

Query Match          1.6%; Score 38; DB 9; Length 16225;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 42
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Db      5049 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 5012

RESULT 10
US-09-764-891-9432/c
; Sequence 9432, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9432
; LENGTH: 16225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9432

Query Match          1.6%; Score 38; DB 9; Length 16225;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 42
      |||
Db      5049 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 5012

RESULT 11
US-09-764-878-370/c
; Sequence 370, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 370
; LENGTH: 16225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-370

Query Match          1.6%; Score 38; DB 10; Length 16225;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 42
      |||
Db      5049 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 5012

RESULT 12
US-10-074-045-70
; Sequence 70, Application US/10074045
; Publication No. US20030092102A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ21C1
; CURRENT APPLICATION NUMBER: US/10/074,045
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 18657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-045-70

Query Match          1.6%; Score 38; DB 9; Length 18657;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 42
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Db      10882 GGGAGCGGAGGTTGCAGTGAGCCAAAGATCAGCCCACT 10919

RESULT 13
US-09-764-891-6868/c
; Sequence 6868, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6868
; LENGTH: 32195
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-764-891-6868

Query Match 1.6%; Score 38; DB 9; Length 32195;  
Best Local Similarity 100.0%; Pred. No. 3.4e-09;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1983 GGGAGCGGAGGTTCAGTCAGTCAGCCAGATCACGCCACT 1946

RESULT 14

US-10-025-187-3/c  
; Sequence 3, Application US/10025187  
; Patent No. US20020150931A1  
; GENERAL INFORMATION:  
; APPLICANT: SHEFFIELD, VAL  
; APPLICANT: NISHIMURA, DARRYL  
; APPLICANT: STONE, EDWARD  
; TITLE OF INVENTION: A BARDET-BIEDL SUSCEPTIBILITY GENE AND USES THEREOF  
; FILE REFERENCE: IOWA:034US  
; CURRENT APPLICATION NUMBER: US/10/025,187  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/256,900  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 45839  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-025-187-3

Query Match 1.6%; Score 38; DB 12; Length 45839;  
Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTCAGTCAGCCAGATCACGCCACT 42  
Db 19401 GGGAGCGGAGGTTCAGTCAGTCAGCCAGATCACGCCACT 19364

RESULT 15

US-09-954-456-2257/c  
; Sequence 2257, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
; FILE REFERENCE: 689290-76  
; CURRENT APPLICATION NUMBER: US/09/954,456  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,923  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,134  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,637  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,638  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,711  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,720  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,840  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,863  
; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 2276  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2257  
; LENGTH: 62944  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-456-2257

Query Match 1.6%; Score 38; DB 10; Length 62944;  
Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGAGCGGAGGTTCAGTCAGCCAGATCACGCCACT 42  
Db 31008 GGGAGCGGAGGTTCAGTCAGTCAGCCAGATCACGCCACT 30971

Search completed: June 17, 2003, 09:59:13  
Job time : 273.144 secs





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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 2731.82 Seconds

(without alignments)  
14252.028 Million cell updates/sec

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Perfect score: 2404

Sequence: 1 agagggagcgagggttc.....gacagggtcttctgtctgcc 2404

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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7: em\_estro:\*\*

8: em\_htc:\*\*

9: gb\_est1:\*\*

10: gb\_est2:\*\*

11: gb\_htc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: gb\_gss:\*\*

18: em\_gss\_hum:\*\*

19: em\_gss\_inv:\*\*

20: em\_gss\_pln:\*\*

21: em\_gss\_vrt:\*\*

22: em\_gss\_fun:\*\*

23: em\_gss\_nam:\*\*

24: em\_gss\_mus:\*\*

25: em\_gss\_other:\*\*

26: em\_gss\_pro:\*\*

27: em\_gss\_rod:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	570	21.7	922	9	AL536293
3	456	19.0	929	13	BM560284
4	383	15.9	1020	12	BF689781
5	296	12.3	296	9	AL134288
6	292	12.1	751	10	BE312985

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BG765063	602737675	939	12	BG765063	9.7	233	8
BF317160	601901286	901	12	BF317160	8.8	212	9
BI034804	RC4-NN117	446	13	BI034804	7.4	177	10
AA020852	ze64b08.r	463	9	AA020852	6.4	153	11
N35845	yx89f10.r1	643	14	N35845	5.6	134	12
BE384676	601276954	558	10	BE384676	4.3	104	13
BE540725	601065002	797	10	BE540725	4.1	98	14
BG769644	602744561	89	3.7	BG769644	3.7	89	15
AL135213	DKFZp762E	247	9	AL135213	3.5	84	16
BE279166	601156630	796	10	BE279166	2.5	60	17
AW47817	UI-M-BH3-	326	10	AW47817	2.2	52	18
BM663827	UI-E-CL1-	700	13	BM663827	1.8	43	19
AA081323	zn33c09.s	214	9	AA081323	1.7	42	20
T06967	EST04856 Fe	370	14	T06967	1.7	42	21
AA641057	nr29a09.s	406	9	AA641057	1.7	42	22
AV720296	AV720296	589	10	AV720296	1.7	42	23
AV718428	AV718428	605	10	AV718428	1.7	42	24
AW855437	CM2-CT027	594	10	AW855437	1.7	41	25
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BF959498	OV2-NN004	168	12	BF959498	1.6	38	28
AI290407	qm59e03.x	217	9	AI290407	1.6	38	29
BE041322	hr80g04.x	217	10	BE041322	1.6	38	30
AW856084	RC1-CT028	218	10	AW856084	1.6	38	31
AA179433	zp45a09.r	240	9	AA179433	1.6	38	32
AA258134	zb32g05.s	261	9	AA258134	1.6	38	33
F03493	HSC12B042.n	262	14	F03493	1.6	38	34
BF815113	MR2-CT012	282	12	BF815113	1.6	38	35
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AI306232	qm80b05.x	320	9	AI306232	1.6	38	37
AI583466	tt69h09.x	326	9	AI583466	1.6	38	38
AW504297	UI-HF-BN0	338	10	AW504297	1.6	38	39
AI085814	ox47b05.s	386	9	AI085814	1.6	38	40
H75720	yu07d05.r1	393	14	H75720	1.6	38	41
AA457655	aag1h02.s	396	9	AA457655	1.6	38	42
AQ349633	RFC11-11	417	17	AQ349633	1.6	38	43
AI054354	qi64b03.x	438	9	AI054354	1.6	38	44
AQ051559	HS 3231.A	441	17	AQ051559	1.6	38	45
AA676875	ae28b04.s	443	9	AA676875	1.6	38	46
AI291961	qm81d06.x	444	9	AI291961	1.6	38	47
BF725595	bx18d01.x	444	12	BF725595	1.6	38	48
AA430514	zw21a08.s	445	9	AA430514	1.6	38	49
AQ877853	HS 2152.B	449	9	AQ877853	1.6	38	50
AL035971	DKFZp564G	457	17	AL035971	1.6	38	51
BE147645	RC1-HT022	471	9	BE147645	1.6	38	52
AI831171	wj81g12.x	475	10	BE147645	1.6	38	53
BE263346	601190845	477	9	AI831171	1.6	38	54
AQ472136	CITBI-E1-	479	10	BE263346	1.6	38	55
AQ542657	RPCI-11-3	490	17	AQ472136	1.6	38	56
BQ082221	K-EST0073	492	17	AQ542657	1.6	38	57
AQ479637	RPCI-11-2	500	14	BQ082221	1.6	38	58
W40469	zb74g05.r1	502	17	AQ479637	1.6	38	59
AW504686	UI-HF-BN0	506	14	W40469	1.6	38	60
AQ784229	HS 3087.B	527	17	AW504686	1.6	38	61
AI734279	zb74g05.y	535	17	AQ784229	1.6	38	62
AG038593	Pan trogl	582	9	AI734279	1.6	38	63
BF212791	601814055	649	17	AG038593	1.6	38	64
AG138366	Pan trogl	667	12	BF212791	1.6	38	65
AG093264	Pan trogl	676	17	AG138366	1.6	38	66
AF010903	AF010903	680	17	AG093264	1.6	38	67
AG009226	Homo sapi	697	17	AF010903	1.6	38	68
AQ009226	Homo sapi	698	17	AG009226	1.6	38	69
AQ782298	HS 3184.B	700	17	AQ009226	1.6	38	70
AQ311647	RPCI11-10	701	17	AQ782298	1.6	38	71
AG117882	Pan trogl	706	17	AQ311647	1.6	38	72
AG117952	Pan trogl	706	17	AG117882	1.6	38	73
AG009228	Homo sapi	711	17	AG117952	1.6	38	74
BG678435	602625085	732	12	AG009228	1.6	38	75
AG009195	Homo sapi	748	17	BG678435	1.6	38	76
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BG778845	602667518	831	12	AA522500	1.6	38	79

C 80	38	1.6	836	12	BE783649	BE783649 601471226	C 153	36	1.5	604	10	AW966758	AW966758 EST378832
C 81	38	1.6	858	14	BQ221178	BQ221178 AGENCOURT	C 154	36	1.5	607	17	B01406	B01406 CSRL-131C10
C 82	38	1.6	869	17	AQ741610	AQ741610 HS_5572_B	C 155	36	1.5	620	9	AL042635	AL042635 DKZP434M
C 83	38	1.6	888	14	BQ988813	BQ988813 AGENCOURT	C 156	36	1.5	632	17	AG149791	AG149791 Pan trogl
C 84	38	1.6	933	14	BQ706641	BQ706641 AGENCOURT	C 157	36	1.5	662	17	AQ379438	AQ379438 RHC111-16
C 85	38	1.6	943	14	BQ058053	BQ058053 AGENCOURT	C 158	36	1.5	736	17	AQ748064	AQ748064 HS_5538_A
C 86	38	1.6	950	14	BQ062719	BQ062719 AGENCOURT	C 159	36	1.5	750	12	BG566041	BG566041 602582640
C 87	38	1.6	979	13	BQ469390	BQ469390 AGENCOURT	C 160	36	1.5	770	12	BG212347	BG212347 601813621
C 88	38	1.6	1002	14	BQ061858	BQ061858 AGENCOURT	C 161	36	1.5	778	12	BG663240	BG663240 602144358
C 89	38	1.6	1015	14	BQ056123	BQ056123 AGENCOURT	C 162	36	1.5	799	17	AQ751118	AQ751118 HS_5575_B
C 90	38	1.6	1012	13	BM469629	BM469629 AGENCOURT	C 163	36	1.5	821	12	BF974661	BF974661 602243396
C 91	38	1.6	1021	14	BQ056173	BQ056173 AGENCOURT	C 164	36	1.5	941	14	BQ711583	BQ711583 AGENCOURT
C 92	38	1.6	1026	14	BQ063043	BQ063043 AGENCOURT	C 165	35	1.5	156	17	AQ266335	AQ266335 RHC111-72
C 93	38	1.6	1041	14	BQ058749	BQ058749 AGENCOURT	C 166	35	1.5	157	13	BM142414	BM142414 if32403.x
C 94	38	1.6	1043	14	BQ058255	BQ058255 AGENCOURT	C 167	35	1.5	211	17	AQ541195	AQ541195 RHC1-11-3
C 95	38	1.6	1063	14	BM800338	BM800338 AGENCOURT	C 168	35	1.5	230	9	AA287872	AA287872 zss1h04.s
C 96	38	1.6	1085	14	BQ059031	BQ059031 AGENCOURT	C 169	35	1.5	302	9	AA303988	AA303988 EST16700
C 97	38	1.6	1124	10	AV762309	AV762309 AV762309	C 170	35	1.5	309	12	BF812434	BF812434 MR2-C1018
C 98	38	1.6	1842	11	BC011119	BC011119 Homo sapi	C 171	35	1.5	318	9	AA292387	AA292387 zt29c05.r
C 99	37	1.5	176	14	N53518	N53518 YZ26d04.sl	C 172	35	1.5	333	17	AQ066918	AQ066918 HS_2227_B
C 100	37	1.5	228	12	BF928074	BF928074 IL5-NT022	C 173	35	1.5	335	9	AA829564	AA829564 od37a10.s
C 101	37	1.5	382	10	AW814730	AW814730 MK1-ST020	C 174	35	1.5	338	9	AA828045	AA828045 od70g02.s
C 102	37	1.5	385	14	H93735	H93735 Ys77a09.sl	C 175	35	1.5	365	12	BF477384	BF477384 nacs59g01.
C 103	37	1.5	389	10	BE206039	BE206039 bb55g07.x	C 176	35	1.5	367	17	AQ041782	AQ041782 CIT-HSP-2
C 104	37	1.5	393	9	AA931162	AA931162 oo70e03.s	C 177	35	1.5	383	9	AA570255	AA570255 nf39e07.s
C 105	37	1.5	398	17	AQ035831	AQ035831 CIT-HSP-2	C 178	35	1.5	397	9	AA490908	AA490908 aa52c01.s
C 106	37	1.5	412	14	T47889	T47889 Yb18a09.sl	C 179	35	1.5	412	10	AW519290	AW519290 xE80c02.x
C 107	37	1.5	421	9	AA593375	AA593375 nm08h10.s	C 180	35	1.5	416	14	TS1572	TS1572 Yb25907.sl
C 108	37	1.5	426	10	AV760528	AV760528 AV760528	C 181	35	1.5	419	14	T65989	T65989 ycl12d04.sl
C 109	37	1.5	459	13	BI493089	BI493089 df97e07.y	C 182	35	1.5	431	17	AQ176276	AQ176276 HS_3209_A
C 110	37	1.5	464	17	B89523	B89523 RHC11-27K1	C 183	35	1.5	432	17	AQ482806	AQ482806 RHC1-11-2
C 111	37	1.5	490	12	BF953490	BF953490 RC3-NN118	C 184	35	1.5	441	9	AA838227	AA838227 oe37d03.s
C 112	37	1.5	513	17	AQ190314	AQ190314 HS_3223_A	C 185	35	1.5	457	17	AQ197732	AQ197732 CIT-HSP-2
C 113	37	1.5	521	12	BF953646	BF953646 RC3-NN118	C 186	35	1.5	459	10	AW963966	AW963966 EST376039
C 114	37	1.5	548	17	AQ485704	AQ485704 RHC1-11-2	C 187	35	1.5	461	13	BM141828	BM141828 if27a02.x
C 115	37	1.5	593	17	AQ351689	AQ351689 CITBI-E1-	C 188	35	1.5	466	17	AQ229478	AQ229478 HS_2021_A
C 116	37	1.5	664	17	AG185369	AG185369 Pan trogl	C 189	35	1.5	489	14	T65778	T65778 ycl11f03.sl
C 117	37	1.5	670	17	AG067776	AG067776 Pan trogl	C 190	35	1.5	501	17	B92576	B92576 CIT-HSP-217
C 118	37	1.5	691	9	AU141371	AU141371 AU141371	C 191	35	1.5	501	17	AQ482803	AQ482803 RHC1-11-2
C 119	37	1.5	751	13	BM007824	BM007824 603617296	C 192	35	1.5	542	9	AL120867	AL120867 DKZP762K
C 120	37	1.5	769	17	AQ900076	AQ900076 HS_3034_B	C 193	35	1.5	566	17	AQ454593	AQ454593 HS_5217_A
C 121	37	1.5	908	10	BE256728	BE256728 601115545	C 194	35	1.5	570	9	AU148264	AU148264 AU148264
C 122	37	1.5	1005	13	BM480128	BM480128 AGENCOURT	C 195	35	1.5	616	17	AQ423170	AQ423170 CITBI-E1-
C 123	37	1.5	1040	14	BQ221982	BQ221982 AGENCOURT	C 196	35	1.5	623	17	AQ036239	AQ036239 Pan trogl
C 124	37	1.5	1051	11	BC022296	BC022296 Homo sapi	C 197	35	1.5	629	14	BM969453	BM969453 UI-CF-DU1
C 125	36	1.5	152	14	N85987	N85987 J5881F Huma	C 198	35	1.5	672	12	BG501601	BG501601 602548640
C 126	36	1.5	209	12	BF880674	BF880674 QV3-ET019	C 199	35	1.5	697	10	AV723135	AV723135 AV723135
C 127	36	1.5	226	12	BF879580	BF879580 PM4-ET015	C 200	35	1.5	706	14	BM975460	BM975460 UI-CF-EN1
C 128	36	1.5	231	12	BF920688	BF920688 RC5-NT018	C 201	35	1.5	777	12	BF219427	BF219427 601884218
C 129	36	1.5	253	9	AA377544	AA377544 EST90150	C 202	35	1.5	842	17	AQ878507	AQ878507 HS_3081_A
C 130	36	1.5	287	9	AA808843	AA808843 nv21b12.r	C 203	35	1.5	870	14	BQ711919	BQ711919 AGENCOURT
C 131	36	1.5	288	9	AA808847	AA808847 nv21d12.r	C 204	34	1.4	219	14	N78609	N78609 za94f09.sl
C 132	36	1.5	288	9	AA569474	AA569474 nm38f11.s	C 205	34	1.4	239	9	AA180815	AA180815 yb44f11.s
C 133	36	1.5	303	9	AA492269	AA492269 ng80a03.s	C 206	34	1.4	261	14	T61163	T61163 zp75h08.r1
C 134	36	1.5	308	9	AA299129	AA299129 EST11596	C 207	34	1.4	265	9	A1264879	A1264879 qk99c04.x
C 135	36	1.5	322	9	AA532700	AA532700 nj59a11.s	C 208	34	1.4	315	14	T61595	T61595 Yb74h05.sl
C 136	36	1.5	378	14	R12765	R12765 Yf44a11.sl	C 209	34	1.4	324	10	AW274191	AW274191 x573b09.x
C 137	36	1.5	385	9	AA995373	AA995373 tp74c07.s	C 210	34	1.4	374	9	AA642088	AA642088 nr30f11.s
C 138	36	1.5	389	9	A1560063	A1560063 tr2a12.x	C 211	34	1.4	384	9	AA847343	AA847343 oe18d10.s
C 139	36	1.5	407	12	BF680068	BF680068 602154792	C 212	34	1.4	400	9	A1167193	A1167193 ok28f05.x
C 140	36	1.5	411	12	BF851368	BF851368 IL5-EN008	C 213	34	1.4	434	17	AQ683459	AQ683459 HS_5432_B
C 141	36	1.5	422	10	AW974135	AW974135 EST386238	C 214	34	1.4	467	9	A1961228	A1961228 wt15c05.x
C 142	36	1.5	433	17	AQ180272	AQ180272 HS_3209_B	C 215	34	1.4	501	17	B02391	B02391 CSRL-152G10
C 143	36	1.5	457	9	AA640314	AA640314 nu01g01.s	C 216	34	1.4	527	12	BG431625	BG431625 602499217
C 144	36	1.5	493	17	AQ351342	AQ351342 RHC11-11	C 217	34	1.4	552	17	AQ0706984	AQ0706984 HS_5551_B
C 145	36	1.5	501	10	BE019467	BE019467 bb56c01.y	C 218	34	1.4	590	9	AA209188	AA209188 zq95d06.r
C 146	36	1.5	509	10	BE294700	BE294700 601173920	C 219	34	1.4	592	10	AW833324	AW833324 QV4-TT000
C 147	36	1.5	518	17	AQ514908	AQ514908 HS_5208_B	C 220	34	1.4	642	17	AQ0309769	AQ0309769 CITBI-E1-
C 148	36	1.5	522	17	AQ155672	AQ155672 HS_3125_A	C 221	34	1.4	668	17	AG163782	AG163782 Pan trogl
C 149	36	1.5	530	17	AQ124065	AQ124065 HS_3121_A	C 222	34	1.4	671	10	AW833742	AW833742 QV4-TT000
C 150	36	1.5	536	17	AQ139263	AQ139263 HS_3079_A	C 223	34	1.4	715	17	AG163684	AG163684 Pan trogl
C 151	36	1.5	550	9	AU148708	AU148708 AU148708	C 224	34	1.4	748	17	AG181959	AG181959 Pan trogl
C 152	36	1.5	572	17	AQ122460	AQ122460 HS_3080_A	C 225	34	1.4	1107	12	BF340713	BF340713 602035470



32	372	32	1.3	753	17	AG029154	Pan trogl	C 445	31	1.3	368	14	H70737	yu69f10.s1
32	373	32	1.3	758	17	AG029792	Pan trogl	C 446	31	1.3	369	10	AW275498	xn07f02..s
32	374	32	1.3	770	12	BF675504	602138482	C 447	31	1.3	377	9	AA602529	no9oA05.s
32	375	32	1.3	796	13	B1835431	603087540	C 448	31	1.3	379	10	AV693021	AV693021
32	376	32	1.3	832	12	BF673957	602137339	C 449	31	1.3	379	17	AQ083206	RPC111-54
32	377	32	1.3	846	17	AQ749752	HS_5573.A	C 450	31	1.3	384	9	AA174016	zpl18h06.r
32	378	32	1.3	869	13	B1598769	603245548	C 451	31	1.3	384	10	AW090392	xc81f02.x
32	379	32	1.3	898	13	BM453640	AGENCOURT	C 452	31	1.3	389	13	BI793141	ie48d10.y
32	380	32	1.3	910	14	BO681678	AGENCOURT	C 453	31	1.3	389	17	AQ550369	RPC1-11-3
32	381	32	1.3	913	12	BF677812	602085323	C 454	31	1.3	390	13	BI793172	ie48h05.y
32	382	32	1.3	917	12	BE732904	601567847	C 455	31	1.3	393	10	BE143560	MRO-HT016
32	383	32	1.3	944	14	BQ709478	AGENCOURT	C 456	31	1.3	393	17	AQ136323	HS_3056.B
32	384	32	1.3	948	17	AQ744098	HS_5501.A	C 457	31	1.3	395	9	AI289050	Qw32a01.x
32	385	32	1.3	956	13	BE756385	603030284	C 458	31	1.3	395	9	AA174017	zpl18h06.s
32	386	32	1.3	1100	13	BM554817	AGENCOURT	C 459	31	1.3	395	14	N71033	za35802.s1
32	387	32	1.3	1485	17	AF101893	AF101893	C 460	31	1.3	396	17	AQ027194	CIT-HSP-2
32	388	32	1.3	2084	11	BC025705	Homo sapi	C 461	31	1.3	398	14	F24745	HSF2p6868B
32	389	32	1.3	2638	11	AF318344	Homo sapi	C 462	31	1.3	399	9	AL700720	DKFZp6868B
32	390	32	1.3	3352	11	AF313681	BC013681	C 463	31	1.3	404	14	H63496	yf548a06.s1
32	391	32	1.3	87	14	N85990	J5884F Huma	C 464	31	1.3	404	17	AQ347410	RPC111-11
32	392	31	1.3	122	9	AI003655	zG01a01.s	C 465	31	1.3	405	10	BE065718	RC2-BT031
32	393	31	1.3	173	12	BE900510	PM1-MT019	C 466	31	1.3	407	9	AI858889	w145b03.x
32	394	31	1.3	187	10	AW080185	xe49f06.x	C 467	31	1.3	408	9	AI362442	qu96a03.x
32	395	31	1.3	202	12	BF811008	CM2-C1017	C 468	31	1.3	409	17	AQ818485	HS_5250.A
32	396	31	1.3	206	13	BM456815	AGENCOURT	C 469	31	1.3	410	9	AI911839	wc79a04.x
32	397	31	1.3	206	17	AQ279397	CITBI-E1-	C 470	31	1.3	411	9	AA564359	nk45e04.s
32	398	31	1.3	216	17	AQ034502	CIT-HSP-2	C 471	31	1.3	411	17	AQ319503	RPC111-97
32	399	31	1.3	231	14	H68240	yu69f08.s1	C 472	31	1.3	411	17	AQ532648	RPC1-11-3
400		31	1.3	239	12	BF876573	QV0-ET014	C 473	31	1.3	412	9	AI055924	ox44b06.s
401		31	1.3	244	12	BF857321	BF857321	C 474	31	1.3	412	14	T83505	y603607.r1
402		31	1.3	248	9	AA525288	n153a10.s	C 475	31	1.3	413	17	AI284092	qt67b11.x
403		31	1.3	248	10	AW945453	PM0-EN000	C 476	31	1.3	413	17	AQ512389	HS_5114.A
404		31	1.3	249	12	BF838584	IL5-HT099	C 477	31	1.3	413	17	AQ512408	HS_5114.A
405		31	1.3	249	14	BQ632526	il28c08.x	C 478	31	1.3	415	10	BE151738	PM1-HT030
406		31	1.3	266	9	AA063139	zif68a03.s	C 479	31	1.3	417	17	AQ566115	HS_5374.A
407		31	1.3	270	10	AW936354	QVA-DT002	C 480	31	1.3	418	17	AQ443330	HS_2231.B
408		31	1.3	271	17	AQ561438	HS_5357.A	C 481	31	1.3	424	9	AI561041	qt29d11.x
409		31	1.3	277	9	AA613761	no95G05.s	C 482	31	1.3	424	17	AQ038204	CIT-HSP-2
410		31	1.3	281	17	BS1151	CIT978SK-76	C 483	31	1.3	425	9	AA856904	oh93e02.s
411		31	1.3	283	9	AA610344	np90h11.s	C 484	31	1.3	425	10	AW513946	xt93a12.x
412		31	1.3	283	12	BF927768	IL2-NT020	C 485	31	1.3	426	10	N62571	za13b12.s1
413		31	1.3	286	9	AA082588	zn23f12.r	C 486	31	1.3	427	14	R64204	y118d06.r1
414		31	1.3	299	17	AQ040045	CIT-HSP-2	C 487	31	1.3	428	10	AW833161	RC3-TT000
415		31	1.3	301	10	AW663162	hh75d08.y	C 488	31	1.3	430	14	H96479	vt98e03.r1
416		31	1.3	302	10	AW886085	RC6-OT007	C 489	31	1.3	430	17	AQ507157	RPC1-11-2
417		31	1.3	303	9	AA483326	ne93a11.s	C 490	31	1.3	432	17	AQ789970	HS_3177.B
418		31	1.3	304	17	BS0766	CIT-HSP-698	C 491	31	1.3	433	9	AI160144	q6b3b09.x
419		31	1.3	305	10	AW993388	RC3-BN003	C 492	31	1.3	435	9	AA112791	zn54d08.r
420		31	1.3	308	9	AA862184	oe13b04.s	C 493	31	1.3	436	14	TS1832	yB54c08.s1
421		31	1.3	317	9	AI637960	tt26h08.x	C 494	31	1.3	438	10	AW303888	xr24h07.x
422		31	1.3	317	17	AQ093667	HS_3022.A	C 495	31	1.3	441	17	AQ179780	HS_3185.B
423		31	1.3	318	10	AW022704	dfr2e11.y	C 496	31	1.3	443	14	BM690267	UI-E-ClO-
424		31	1.3	322	17	AQ504293	RPC1-11-2	C 497	31	1.3	444	10	AW150111	xg48d10.x
425		31	1.3	327	14	W45283	zc80c08.s1	C 498	31	1.3	444	17	AQ207583	HS_2243.B
426		31	1.3	329	14	W45298	zc80d07.s1	C 499	31	1.3	446	9	AA584241	mn71g12.s
427		31	1.3	331	12	BG222405	naj74b12.	C 500	31	1.3	447	9	AI570805	tr67d06.x
428		31	1.3	333	17	B63128	CIT978SK-A-	C 501	31	1.3	447	9	AI953764	wx69b01.x
429		31	1.3	335	9	AL712159	DKFZp686C	C 502	31	1.3	447	10	AW250029	2819251.3
430		31	1.3	337	17	AQ067790	HS_2233.B	C 503	31	1.3	447	17	B33682	HS-1023-AI-
431		31	1.3	342	9	AA053253	z172e09.s	C 504	31	1.3	449	9	AA205399	zq79g01.s
432		31	1.3	345	12	BG223550	naj52h02.	C 505	31	1.3	449	9	AA504996	ab04f03.r
433		31	1.3	345	17	AQ097220	HS_3038.B	C 506	31	1.3	450	17	AQ064450	HS_2198.B
434		31	1.3	347	10	AW804963	QVA-UM009	C 507	31	1.3	451	17	B65846	CIT-HSP-202
435		31	1.3	350	17	AQ695996	HS_5486.B	C 508	31	1.3	452	10	AW235522	xn19b11.x
436		31	1.3	351	12	BF906827	RC3-ST019	C 509	31	1.3	453	17	AQ793843	HS_5252.B
437		31	1.3	356	17	AQ060968	AQ063968	C 510	31	1.3	454	17	B56476	CIT-HSP-200
438		31	1.3	357	9	AI433131	th41g10.x	C 511	31	1.3	456	14	T08075	EST05966
439		31	1.3	357	9	AA493464	ng75d06.s	C 512	31	1.3	457	9	AI954248	wx95a02.x
440		31	1.3	357	17	AQ151129	HS_2186.A	C 513	31	1.3	457	17	AQ220208	HS_2006.B
441		31	1.3	359	9	AA569089	nm35g04.s	C 514	31	1.3	459	9	AI598003	ts05d01.x
442		31	1.3	361	9	AI366993	tb80d10.x	C 515	31	1.3	460	17	BI5692	345N8.TP.CI
443		31	1.3	363	10	AV762979	AV762979	C 516	31	1.3	464	9	AI342622	qt33e08.x
444		31	1.3	367	9	AI453476	tj28d07.x	C 517	31	1.3	465	10	AW972801	EST384996

c 518	31	1.3	466	14	BQ575431	UI-H-EZ1-	BQ575431	31	1.3	585	9	AU145035	AU145035
c 519	31	1.3	472	12	BF874974	MR1-ET014	BF874974	31	1.3	592	10	AV716255	AV716255
c 520	31	1.3	472	14	T78512	Yd68c01.r1	T78512	31	1.3	592	10	AQ008952	RPC111-22
c 521	31	1.3	472	14	T78512	Yd68c01.r1	T78512	31	1.3	592	10	AQ008952	RPC111-22
c 522	31	1.3	473	9	AA494452	ne38a09.s	AA494452	31	1.3	595	17	AQ344454	RPC111-11
c 523	31	1.3	475	17	AQ123045	HS 3095.B	AQ123045	31	1.3	595	17	AQ242414	CITBI-E1-
c 524	31	1.3	476	13	BI436628	BI436628	BI436628	31	1.3	596	17	AQ242414	CITBI-E1-
c 525	31	1.3	477	9	AI591174	AI591174	AI591174	31	1.3	600	12	BF678990	602153630
c 526	31	1.3	478	9	AA526099	AA526099	AA526099	31	1.3	601	12	BF678990	602153630
c 527	31	1.3	480	10	BE143258	MR0-HT016	BE143258	31	1.3	602	17	AQ54076	RPC111-3
c 528	31	1.3	481	9	AI986165	AI986165	AI986165	31	1.3	613	17	AQ414472	RPC111-1
c 529	31	1.3	482	12	BF845248	BF845248	BF845248	31	1.3	613	17	AQ414472	RPC111-1
c 530	31	1.3	483	10	AV719884	AV719884	AV719884	31	1.3	616	10	AV732982	AV732982
c 531	31	1.3	483	17	B87837	B87837	B87837	31	1.3	616	10	AV732982	AV732982
c 532	31	1.3	486	17	B87844	B87844	B87844	31	1.3	616	10	AV732982	AV732982
c 533	31	1.3	487	9	AA634095	AA634095	AA634095	31	1.3	623	17	AG058831	Pan trogl
c 534	31	1.3	492	12	BF889156	BF889156	BF889156	31	1.3	623	17	AG058831	Pan trogl
c 535	31	1.3	493	17	AQ142111	AQ142111	AQ142111	31	1.3	624	10	AV718908	AV718908
c 536	31	1.3	495	17	AQ342662	AQ342662	AQ342662	31	1.3	624	10	AV718908	AV718908
c 537	31	1.3	497	9	AA037725	AA037725	AA037725	31	1.3	626	17	AQ804056	PW2-UM008
c 538	31	1.3	497	12	BE968744	BE968744	BE968744	31	1.3	626	17	AQ804056	PW2-UM008
c 539	31	1.3	503	14	BQ015442	BQ015442	BQ015442	31	1.3	628	17	AQ417535	RPC111-1
c 540	31	1.3	503	17	AQ732529	HS 5543.B	AQ732529	31	1.3	631	17	AQ061135	CIT-HSP-2
c 541	31	1.3	503	17	AZ755833	AZ755833	AZ755833	31	1.3	631	17	AQ382985	RPC111-13
c 542	31	1.3	506	9	AI126238	AI126238	AI126238	31	1.3	636	10	AV761707	AV761707
c 543	31	1.3	506	9	AI640367	AI640367	AI640367	31	1.3	637	10	AV761729	AV761729
c 544	31	1.3	511	9	AI885488	AI885488	AI885488	31	1.3	637	10	AV761729	AV761729
c 545	31	1.3	514	17	AQ884228	HS 5504.B	AQ884228	31	1.3	638	17	AG101075	Pan trogl
c 546	31	1.3	515	9	AA577706	AA577706	AA577706	31	1.3	638	17	AG101075	Pan trogl
c 547	31	1.3	515	12	BF878961	BF878961	BF878961	31	1.3	638	17	AG101075	Pan trogl
c 548	31	1.3	516	17	AQ347616	AQ347616	AQ347616	31	1.3	645	17	AQ315803	RPC111-94
c 549	31	1.3	517	17	AQ155788	HS 3185.B	AQ155788	31	1.3	645	17	AQ315803	RPC111-94
c 550	31	1.3	517	17	AZ757035	AZ757035	AZ757035	31	1.3	646	17	AG138843	Pan trogl
c 551	31	1.3	518	17	AQ425239	AQ425239	AQ425239	31	1.3	646	17	BE072376	OV0-BT053
c 552	31	1.3	519	9	AI814721	AI814721	AI814721	31	1.3	648	10	BE072376	OV0-BT053
c 553	31	1.3	519	9	AI702651	AI702651	AI702651	31	1.3	648	10	BE072376	OV0-BT053
c 554	31	1.3	519	14	BM997623	BM997623	BM997623	31	1.3	648	10	BE072376	OV0-BT053
c 555	31	1.3	520	10	BE066487	BE066487	BE066487	31	1.3	650	17	AG180765	Pan trogl
c 556	31	1.3	521	9	AA134472	AA134472	AA134472	31	1.3	651	10	AV733239	AV733239
c 557	31	1.3	521	17	AQ462183	AQ462183	AQ462183	31	1.3	651	10	AV733239	AV733239
c 558	31	1.3	523	9	AI054414	AI054414	AI054414	31	1.3	653	17	AG052307	Pan trogl
c 559	31	1.3	527	10	AW966777	AW966777	AW966777	31	1.3	653	17	AG052307	Pan trogl
c 560	31	1.3	528	9	AA707137	AA707137	AA707137	31	1.3	657	13	BI492664	df27e02.w
c 561	31	1.3	529	12	BG402924	BG402924	BG402924	31	1.3	657	13	BI492664	df27e02.w
c 562	31	1.3	529	17	AQ464785	AQ464785	AQ464785	31	1.3	659	17	AG155371	Pan trogl
c 563	31	1.3	531	17	AQ452366	HS 5154.A	AQ452366	31	1.3	660	17	AG155371	Pan trogl
c 564	31	1.3	535	12	BF851643	BF851643	BF851643	31	1.3	660	17	AG155371	Pan trogl
c 565	31	1.3	536	17	AZ254536	AZ254536	AZ254536	31	1.3	668	17	AG045483	Pan trogl
c 566	31	1.3	536	17	AQ236378	HS 2041.A	AQ236378	31	1.3	668	17	AG045483	Pan trogl
c 567	31	1.3	539	14	R76565	R76565	R76565	31	1.3	668	17	AG045483	Pan trogl
c 568	31	1.3	539	17	AQ450654	AQ450654	AQ450654	31	1.3	668	17	AG045483	Pan trogl
c 569	31	1.3	542	9	AI871103	AI871103	AI871103	31	1.3	668	17	AG045483	Pan trogl
c 570	31	1.3	542	17	AQ635546	AQ635546	AQ635546	31	1.3	668	17	AG045483	Pan trogl
c 571	31	1.3	545	17	AQ712209	HS 2114.A	AQ712209	31	1.3	668	17	AG045483	Pan trogl
c 572	31	1.3	546	10	AW836779	AW836779	AW836779	31	1.3	668	17	AG045483	Pan trogl
c 573	31	1.3	546	12	BG422108	BG422108	BG422108	31	1.3	668	17	AG045483	Pan trogl
c 574	31	1.3	547	17	AQ800801	HS 5299.A	AQ800801	31	1.3	668	17	AG045483	Pan trogl
c 575	31	1.3	547	17	AQ344772	AQ344772	AQ344772	31	1.3	668	17	AG045483	Pan trogl
c 576	31	1.3	548	17	AQ318090	AQ318090	AQ318090	31	1.3	668	17	AG045483	Pan trogl
c 577	31	1.3	551	9	AL698703	AL698703	AL698703	31	1.3	668	17	AG045483	Pan trogl
c 578	31	1.3	551	12	BG189142	BG189142	BG189142	31	1.3	668	17	AG045483	Pan trogl
c 579	31	1.3	558	17	AQ603083	AQ603083	AQ603083	31	1.3	668	17	AG045483	Pan trogl
c 580	31	1.3	559	14	BM874128	BM874128	BM874128	31	1.3	668	17	AG045483	Pan trogl
c 581	31	1.3	560	13	BM505425	BM505425	BM505425	31	1.3	668	17	AG045483	Pan trogl
c 582	31	1.3	571	17	AQ802982	AQ802982	AQ802982	31	1.3	668	17	AG045483	Pan trogl
c 583	31	1.3	572	14	BQ020816	BQ020816	BQ020816	31	1.3	668	17	AG045483	Pan trogl
c 584	31	1.3	575	17	AQ563986	HS 5334.B	AQ563986	31	1.3	668	17	AG045483	Pan trogl
c 585	31	1.3	576	10	AV714886	AV714886	AV714886	31	1.3	668	17	AG045483	Pan trogl
c 586	31	1.3	578	9	AL047793	AL047793	AL047793	31	1.3	668	17	AG045483	Pan trogl
c 587	31	1.3	578	13	BM509841	BM509841	BM509841	31	1.3	668	17	AG045483	Pan trogl
c 588	31	1.3	578	17	B93700	B93700	B93700	31	1.3	668	17	AG045483	Pan trogl
c 589	31	1.3	581	10	AV761497	AV761497	AV761497	31	1.3	668	17	AG045483	Pan trogl
c 590	31	1.3	581	12	BG623941	BG623941	BG623941	31	1.3	668	17	AG045483	Pan trogl

c 664	31	1.3	726	17	AZ254557	HSC 00177	737	30	1.2	219	17	AQ538879	AQ538879	RPIC1-11-3
c 665	31	1.3	734	17	AG166338	Pan trogl	c 738	30	1.2	221	9	AI886056	AI886056	w08h04.x
c 666	31	1.3	737	14	BM975105	UT-CF-ECL	c 739	30	1.2	223	9	AA812287	AA812287	nr82f08.s
c 667	31	1.3	739	17	AG000964	Homo sapi	c 740	30	1.2	234	9	AA610803	AA610803	np92e03.s
c 668	31	1.3	741	17	AG088253	Pan trogl	c 741	30	1.2	237	17	AQ274956	AQ274956	RPIC1-4-72
c 669	31	1.3	748	17	AG000963	Homo sapi	c 742	30	1.2	241	9	AA773424	AA773424	ab58b02.s
c 670	31	1.3	748	17	AG000970	Homo sapi	c 743	30	1.2	244	14	BQ360810	BQ360810	RC1-OT008
c 671	31	1.3	751	17	AG000944	Homo sapi	c 744	30	1.2	246	10	AA834473	AA834473	MR2-TT001
c 672	31	1.3	753	14	BQ053071	AGENCOURT	c 745	30	1.2	247	9	AA715201	AA715201	n749i2.x
c 673	31	1.3	754	17	AG000969	Homo sapi	c 746	30	1.2	250	10	BE062239	BE062239	RC1-ET025
c 674	31	1.3	755	17	AG000945	Homo sapi	c 747	30	1.2	251	12	BE783829	BE783829	601471056
c 675	31	1.3	761	17	AQ745261	HS 5503.A	c 748	30	1.2	252	10	AA834369	AA834369	MR2-TT001
c 676	31	1.3	766	17	AQ788194	HS 3135.A	c 749	30	1.2	255	9	AI886434	AI886434	w094g04.x
c 677	31	1.3	776	17	AG000971	Homo sapi	c 750	30	1.2	255	10	BE063646	BE063646	IL5-ET028
c 678	31	1.3	779	12	BF675202	602138131	c 751	30	1.2	256	9	AI926240	AI926240	w041g01.x
c 679	31	1.3	779	12	BG197390	RST16633	c 752	30	1.2	256	14	F13808	F13808	HSF1M1008.S
c 680	31	1.3	804	12	BG179552	602328163	c 753	30	1.2	258	17	AQ373299	AQ373299	RPIC11-14
c 681	31	1.3	804	12	BG179552	602328163	c 754	30	1.2	258	10	BE081332	BE081332	QV1-BT063
c 682	31	1.3	809	12	BG207230	RST26698	c 755	30	1.2	259	14	T07414	T07414	EST05303.Fe
c 683	31	1.3	810	12	BG214593	RST34236	c 756	30	1.2	267	9	AI872513	AI872513	w09b04.x
c 684	31	1.3	819	17	AQ741638	HS 5572.B	c 757	30	1.2	271	9	AA370455	AA370455	EST82092
c 685	31	1.3	831	13	BI818348	603032973	c 758	30	1.2	271	10	AA834419	AA834419	MR2-TT001
c 686	31	1.3	838	17	AQ782284	HS 3184.B	c 759	30	1.2	272	10	BE153150	BE153150	PWO-HT033
c 687	31	1.3	839	17	AQ781535	HS 3174.A	c 760	30	1.2	274	9	AA054055	AA054055	zf48e07.r
c 688	31	1.3	853	17	AQ739924	HS 5506.A	c 761	30	1.2	275	9	AA578925	AA578925	n330c01.s
c 689	31	1.3	861	12	BG752933	602732584	c 762	30	1.2	275	9	AA581238	AA581238	n038b01.s
c 690	31	1.3	886	17	AQ787966	HS 3100.A	c 763	30	1.2	275	10	AW131272	AW131272	x660h05.x
c 691	31	1.3	896	17	AQ738735	HS 5382.B	c 764	30	1.2	279	9	AA570136	AA570136	n046h08.s
c 692	31	1.3	898	12	BF215757	601881252	c 765	30	1.2	280	9	AA050502	AA050502	nh96d11.s
c 693	31	1.3	911	14	BQ719276	AGENCOURT	c 766	30	1.2	282	9	AA078084	AA078084	7P01D01.C
c 694	31	1.3	927	9	AL536593	AL536593	c 767	30	1.2	283	14	F02611	F02611	HSC14C112.n
c 695	31	1.3	952	14	BQ711992	AGENCOURT	c 768	30	1.2	288	14	F12053	F12053	HSC35B071.n
c 696	31	1.3	964	12	BG483309	602504172	c 769	30	1.2	290	9	AI241851	AI241851	qu69b01.x
c 697	31	1.3	967	13	BM466372	AGENCOURT	c 770	30	1.2	292	17	AZ757648	AZ757648	ew10f08.r
c 698	31	1.3	1001	14	BQ070984	AGENCOURT	c 771	30	1.2	293	17	AQ093533	AQ093533	HS 3026.B
c 699	31	1.3	1040	13	BM559264	AGENCOURT	c 772	30	1.2	293	17	AQ489212	AQ489212	RPIC1-11-2
c 700	31	1.3	1072	14	BQ071445	AGENCOURT	c 773	30	1.2	294	10	AA886953	AA886953	RC1-OT008
c 701	31	1.3	1103	13	BM479678	AGENCOURT	c 774	30	1.2	294	17	AQ067336	AQ067336	HS 2237.A
c 702	31	1.3	2435	11	AF289560	Homo sapi	c 775	30	1.2	300	9	AI824740	AI824740	ws57f02.x
c 703	31	1.2	95	9	AA669571	ac18d10.s	c 776	30	1.2	300	9	AA381675	AA381675	EST94781
c 704	30	1.2	104	9	AA129957	zn86h04.r	c 777	30	1.2	301	9	AA742818	AA742818	nv34g04.r
c 705	30	1.2	112	10	AA589602	x013a01.x	c 778	30	1.2	302	9	AA853397	AA853397	NHTBCae05
c 706	30	1.2	126	9	AA228768	nc14b07.s	c 779	30	1.2	305	9	AA747607	AA747607	wx73g09.s
c 707	30	1.2	128	14	BQ353357	IL3-BT061	c 780	30	1.2	305	9	AI932902	AI932902	nx039d10.x
c 708	30	1.2	131	9	AI251360	qvs6e03.x	c 781	30	1.2	306	9	AA728812	AA728812	nx57g08.s
c 709	30	1.2	132	9	AA873660	oe02g11.s	c 782	30	1.2	306	9	AA985243	AA985243	ng80e02.s
c 710	30	1.2	137	10	AA878190	MR3-OT000	c 783	30	1.2	306	9	AA941415	AA941415	ng98b08.s
c 711	30	1.2	139	9	AF137025	AF137025	c 784	30	1.2	306	9	AA581183	AA581183	nd38b01.r
c 712	30	1.2	141	9	AA582889	nn72d01.s	c 785	30	1.2	306	12	BF941940	BF941940	nac37f05.
c 713	30	1.2	151	12	BF920430	QV2-NT014	c 786	30	1.2	309	10	AA841318	AA841318	RC6-CN001
c 714	30	1.2	155	9	AI254980	qv48a11.x	c 787	30	1.2	309	10	AA841370	AA841370	RC6-CN001
c 715	30	1.2	156	14	N52227	yv46c12.s1	c 788	30	1.2	312	9	AA363152	AA363152	EST72963
c 716	30	1.2	162	9	AA354535	EST62814	c 789	30	1.2	313	17	BE7600	BE7600	CIT-HSP-201
c 717	30	1.2	165	17	AQ045666	RPIC11-34	c 790	30	1.2	314	17	AA834851	AA834851	oe02a08.s
c 718	30	1.2	170	9	AA775154	ac78e02.s	c 791	30	1.2	315	10	AA339296	AA339296	hb72b01.x
c 719	30	1.2	174	9	AI555803	to31c10.x	c 792	30	1.2	315	10	AA279125	AA279125	z683c05.s
c 720	30	1.2	180	12	BG272027	na16g12.	c 793	30	1.2	316	14	F09946	F09946	HSC38E072.n
c 721	30	1.2	187	9	AA504921	ab03b09.r	c 794	30	1.2	316	17	AQ061991	AQ061991	CIT-HSP-2
c 722	30	1.2	188	14	BQ360836	RC1-OT008	c 795	30	1.2	317	10	AA875173	AA875173	RC0-PT000
c 723	30	1.2	196	9	AI611736	tu7g09.x	c 796	30	1.2	318	14	F11080	F11080	HSC3FC112.n
c 724	30	1.2	197	10	BE158883	RC5-HT040	c 797	30	1.2	319	14	F27738	F27738	HSPD15869.H
c 725	30	1.2	200	9	AA484901	ne81h11.s	c 798	30	1.2	320	14	HS1061	HS1061	YP84g09.r1
c 726	30	1.2	201	9	AA877303	nr08d05.s	c 799	30	1.2	322	10	BE155708	BE155708	PM4-HT035
c 727	30	1.2	202	9	AF202336	AF202336	c 800	30	1.2	324	14	R76682	R76682	y161d07.s1
c 728	30	1.2	202	14	N91357	zb39d02.s1	c 801	30	1.2	325	17	AQ000933	AQ000933	CIT-HSP-2
c 729	30	1.2	203	17	AQ059130	CIT-HSP-2	c 802	30	1.2	329	9	AA224236	AA224236	zr14g09.s
c 730	30	1.2	206	9	AA975291	q036g04.s	c 803	30	1.2	330	14	Z21713	Z21713	HSB25C04.S
c 731	30	1.2	206	10	AA878020	MR3-OT000	c 804	30	1.2	332	17	B80516	B80516	CIT-HSP-205
c 732	30	1.2	208	9	AA374775	EST86967	c 805	30	1.2	333	9	AA826844	AA826844	nr50a06.s
c 733	30	1.2	209	9	AA599556	ag08b03.s	c 806	30	1.2	334	9	AI754544	AI754544	cr26f08.x
c 734	30	1.2	213	10	AA855982	RC3-CT028	c 807	30	1.2	334	10	AW194802	AW194802	xn31603.x
c 735	30	1.2	215	10	BE002911	QV4-BN009.	c 808	30	1.2	335	12	BF813915	BF813915	RC4-CI019
c 736	30	1.2	215	17	AQ044864	CIT-HSP-2	c 809	30	1.2	335	14	M77870	M77870	EST01454.Fe

810	30	1.2	340	9	AA666295	AA666295 ac39a10.s	883	30	1.2	394	10	BE677029	BE677029 7d51f07.x
811	30	1.2	342	12	BF859011	BF859011 MR0-FT018	884	30	1.2	394	12	BF061272	BF061272 7d55906.x
812	30	1.2	343	10	BE243948	BE243948 TCBAPE14	C 885	30	1.2	395	10	AA666059	AA666059 ac41b06.s
813	30	1.2	345	17	AQ676759	AQ676759 HS 5496_B	C 886	30	1.2	395	9	AI240701	AI240701 qh53e06.x
814	30	1.2	346	9	AA345064	AA345064 EST51047	C 887	30	1.2	395	9	AI112925	AI112925 zn54912.x
815	30	1.2	346	17	B35322	B35322 HS-1028-B1-	C 888	30	1.2	395	9	AI690497	AI690497 tx99e08.x
816	30	1.2	347	9	AA643448	AA643448 nui3h11.s	C 889	30	1.2	396	9	AA167178	AA167178 zp15a11.x
817	30	1.2	347	9	AI247002	AI247002 qx52b04.x	C 890	30	1.2	397	9	AA167556	AA167556 zp15a11.x
818	30	1.2	349	10	BE155734	BE155734 PM4-HT035	C 891	30	1.2	398	10	AW696374	AW696374 AV696374
819	30	1.2	349	10	BE155735	BE155735 PM4-HT035	C 892	30	1.2	398	10	AW696374	AW696374 AV696374
820	30	1.2	351	9	AA864575	AA864575 oh31c11.s	C 893	30	1.2	399	13	BM313409	BM313409 is71g11.x
821	30	1.2	351	9	AA347203	AA347203 EST53463	C 894	30	1.2	400	14	R73754	R73754 yis5e08.r1
822	30	1.2	353	10	AV760169	AV760169 AV760169	C 895	30	1.2	400	17	Q583654	Q583654 RPC1-11-4
823	30	1.2	353	12	EG152753	EG152753 nag84e12.	C 896	30	1.2	401	9	AI367544	AI367544 qv33d04.x
824	30	1.2	354	9	AA806762	AA806762 ob91c11.s	C 897	30	1.2	402	9	AA652332	AA652332 ns50g03.s
825	30	1.2	355	14	BQ130165	BQ130165 j185g03.x	C 898	30	1.2	402	9	AA486174	AA486174 ab14f05.r
826	30	1.2	355	17	B71387	B71387 RPC11-7P3.	C 899	30	1.2	402	10	AV764009	AV764009 AV764009
827	30	1.2	356	9	AA911584	AA911584 od30a06.s	C 900	30	1.2	402	17	Q262843	Q262843 CITBI-E1-
828	30	1.2	358	10	AV709871	AV709871 AV709871	C 901	30	1.2	403	9	AA865508	AA865508 oh30a12.s
829	30	1.2	358	14	R79873	R79873 y185a05.r1	C 902	30	1.2	404	9	AI310343	AI310343 oh70h12.x
830	30	1.2	359	14	BQ445989	BQ445989 UT-H-EUL-	C 903	30	1.2	404	17	AQ092724	AQ092724 HS 3005_A
831	30	1.2	360	9	AI537014	AI537014 to15a03.x	C 904	30	1.2	405	17	AQ031211	AQ031211 HS 2228_A
832	30	1.2	361	9	AA688267	AA688267 nv57g02.s	C 905	30	1.2	406	9	AI360521	AI360521 qx18d10.x
833	30	1.2	361	9	AA128511	AA128511 zn86h04.s	C 906	30	1.2	407	9	AA085863	AA085863 zn86e10.s
834	30	1.2	362	9	AA643444	AA643444 nui3f12.s	C 907	30	1.2	408	17	AQ043493	AQ043493 CIT-HSP-2
835	30	1.2	364	13	BI491116	BI491116 df04a09.w	C 908	30	1.2	409	10	BE152256	BE152256 QV4-HT031
836	30	1.2	365	10	AW020088	AW020088 df04a09.y	C 909	30	1.2	410	9	AA971630	AA971630 op94d04.s
837	30	1.2	366	10	BE143936	BE143936 MR0-HT016	C 910	30	1.2	410	9	AI278592	AI278592 qo43c04.x
838	30	1.2	366	10	BE143990	BE143990 MR0-HT016	C 911	30	1.2	410	14	H65404	H65404 yu63a12.r1
839	30	1.2	366	14	BQ024136	BQ024136 UT-1-BB1p	C 912	30	1.2	411	10	BE152291	BE152291 QV4-HT031
840	30	1.2	367	9	AA862035	AA862035 oi46f01.s	C 913	30	1.2	412	9	AA525879	AA525879 ni57f03.s
841	30	1.2	367	12	BG152612	BG152612 naf57h02.	C 914	30	1.2	412	14	D58429	D58429 HUM500803B
842	30	1.2	367	17	AQ137721	AQ137721 HS 3065_B	C 915	30	1.2	412	17	AQ260163	AQ260163 CITBI-E1-
843	30	1.2	369	14	R21450	R21450 YG05a11.r1	C 916	30	1.2	414	9	AI160117	AI160117 qb51g09.x
844	30	1.2	370	10	AV741072	AV741072 AV741072	C 917	30	1.2	415	9	AI204981	AI204981 an03a07.x
845	30	1.2	370	10	AV743401	AV743401 AV743401	C 918	30	1.2	417	17	AQ303072	AQ303072 RPC1-11-3
846	30	1.2	371	10	AW886251	AW886251 RC5-OT007	C 919	30	1.2	417	17	AQ661804	AQ661804 HS 2137_A
847	30	1.2	371	10	AW886329	AW886329 RC5-OT007	C 920	30	1.2	418	9	AI360690	AI360690 qx64g03.x
848	30	1.2	371	10	AW886331	AW886331 RC5-OT007	C 921	30	1.2	421	10	BE348907	BE348907 hs90h04.x
849	30	1.2	371	10	AW887931	AW887931 RC5-OT070	C 922	30	1.2	421	17	AQ020506	AQ020506 CIT-HSP-2
850	30	1.2	371	10	AW887933	AW887933 RC5-OT070	C 923	30	1.2	422	10	AW081194	AW081194 xc40s08.x
851	30	1.2	372	9	AA652064	AA652064 ns50a03.s	C 924	30	1.2	423	9	AA774027	AA774027 ab67h03.r
852	30	1.2	372	10	AV736037	AV736037 AV736037	C 925	30	1.2	423	10	AW819125	AW819125 RC3-ST028
853	30	1.2	373	14	R10602	R10602 yf35f09.s1	C 926	30	1.2	423	14	H69000	H69000 yul7d05.s1
854	30	1.2	374	17	AQ383763	AQ383763 RPC11-12	C 927	30	1.2	426	9	AA558710	AA558710 nl42d02.s
855	30	1.2	375	17	AQ100384	AQ100384 HS 3055_A	C 928	30	1.2	426	14	N45314	N45314 yz17c10.s1
856	30	1.2	377	14	BQ360734	BQ360734 RC5-OT007	C 929	30	1.2	426	17	AQ675034	AQ675034 HS 2139_A
857	30	1.2	377	17	AQ038465	AQ038465 CIT-HSP-2	C 930	30	1.2	427	17	BQ360680	BQ360680 RCI-OT008
858	30	1.2	378	9	AA190854	AA190854 zp85a01.s	C 931	30	1.2	427	17	AQ040782	AQ040782 HS 5044_A
859	30	1.2	378	10	BE183069	BE183069 CM2-HT065	C 932	30	1.2	430	10	AW189336	AW189336 x104h09.x
860	30	1.2	380	9	AA828800	AA828800 od76f02.s	C 933	30	1.2	430	10	AW189336	AW189336 x104h09.x
861	30	1.2	382	9	AI049512	AI049512 an21c07.s	C 934	30	1.2	430	10	AW438661	AW438661 xu37g02.x
862	30	1.2	382	9	AI285578	AI285578 qh08e02.x	C 935	30	1.2	431	9	AA804731	AA804731 nm29e11.s
863	30	1.2	382	10	AW862568	AW862568 QV0-CT038	C 936	30	1.2	431	9	AI801540	AI801540 to90g05.x
864	30	1.2	384	14	BQ360693	BQ360693 RC5-OT007	C 937	30	1.2	431	14	H69653	H69653 yr92a01.s1
865	30	1.2	386	10	AW866188	AW866188 QV4-SN002	C 938	30	1.2	431	10	AW054710	AW054710 w296g07.x
866	30	1.2	387	10	AW894960	AW894960 CM1-NN003	C 939	30	1.2	433	10	AW192471	AW192471 x144e10.x
867	30	1.2	388	9	AA371570	AA371570 EST83375	C 940	30	1.2	433	10	AW054710	AW054710 w296g07.x
868	30	1.2	389	9	AI561192	AI561192 tq37g11.x	C 941	30	1.2	433	14	BQ083695	BQ083695 K-EST0146
869	30	1.2	389	10	AW866252	AW866252 RC5-OT007	C 942	30	1.2	433	14	BQ083695	BQ083695 K-EST0146
870	30	1.2	389	10	AW887894	AW887894 RC5-OT070	C 943	30	1.2	433	17	AQ088806	AQ088806 HS 3002_A
871	30	1.2	389	12	BG014939	BG014939 RC4-GN032	C 944	30	1.2	434	17	AQ117512	AQ117512 HS 2187_B
872	30	1.2	390	9	AI014671	AI014671 os36d08.s	C 945	30	1.2	434	10	AW86249	AW86249 RC5-OT007
873	30	1.2	391	12	BF814354	BF814354 MR2-C1012	C 946	30	1.2	435	10	AV720567	AV720567 AV720567
874	30	1.2	391	17	AQ153758	AQ153758 HS 2245_B	C 947	30	1.2	436	9	AI278865	AI278865 qo42g05.x
875	30	1.2	392	10	AW866301	AW866301 RC5-OT007	C 948	30	1.2	436	9	AI684097	AI684097 tx79b07.x
876	30	1.2	392	14	R05313	R05313 ye91h03.s1	C 949	30	1.2	436	9	AA452521	AA452521 ng98h03.s
877	30	1.2	392	14	T53408	T53408 ya88g10.s1	C 950	30	1.2	436	17	AQ089756	AQ089756 HS 3006_B
878	30	1.2	393	14	AA427747	AA427747 zw26h03.s	C 951	30	1.2	437	14	H10143	H10143 ym05a11.s1
879	30	1.2	393	9	AA427747	AA427747 zw26h03.s	C 952	30	1.2	438	14	R79496	R79496 yi88e02.r1
880	30	1.2	393	10	AV703785	AV703785 AV703785	C 953	30	1.2	438	14	R79496	R79496 yi88e02.r1
881	30	1.2	394	9	AI874201	AI874201 wm50b08.x	C 954	30	1.2	438	14	R83708	R83708 yq14f09.r1
882	30	1.2	394	9	AA244339	AA244339 nc07c08.r	C 955	30	1.2	438	17	AQ059866	AQ059866 CIT-HSP-2

956	30	1.2	439	14	BQ360684	BQ360684 RC5-OT007
957	30	1.2	439	14	BQ360694	BQ360694 RC5-OT007
958	30	1.2	440	12	BF773446	BF773446 CM2-IT003
959	30	1.2	440	14	BQ360683	BQ360683 RC5-OT007
960	30	1.2	440	17	AQ596450	AQ596450 HS 5198.A
961	30	1.2	441	9	AA630535	AA630535 ab96d05.5
962	30	1.2	441	12	BF800786	BF800786 CM1-CI009
963	30	1.2	442	9	AA569734	AA569734 nf25c05.8
964	30	1.2	443	9	AA486111	AA486111 ab14f05.8
965	30	1.2	443	10	AW402143	AW402143 UI-HF-BK0
966	30	1.2	444	9	AI188340	AI188340 qd08a03.x
967	30	1.2	444	10	AW151022	AW151022 xq43f06.x
968	30	1.2	444	17	AQ543409	AQ543409 RPI-11-3
969	30	1.2	445	14	N74747	N74747 yv52a10.r
970	30	1.2	445	17	B43746	B43746 HS-1058-A2-
971	30	1.2	446	10	AW579721	AW579721 MR0-HT024
972	30	1.2	446	17	N73719	N73719 za61a02.s1
973	30	1.2	446	17	B45868	B45868 HS-1062-B1-
974	30	1.2	447	10	AW886230	AW886230 RC5-OT007
975	30	1.2	447	17	AQ450875	AQ450875 HS-5158.A
976	30	1.2	448	14	H54292	H54292 yq93ell.s1
977	30	1.2	448	14	R80655	R80655 y193d04.s1
978	30	1.2	448	17	AQ571868	AQ571868 HS 2094.A
979	30	1.2	449	10	AW886319	AW886319 RC5-OT007
980	30	1.2	449	10	AW887921	AW887921 RC5-OT070
981	30	1.2	450	12	BF725318	BF725318 bx14e10.x
982	30	1.2	450	17	AQ061101	AQ061101 CIT-HSP-2
983	30	1.2	451	17	B66387	B66387 CIT-HSP-200
984	30	1.2	452	10	AW977578	AW977578 EST389687
985	30	1.2	452	14	BM845661	BM845661 K-EST0124
986	30	1.2	452	14	N33374	N33374 yv40c10.s1
987	30	1.2	452	17	AQ231638	AQ231638 HS 2057.A
988	30	1.2	453	10	BE147879	BE147879 RC3-HT023
989	30	1.2	453	14	H29404	H29404 ym60c04.r1
990	30	1.2	454	9	AA682967	AA682967 ae92h11.s
991	30	1.2	454	10	AW886239	AW886239 RC5-OT007
992	30	1.2	454	14	H70066	H70066 yr92a01.r1
993	30	1.2	456	9	AI305255	AI305255 qm08e02.x
994	30	1.2	456	17	AQ122741	AQ122741 HS 3088.A
995	30	1.2	457	9	AI340280	AI340280 qp85a11.x
996	30	1.2	457	17	AQ184602	AQ184602 HS 2212.A
997	30	1.2	458	9	AA808796	AA808796 nv22a05.F
998	30	1.2	458	9	AI138119	AI138119 DKEP2547D
999	30	1.2	458	9	AA601084	AA601084 ns03e05.8
1000	30	1.2	458	10	AW151247	AW151247 xg34h04.x

ALIGNMENTS

RESULT 1

AL118597

LOCUS

DEFINITION

705 bp mRNA linear EST 29-FEB-2000

DKFPZ761D0110 r1 761 (synonym: hamy2) Homo sapiens cDNA clone

DKFPZ761D0110 5', mRNA sequence.

AL118597

AL118597.1

GI:5924496

EST.

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 705)

Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

EST (Blum, et al.)

Unpublished (1999)

Contact: Blum H

MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by LMU (Ludwig Maximilians University,

FEATURES	Location/Qualifiers	source
1..705	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="DKFPZ761D0110"	
	/clone_lib="761 (synonym: hamy2)"	
	/tissue_type="amygdala"	
	/dev_stage="adult"	
	/lab_host="DH10B"	
	/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI"	
BASE COUNT	148 a 205 c 203 g 149 t	
ORIGIN		
Query Match	25.1%; Score 603; DB 9; Length 705;	
Best Local Similarity	99.7%; Pred. No. 5.3e-287;	
Matches 703; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
1631	CCAGTGGCGGGTGTGATGCCAGCCCTGGGGCCCGCCCTGTTTACTGGTCTTTCGAAAT	1690
1	CCAGTGGCGGGTGTGATGCCAGCCCTGGGGCCCGCCCTGTTTACTGGTCTTTCGAAAT	60
1691	GGAGCTGAGCAGCCTCTGACAGCAGTACCTTTGACCTCGGTGACCACTCTCTTTTA	1750
61	GGGAGCTGAGCAGCCTCTGACAGCAGTACCTTTGACCTCGGTGACCACTCTCTTTTA	120
1751	AGCATAGACCTTGGCCCTGGGCTGGGCTGGGAAGGGAGGTTGAAACCACTGTA	1810
121	AGCATAGACCTTGGCCCTGGGCTGGGCTGGGAAGGGAGGTTGAAACCACTGTA	180
1811	ACCAGAGGGTGTGGCTTTCAGKACACCTCCAGGAGCCTCCCATCTGTCCAGTGGGGC	1870
181	ACCAGAGGGTGTGGCTTTCAGTCCAGTCCAGGAGCCTCCCATCTGTCCAGTGGGGC	240
1871	CAGAGCTGGAGTCCCTACCTGCTTCACTGGCGGGGGCTACTCTGAAATGTTTTTC	1930
241	CAGAGCTGGAGTCCCTACCTGCTTCACTGGCGGGGGCTACTCTGAAATGTTTTTC	300
1931	CTTCCCCAGAAATCAAGCTTTTGTGATCCAGAGAGCCCATCATCTAGATGGCATAT	1990
301	CTTCCCCAGAAATCAAGCTTTTGTGATCCAGAGAGCCCATCATCTAGATGGCATAT	360
1991	ATGTGATCTGGGCATTTTCTCTCTCTCTACAGCCAGGTTTAGCGGCAAACTTTCCCC	2050
361	ATGTGATCTGGGCATTTTCTCTCTCTCTACAGCCAGGTTTAGCGGCAAACTTTCCCC	420
2051	CTTAGCAGCTTACAGGCTGAGTCTTGGGTTTCTAGAGGTGAGGCTCTCTAGAGGC	2110
421	CTTAGCAGCTTACAGGCTGAGTCTTGGGTTTCTAGAGGTGAGGCTCTCTAGAGGC	480
2111	CAGAGAGCCAGAGCCCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2170
481	CAGAGAGCCAGAGCCCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	540
2171	CTGGCCACCAAGCCATCT	2230
541	CTGGCCACCAAGCCATCT	600
2231	CAGAGAGCAGCT	2290
601	CAGAGAGCAGCT	660
2291	TGCAGATGTGCGAGCGGAGGCGGTGTGATAGAGAGATATAAGG	2335
661	TGCAGATGTGCGAGCGGAGGCGGTGTGATAGAGAGATATAAGG	705

RESULT 2



```

AL536293      AL536293      922 bp      mRNA      linear      EST 13-FEB-2001
LOCUS         AL536293 LTI_FLO13_FBrnl Homo sapiens cDNA clone CS0DF014YH20 5
DEFINITION    prime, mRNA sequence.
ACCESSION     AL536293
VERSION       AL536293.1 GI:12799786
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               /db_xref="taxon:9606"
               /clone="CS0DF014YH20"
               /clone_lib="LTI_FLO13_FBrnl"
               /dev_stage="pooled tissue from post conception fetuses (20
               week, 24 week and 26 week)"
               /lab_host="DH10B"
               /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
               cDNA was primed with a NotI-oligo(dT) primer. Five prime
               end enriched, double-stranded cDNA was digested with Not I
               and cloned into the Not I and Eco RV sites of the
               pCMVSPORT 6 vector. Library was constructed by Life
               Technologies. Contact : Peng Liang Life Technologies, a
               division of Invitrogen 9800 Medical Center Drive Rockville
               , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
               fliang@lifetech.com URL :
               http://fulllength.invitrogen.com"
BASE COUNT    198 a      248 c      278 g      196 t      2 others
ORIGIN
Query Match   23.7%; Score 570; DB 9; Length 922;
Best Local Similarity 99.6%; Pred. No. 1.3e-270;
Matches 790; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1479 GTGAATGAGCGCGGGAAGCTGGCTTTGAACCTCAGGCTGTCCAGCCCGCGCAAG 1538
DB 1 GTGAATGAGCGCGGGAAGCTGGCTTTGAACCTCAGGCTGTCCAGCCCGCGCAAG 60

QY 1539 CCACAGGAAGGGGAGACAGGACAGCCAGCAGTGTGGAGACCTGCCACAGCCAGA 1598
DB 61 CCACAGGAAGGGGAGACAGGACAGCCAGCAGTGTGGAGACCTGCCACAGCCAGA 120

QY 1599 GGAGGGCAGAGGAGAAATCAAGGTTGAGAGCCAGTGGCGG-GTATGGCCAGCCCTG 1657
DB 121 GGAGGGCAGAGGAGAAATCAAGGTTGAGAGCCAGTGGCGGNGTGTATGGCCAGCCCTG 180

QY 1658 GGGCCAGCCCTGTCTTACTGTTCTTGAATGGGAGCTGAGCAGCTCTGGACAGCCA 1717
DB 181 GGGCCAGCCCTGTCTTACTGTTCTTGAATGGGAGCTGAGCAGCTCTGGACAGCCA 240

QY 1718 GTGACCTTTGACCTCGGTGACCACTCTTCTTAAAGCCATAGACCCCTGAGGCCCTGGGCTG 1777
DB 241 GTGACCTTTGACCTCGGTGACCACTCTTCTTAAAGCCATAGACCCCTGAGGCCCTGGGCTG 300

QY 1778 GTGCTGGGAGGAGGGTTGAAACCAACCGTGAAACAGAGGGTGTGGCTTTCCAGKACC 1837
DB 301 GTGCTGGGAGGAGGGTTGAAACCAACCGTGAAACAGAGGGTGTGGCTTTCCAGTCAAC 360

QY 1838 CTAGGGAGGCTCCCATCTGTCAGCTGGGGCAGAGGCTGGAGTCCCTACTGCTTC 1897
DB 361 CTAGGGAGGCTCCCATCTGTCAGCTGGGGCAGAGGCTGGAGTCCCTACTGCTTC 420

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QY 1898 ACCTTGGCGCGGCTACTCTGGAATGTTTTTCCCTCCCAGAAATCAAGCTTTTGTCTGA 1957
DB 421 ACCTTGGCGCGGCTACTCTGGAATGTTTTTCCCTCCCAGAAATCAAGCTTTTGTCTGA 480

QY 1958 TCCAGAGAGCCCATATCACTAGATGGCATATATGTGATCTGGGCATTTTCTCTCTG 2017
DB 481 TCCAGAGAGCCCATATCACTAGATGGCATATATGTGATCTGGGCATTTTCTCTCTG 540

QY 2018 CTTACAGCCAGGTTTAGCGGCAAACTTTCCCTCTTAGCACCTTTCAGGGCTGAGTTCTGG 2077
DB 541 CTTACAGCCAGGTTTAGCGGCAAACTTTCCCTCTTAGCACCTTTCAGGGCTGAGTTCTGG 600

QY 2078 GTTTCTAGAGTTCAGACGGCTCTCTAGAGCGCCAGGAAAGCCAGAGCCCAAGAGAGC 2137
DB 601 GTTTCTAGAGTTCAGACGGCTCTCTAGAGCGCCAGGAAAGCCAGAGCCCAAGAGAGC 660

QY 2138 AAAAGAGGCATACACACAGCAGTGTGAATAGCTGGCCACAGCCATCTCTCTCCACC 2197
DB 661 AAAAGAGGCATACACACAGCAGTGTGAATAGCTGGCCACAGCCATCTCTCTCCACC 720

QY 2198 TCAAGACCCCTTGTCTCSAGACTAAAGGATCCAGAGAGCAGCTCCCTTTCTCAGGAGC 2257
DB 721 TCAAGACCCCTTGTCTCSAGACTAAAGGATCCAGAGAGCAGCTCCCTTTCTCAGGAGC 780

QY 2258 TTGGGCAAGTGCCT 2270
DB 781 TTGGGCAAGTGCCT 793

RESULT 3
BM560284
LOCUS         BM560284      929 bp      mRNA      linear      EST 20-FEB-2002
DEFINITION    AGENCOURT 5597802 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5432019
               5', mRNA sequence.
ACCESSION     BM560284
VERSION       BM560284.1 GI:18804585
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1 (bases 1 to 929)
               /db_xref="taxon:9606"
               /clone="IMAGE:5432019"
               /clone_lib="NIH_MGC_98"
               /tissue_type="astrocytoma grade IV, cell line"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
               EcoRI; cDNA made by oligo-dT priming. Directionally
               cloned into EcoRI/XhoI sites using the following 5'
               adaptor: GGCACGAG(G). Library constructed by Ling Hong
               in the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH MGC library."
BASE COUNT    198 a      288 c      264 g      179 t

```

FEATURES  
source



## MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.

No 81 sequence available.  
This clone (DKFZp547J194) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 5, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

## source

1. .296  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp547J194"  
/clone\_lib="547 (synonym: hfbr1)"  
/tissue\_type="brain"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/note="Vector: pAMP1; Site 1: NotI; Site 2: SalI"

BASE COUNT 64 a 87 c 71 g 74 t

## ORIGIN

Query Match 12.3%; Score 296; DB 9; Length 296;  
Best Local Similarity 100.0%; Pred. NO. 4.4e-135;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1191 CCTGACTCCTCTGGCTTTCCAGAGATGGTCCAGGGCTGTCTCTTTGGTTAAGG 1250  
Db 1 CCTGACTCCTCTGGCTTTCCAGAGATGGTCCAGGGCTGTCTCTTTGGTTAAGG 60  
QY 1251 CTCCTAAACTTTGGCTTTTTCGAAATAGATCTCTCCCTCTCTCCAGGAAGT 1310  
Db 61 CTCCTAAACTTTGGCTTTTTCGAAATAGATCTCTCTCTCTCCAGGAAGT 120  
QY 1311 GGCCACAGCAAGACAGCGGCTCCCTCCGCTTCTCATCCCAACTCTTTTCTCTCTGG 1370  
Db 121 GGCCACAGCAAGACAGCGGCTCCCTCCGCTTCTCATCCCAACTCTTTTCTCTCTGG 180  
QY 1371 ACACATTGGATGCTTGGAAATAGAAAGCATTATATGACAGAGCTTGGAAACCA 1430  
Db 181 ACACATTGGATGCTTGGAAATAGAAAGCATTATATGACAGAGCTTGGAAACCA 240  
QY 1431 GCCCATCAGAACCTGAGCTATTTTCTCTGGCGCAGAGGTGTAGGGTGGATG 1486  
Db 241 GCCCATCAGAACCTGAGCTATTTTCTCTGGCGCAGAGGTGTAGGGTGGATG 296

RESULT 6  
BE312985  
LOCUS BE312985 751 bp mRNA linear EST 26-OCT-2000  
DEFINITION 601150246F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3503003 5',  
mRNA sequence.  
ACCESSION BE312985  
VERSION BE312985.1 GI:9132352  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 751)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCMI75 row: 1 column: 12  
High quality sequence stop: 640.

## FEATURES

## source

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/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: This is a NIH MGC Library."

BASE COUNT 138 a 233 c 234 g 146 t

## ORIGIN

Query Match 12.1%; Score 292; DB 10; Length 751;  
Best Local Similarity 100.0%; Pred. NO. 5.8e-133;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 937 GGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCCCTGGGAAG 996  
Db 1 GGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATCTGAGGGGCTGCCCTGGGAAG 60  
QY 997 GCGAGTCTGGGACCTTGGCACTGGGAGGAGGCTCTCCCGTGCATCCCCCTGCTCAGC 1056  
Db 61 GCGAGTCTGGGACCTTGGCACTGGGAGGAGGCTCTCCCGTGCATCCCCCTGCTCAGC 120  
QY 1057 AATTCAGACCCCTCTGAGAGACGCCACTCCCTGGACACAGACCCAGGACCCCGAGGG 1116  
Db 121 AATTCAGACCCCTCTGAGAGACGCCACTCCCTGGACACAGACCCAGGACCCCGAGGG 180  
QY 1117 AGGCGAGGATGGCTTTCCCTCTCTGATGTCCTCAGTGCCTCAGGAGATGGTCCAGCC 1176  
Db 181 AGGCGAGGATGGCTTTCCCTCTCTGATGTCCTCAGTGCCTCAGGAGATGGTCCAGCC 240  
QY 1177 ACCAGACGTGAGCCCTGACTCTCTGGCTTTCCAGGAGATGGTCCAGGG 1228  
Db 241 ACCAGACGTGAGCCCTGACTCTCTGGCTTTCCAGGAGATGGTCCAGGG 292

RESULT 7  
BF313433  
LOCUS BF313433 432 bp mRNA linear EST 21-NOV-2000  
DEFINITION 601900020F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4129205 5',  
mRNA sequence.  
ACCESSION BF313433  
VERSION BF313433.1 GI:11261437  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 432)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCMI023 row: h column: 06  
High quality sequence stop: 429.



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/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      199 a      247 c      311 g      144 t
ORIGIN
Query Match      8.8%; Score 212; DB 12; Length 901;
Best Local Similarity 100.0%; Pred. No. 2.6e-93;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 918 TTGAGAGTTGACCTGGAGGGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATC 977
Db 3 TTGAGAGTTGACCTGGAGGGGCTGACATCCCTACGAGGACATCATAGCCACTGAGATC 62
Qy 978 TGAGGGGCTGCTGGGAGGCGAGTCTGGGACCTGGGACCTGGGAGGCGAGGCTCTCCCG 1037
Db 63 TGAGGGGCTGCTGGGAGGCGAGTCTGGGACCTGGGACCTGGGAGGCGAGGCTCTCCCG 122
Qy 1038 TGCATCCCCCTGCTCAGCAATTCAGACCCCTCTGAGAGGCGCCACTCCCTGGGACACAG 1097
Db 123 TGCATCCCCCTGCTCAGCAATTCAGACCCCTCTGAGAGGCGCCACTCCCTGGGACACAG 182
Qy 1098 ACCGAGGACCCCGAGGGGAGGAGGATGCG 1129
Db 183 ACCGAGGACCCCGAGGGGAGGAGGATGCG 214
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RESULT 10
BI034804/c
LOCUS      BI034804      446 bp      mRNA      linear      EST 14-JUN-2001
DEFINITION RC4-NN1176-090401-013-g03 NN1176 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BI034804
VERSION     BI034804.1 GI:14441430
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 446)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-NN1176-
090401-013-g03&t3=2001-04-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 67
High quality sequence stop: 389.
Location/Qualifiers
    . 446
    /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="NN1176"
/dev_stage="Adult"
/notes="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      102 a      106 c      134 g      104 t
ORIGIN
Query Match      7.4%; Score 177; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 4.4e-76;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2020 TACAGCCAGTTTACGGGCAAACTTTCCCTTAGCCTTACGGGCTAGTTCGGGT 2079
Db 305 TACAGCCAGTTTACGGGCAAACTTTCCCTTAGCCTTACGGGCTAGTTCGGGT 246
Qy 2080 TTCTAGAGGTTCAGAGCGGCTCTCAGAGCGCCAGGAGCCAGAGCCCAAGCAGGACGAA 2139
Db 245 TTCTAGAGGTTCAGAGCGGCTCTCAGAGCGCCAGGAGCCCAAGCAGGACGAA 186
Qy 2140 AAAGAGGCATACACACAGCAGTGTGAATAGCTGGCCAGCAGCATCTCCCTCCAC 2196
Db 185 AAAGAGGCATACACACAGCAGTGTGAATAGCTGGCCAGCAGCATCTCCCTCCAC 129
RESULT 11
AA020852/c
LOCUS      AA020852      463 bp      mRNA      linear      EST 30-JAN-1997
DEFINITION ze64b08.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:363735 5', mRNA sequence.
ACCESSION  AA020852
VERSION     AA020852.1 GI:1484623
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 463)
AUTHORS    Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., DuBuque,T., Pavello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Matra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 4323 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 342.
Location/Qualifiers
    . 463
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    /tissue_type="retina"
    /dev_stage="55 year old"
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California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 122 a 160 c 175 g 101 t

ORIGIN

Query Match 4.3%; Score 104; DB 10; Length 558;  
Best Local Similarity 100.0%; Pred. No. 6.7e-40;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1499 GCTGGCTTTGAAACCTCAGGCTCTCCAGCCCGCAAGCCACAGGAGGGGAGAG 1558  
Db 63 GCTGGCTTTGAAACCTCAGGCTCTCCAGCCCGCAAGCCACAGGAGGGGAGAG 122

Qy 1559 ACAGGACCCAGCAGTGTGAGACCTTGCACAGCCAGAGGAG 1602  
Db 123 ACAGGACCCAGCAGTGTGAGACCTTGCACAGCCAGAGGAG 166

RESULT 14  
BE540725  
LOCUS BE540725 797 bp mRNA linear EST 09-AUG-2000  
DEFINITION 601065002P1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:3451321 5', mRNA sequence.  
ACCESSION BE540725  
VERSION BE540725.1 GI:9769370  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 797)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLAM8431 row: c column: 02  
High quality sequence start: 4  
High quality sequence stop: 677.  
Location/Qualifiers  
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BASE COUNT 158 a 219 c 235 g 184 t 1 others

ORIGIN

Query Match 4.1%; Score 98; DB 10; Length 797;  
Best Local Similarity 100.0%; Pred. No. 7.1e-37;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2218 AGACTAAGGATCCAGAGAGCAGTCCCTTTCTCAGGAGCTGGCGAGTCCCCAGGAG 2277  
Db 304 AGACTAAGGATCCAGAGAGCAGTCCCTTTCTCAGGAGCTGGCGAGTCCCCAGGAG 363

Qy 2278 TCCAGGGTTTCTCTGCAGATGTCGGAGCGGAGCGG 2315  
Db 364 TCCAGGGTTTCTCTGCAGATGTCGGAGCGGAGCGG 401

RESULT 15  
BG769644  
LOCUS BG769644 1120 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602744561F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4877655 5', mRNA sequence.  
ACCESSION BG769644  
VERSION BG769644.1 GI:14080297  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1120)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLCMI762 row: i column: 16  
High quality sequence start: 22  
High quality sequence stop: 611.  
Location/Qualifiers  
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/db xref="taxon:9606"  
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/cell\_line="NIH\_MGC\_49"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 328 a 278 c 343 g 171 t

ORIGIN

Query Match 3.7%; Score 89; DB 12; Length 1120;  
Best Local Similarity 100.0%; Pred. No. 2.3e-32;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CCCATCAGAACCTGAGCTATTTCTCTGCGCGACAGGTGTAGGGGTGAATGACCG 80

Qy 1492 CGGGGAGCTGGCTTTGAACCTCAGGCG 1520  
Db 81 CGGGGAGCTGGCTTTGAACCTCAGGCG 109

Search completed: June 17, 2003, 06:24:58  
Job time : 2779.07 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 344.575 Seconds  
(without alignments)  
15794.017 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_6939\_7125

Perfect score: 187

Sequence: 1 atgatcatgctcactgag.....tggcctcaagcaatccacct 187

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	187	100.0	5492	9	AF123659 Homo sapi
2	187	100.0	9108	9	AF123653 Homo sapi
3	187	100.0	173284	2	AC025853 Homo sapi
C 4	42	22.5	105051	2	AC009449 Homo sapi
C 5	42	22.5	147760	9	AC011846 Homo sapi
C 6	42	22.5	156197	9	HS97K10
C 7	42	22.5	198295	9	AC105129 Homo sapi
C 8	42	22.5	212505	2	AC027220 Homo sapi
C 9	41	21.9	112732	2	AC092367 Homo sapi
C 10	41	21.9	120186	9	AF001184 Homo sapi
C 11	41	21.9	155877	2	AC073631 Homo sapi
C 12	41	21.9	165662	9	AC009930 Homo sapi
C 13	41	21.9	166098	9	AC020641 Homo sapi
C 14	41	21.9	180423	9	AC012152 Homo sapi
C 15	41	21.9	187266	2	AC073984 Homo sapi
C 16	41	21.9	202760	2	AC021987 Homo sapi
C 17	40	21.4	2580	9	AK026402 Homo sapi
C 18	40	21.4	11170	9	AL512429 Human DNA
C 19	40	21.4	18999	6	AX473126 Sequence
C 20	40	21.4	53269	9	AP002404 Homo sapi
C 21	40	21.4	56867	2	AC073170 Homo sapi
C 22	40	21.4	71091	9	AC106052 Homo sapi
C 23	40	21.4	79560	9	AL591471 Human DNA
C 24	40	21.4	86295	2	AC078810 Homo sapi
C 25	40	21.4	92651	9	AC002527 Human BAC
C 26	40	21.4	100000	9	AP000081 Homo sapi
C 27	40	21.4	109296	9	AC083949 Homo sapi
C 28	40	21.4	110000	2	AC125619_4
C 29	40	21.4	110000	2	AC027294_2
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C 31	40	21.4	120488	9	AC073257 Homo sapi
C 32	40	21.4	123070	9	AC020656 Homo sapi
C 33	40	21.4	125146	9	AL512770 Human DNA
C 34	40	21.4	140974	9	AC068533 Homo sapi
C 35	40	21.4	141771	9	AC091821 Homo sapi
C 36	40	21.4	142666	9	AC114745 Homo sapi
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C 40	40	21.4	150526	2	AC092339 Homo sapi
C 41	40	21.4	153201	9	AC006454 Homo sapi
C 42	40	21.4	153342	2	AL591646 Homo sapi
C 43	40	21.4	153832	2	AC116447 Homo sapi
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C 53	40	21.4	161737	2	AC087809 Homo sapi
C 54	40	21.4	162427	9	AC010205 Homo sapi
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C 63	40	21.4	168862	9	AC073464 Homo sapi
C 64	40	21.4	169552	9	AC015976 Homo sapi
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c 66	40	21.4	171173	2	AC127454	AC127454 Homo sapi	139	38	20.3	204505	9	AC089983	Homo sapi
c 67	40	21.4	177219	2	AC021286	AC021286 Homo sapi	c 140	38	20.3	209162	9	AC090955	Homo sapi
c 68	40	21.4	177527	9	AC092719	AC092719 Homo sapi	c 141	38	20.3	210791	9	CNS01D7	Human Chr
c 69	40	21.4	178377	9	AC007685	AC007685 Homo sapi	c 142	38	20.3	236486	9	CNS01D188	Homo sapi
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c 71	40	21.4	185000	2	AC007799	AC007799 Homo sapi	c 144	38	20.3	254437	9	AP000500	Homo sapi
c 72	40	21.4	186202	9	AC108516	AC108516 Homo sapi	c 145	37	19.8	41313	2	U82205	Homo sapien
c 73	40	21.4	186886	2	AC016297	AC016297 Homo sapi	c 146	37	19.8	50843	2	AC074114	Homo sapi
c 74	40	21.4	187431	9	AC107219	AC107219 Homo sapi	c 147	37	19.8	74509	2	AF260012	Homo sapi
c 75	40	21.4	188256	2	AP001927	AP001927 Homo sapi	c 148	37	19.8	75148	9	AC091545	Homo sapi
c 76	40	21.4	188410	2	AC124073	AC124073 Homo sapi	c 149	37	19.8	76075	9	AL590387	Human DNA
c 77	40	21.4	192554	2	AC024170	AC024170 Homo sapi	c 150	37	19.8	82151	9	AC079987	Homo sapi
c 78	40	21.4	194832	9	AC025287	AC025287 Homo sapi	c 151	37	19.8	99408	9	AL359385	Human DNA
c 79	40	21.4	195529	2	AC025714	AC025714 Homo sapi	c 152	37	19.8	104656	9	AL731576	Human DNA
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c 82	40	21.4	210723	9	AC012215	AC012215 Homo sapi	c 155	37	19.8	125674	2	AP002018	Homo sapi
c 83	40	21.4	215994	9	AC067941	AC067941 Homo sapi	c 156	37	19.8	125674	9	AL451125	Human DNA
c 84	40	21.4	232964	2	AC015501	AC015501 Homo sapi	c 157	37	19.8	135405	9	AC000025	Homo sapi
c 85	40	21.4	249325	2	AC015501	AC015501 Homo sapi	c 158	37	19.8	139485	2	AC025597	Homo sapi
c 86	40	21.4	250625	2	AL442068	AL442068 Homo sapi	c 159	37	19.8	143146	9	AC079855	Homo sapi
c 87	39	20.9	71404	2	AC103701	AC103701 Homo sapi	c 160	37	19.8	145428	2	AC026068	Homo sapi
c 88	39	20.9	83798	9	HS1013A22	AL132772 Human DNA	c 161	37	19.8	146889	9	AL358937	Human DNA
c 89	39	20.9	100664	9	AL512651	AL512651 Human DNA	c 162	37	19.8	147484	2	AL590088	Homo sapi
c 90	39	20.9	109876	2	AC091497	AC091497 Homo sapi	c 163	37	19.8	149308	9	AC005527	Homo sapi
c 91	39	20.9	120192	2	AC093220	AC093220 Homo sapi	c 164	37	19.8	151853	9	CNS01RHL	Human Chr
c 92	39	20.9	140469	2	AC025066	AC025066 Homo sapi	c 165	37	19.8	152118	2	AC013263	Homo sapi
c 93	39	20.9	159910	9	AC009235	AC009235 Homo sapi	c 166	37	19.8	154606	9	AC097358	Homo sapi
c 94	39	20.9	167206	9	AL392044	AL392044 Human DNA	c 167	37	19.8	156378	2	AC084267	Homo sapi
c 95	39	20.9	169988	9	AC064846	AC064846 Homo sapi	c 168	37	19.8	157672	9	AC113143	Homo sapi
c 96	39	20.9	170758	9	AC004965	AC004965 Homo sapi	c 169	37	19.8	159098	2	AC016484	Homo sapi
c 97	39	20.9	170926	9	AC095034	AC095034 Homo sapi	c 170	37	19.8	162314	9	AC061965	Homo sapi
c 98	39	20.9	171343	2	AC016676	AC016676 Homo sapi	c 171	37	19.8	165260	2	AC093928	Homo sapi
c 99	39	20.9	178446	2	AC109450	AC109450 Homo sapi	c 172	37	19.8	167386	2	AL159993	Homo sapi
c 100	39	20.9	182703	2	AC022939	AC022939 Homo sapi	c 173	37	19.8	168056	9	AC004458	Homo sapi
c 101	39	20.9	185784	2	AC009719	AC009719 Homo sapi	c 174	37	19.8	169650	2	AC024629	Homo sapi
c 102	39	20.9	186531	2	AC109464	AC109464 Homo sapi	c 175	37	19.8	170404	9	AC012493	Homo sapi
c 103	38	20.3	33931	2	AC022156	AC022156 Homo sapi	c 176	37	19.8	170586	2	AL356126	Homo sapi
c 104	38	20.3	58826	2	AC116536	AC116536 Homo sapi	c 177	37	19.8	178137	9	AC011302	Homo sapi
c 105	38	20.3	71406	2	AC027434	AC027434 Homo sapi	c 178	37	19.8	179372	2	AC040922	Homo sapi
c 106	38	20.3	81951	2	AC022814	AC022814 Homo sapi	c 179	37	19.8	180595	9	AC008280	Homo sapi
c 107	38	20.3	96253	9	AC090083	AC090083 Homo sapi	c 180	37	19.8	181856	9	AC093227	Homo sapi
c 108	38	20.3	102517	2	AP002876	AP002876 Homo sapi	c 181	37	19.8	182241	9	AC022909	Homo sapi
c 109	38	20.3	110000	2	AC008576	Continuation (2 of	c 182	37	19.8	190076	9	AC008403	Homo sapi
c 110	38	20.3	120890	2	AC079517	Continuation (4 of	c 183	37	19.8	194034	2	AL592148	Human DNA
c 111	38	20.3	120890	9	AL606760	AL606760 Human DNA	c 184	37	19.8	195773	2	AC073134	Homo sapi
c 112	38	20.3	122176	2	AL358233	AL358233 Homo sapi	c 185	37	19.8	198396	9	AC010355	Homo sapi
c 113	38	20.3	131398	9	HS445C9	Z95115 Human DNA s	c 186	37	19.8	198751	9	AC022148	Homo sapi
c 114	38	20.3	142391	2	AC092507	AC092507 Homo sapi	c 187	37	19.8	222106	2	AC018570	Homo sapi
c 115	38	20.3	142839	9	AL356218	AL356218 Human DNA	c 188	37	19.8	22275	9	CNS05TCN	Human Chr
c 116	38	20.3	152741	2	AC021606	AC021606 Homo sapi	c 189	37	19.8	226171	9	AP003730	Homo sapi
c 117	38	20.3	152824	9	AC107072	AC107072 Homo sapi	c 190	37	19.8	266941	9	AF213884S2	Homo sapi
c 118	38	20.3	157442	9	AC105001	AC105001 Homo sapi	c 191	36	19.3	318488	9	AC005529	Homo sapi
c 119	38	20.3	157921	2	AC027726	AC027726 Homo sapi	c 192	36	19.3	41907	9	AC090901	Homo sapi
c 120	38	20.3	159488	2	AC025141	AC025141 Homo sapi	c 193	36	19.3	44679	9	AD001502	Homo sapi
c 121	38	20.3	166007	9	CNS01DRC	AL117186 Human Chr	c 194	36	19.3	50793	9	AC092592	Homo sapi
c 122	38	20.3	167358	2	AC010673	AC010673 Homo sapi	c 195	36	19.3	58035	9	AL158199	Human DNA
c 123	38	20.3	168672	2	AC027102	AC027102 Homo sapi	c 196	36	19.3	75547	9	AC004919	Homo sapi
c 124	38	20.3	168798	2	AC012683	AC012683 Homo sapi	c 197	36	19.3	89944	9	AC093127	Papio cyn
c 125	38	20.3	169223	2	AL353675	AL353675 Homo sapi	c 198	36	19.3	112416	2	AP000482	Homo sapi
c 126	38	20.3	173137	2	AC107017	AC107017 Homo sapi	c 199	36	19.3	112875	2	AP000638	Homo sapi
c 127	38	20.3	173845	9	AC018662	AC018662 Human Chr	c 200	36	19.3	119555	9	AL353790	Human DNA
c 128	38	20.3	175046	2	AC022728	AC022728 Homo sapi	c 201	36	19.3	127051	9	AL355538	Human DNA
c 129	38	20.3	176046	9	AC073366	AC073366 Homo sapi	c 202	36	19.3	130932	9	AC092658	Homo sapi
c 130	38	20.3	176584	2	AC027812	AC027812 Homo sapi	c 203	36	19.3	137830	9	AC003029	Homo sapi
c 131	38	20.3	178628	2	AC015715	AC015715 Homo sapi	c 204	36	19.3	145616	9	Z85986	Human DNA s
c 132	38	20.3	181629	2	AC087738	AC087738 Homo sapi	c 205	36	19.3	154738	9	AC023355	Homo sapi
c 133	38	20.3	183099	2	AC034144	AC034144 Homo sapi	c 206	36	19.3	156300	2	AC087739	Homo sapi
c 134	38	20.3	189636	9	HUAC002287	AC002287 Homo sapi	c 207	36	19.3	157347	2	AP001882	Homo sapi
c 135	38	20.3	191265	2	AC130450	AC130450 Homo sapi	c 208	36	19.3	158952	9	AC096745	Homo sapi
c 136	38	20.3	198402	9	AC069546	AC069546 Homo sapi	c 209	36	19.3	161487	2	AC119571	Homo sapi
c 137	38	20.3	202750	2	AC116942	AC116942 Pan trogl	c 210	36	19.3	161874	9	AC114482	Homo sapi
c 138	38	20.3	203200	9	AC008744	AC008744 Homo sapi	c 211	36	19.3	164646	2	AP002877	Homo sapi

212	36	19.3	167005	9	AL158070	AL158070 Human DNA
213	36	19.3	167633	2	AC129096	Papio cyn
214	36	19.3	169505	2	CNS01DVT	Human chr
215	36	19.3	169871	9	AC087485	Homo sapi
216	36	19.3	169867	2	AC087485	Homo sapi
217	36	19.3	170102	9	AC080879	Homo sapi
218	36	19.3	171449	9	AC007284	Homo sapi
219	36	19.3	172327	2	AC012345	Homo sapi
220	36	19.3	175108	2	AC031982	Homo sapi
221	36	19.3	175249	9	AC119038	Homo sapi
222	36	19.3	175776	2	AC112511	Homo sapi
223	36	19.3	175837	2	AC022045	Homo sapi
224	36	19.3	176010	2	AC069125	Homo sapi
225	36	19.3	176117	9	AC092352	Homo sapi
226	36	19.3	176421	9	AC096888	Homo sapi
227	36	19.3	176512	9	AC012323	Homo sapi
228	36	19.3	179460	9	AC012512	Homo sapi
229	36	19.3	179611	2	AC084348	Homo sapi
230	36	19.3	179844	9	AC009265	Homo sapi
231	36	19.3	182617	9	AC007731	Homo sapi
232	36	19.3	183337	9	AL1139002	Human DNA
233	36	19.3	184138	2	AC087177	Homo sapi
234	36	19.3	187863	9	AL589740	Human DNA
235	36	19.3	188034	2	AC036169	Homo sapi
236	36	19.3	190305	2	AC090267	Homo sapi
237	36	19.3	190415	9	AC066612	Homo sapi
238	36	19.3	191098	2	AC073518	Homo sapi
239	36	19.3	191329	2	AC090269	Homo sapi
240	36	19.3	191957	9	AC015845	Homo sapi
241	36	19.3	192592	9	AC005500	Homo sapi
242	36	19.3	193963	9	AC007736	Homo sapi
243	36	19.3	194197	9	AC064871	Homo sapi
244	36	19.3	199869	9	AC092378	Homo sapi
245	36	19.3	202414	2	AC090966	Papio cyn
246	36	19.3	207183	9	AP001533	Homo sapi
247	36	19.3	215223	9	AP001972	Homo sapi
248	36	19.3	219436	9	AC005046	Homo sapi
249	35	18.7	272	9	AF032273	Eulemur m
250	35	18.7	275	9	AF032256	Eulemur m
251	35	18.7	275	9	AF032322	Propithec
252	35	18.7	300	9	HJ19344	Homo sapi
253	35	18.7	417	6	AX072460	Sequence
254	35	18.7	535	11	HUMT6283	Human STS U
255	35	18.7	567	6	AX387669	Sequence
256	35	18.7	1000	9	S83170	tissue-type
257	35	18.7	1203	9	HUMDYSKW	Human dystr
258	35	18.7	1341	9	HS244000	Homo sapi
259	35	18.7	1341	9	HSG6P	H. sapiens g
260	35	18.7	1580	9	BC000052	Homo sapi
261	35	18.7	1690	9	AF218028	Homo sapi
262	35	18.7	1777	9	HSTECTXT11	Human tyros
263	35	18.7	1817	9	AK024132	Homo sapi
264	35	18.7	1927	9	HSM803388	Homo sapi
265	35	18.7	1949	9	AK055117	Homo sapi
266	35	18.7	2138	9	HSM802532	Homo sapi
267	35	18.7	2308	6	AX399200	Sequence
268	35	18.7	2320	9	AK096458	Homo sapi
269	35	18.7	2335	6	AX399198	Sequence
270	35	18.7	2335	9	HS112REC	Human mRNA
271	35	18.7	2391	9	HSM804140	Homo sapi
272	35	18.7	2439	9	AK025301	Homo sapi
273	35	18.7	2642	9	AF160477	Homo sapi
274	35	18.7	2674	9	HSM805065	Homo sapi
275	35	18.7	2744	9	AK027753	Homo sapi
276	35	18.7	2841	9	AK051320	Homo sapi
277	35	18.7	2870	9	AK056213	Homo sapi
278	35	18.7	2995	9	HSM804013	Homo sapi
279	35	18.7	3040	9	HSATP2A1S9	Human Cg2+
280	35	18.7	3251	9	AK001638	Homo sapi
281	35	18.7	3840	9	HSAPQC2G	Homo sapi
282	35	18.7	4034	6	A98026	Sequence 1
283	35	18.7	4034	9	AF051355	Homo sapi
284	35	18.7	4057	9	HUMAPOC2	Human apoli

AK023833	Homo sapi	9	AK023833	6133	18.7	35	285	9	AK023833	Homo sapi
U12022	Human prost	9	HSCALMG2	6581	18.7	35	286	9	HSCALMG2	Human prost
U33446	Human chr	9	U33446	7008	18.7	35	287	9	U33446	Human chr
AL590374	Human DNA	9	AL590374	9775	18.7	35	288	9	AL590374	Human DNA
AL592286	Human DNA	9	AL592286	10988	18.7	35	289	9	AL592286	Human DNA
AL034404	Human DNA	9	HS417C12	11663	18.7	35	290	9	HS417C12	Human DNA
AF494057	Homo sapi	9	AF494057	12064	18.7	35	291	9	AF494057	Homo sapi
AY027894	Homo sapi	9	AY027894	12248	18.7	35	292	9	AY027894	Homo sapi
AC084280	Homo sapi	9	AC084280	15966	18.7	35	293	9	AC084280	Homo sapi
AC109828	Homo sapi	9	AC109828	18332	18.7	35	294	9	AC109828	Homo sapi
AF141309	Homo sapi	9	HSPMFG2	22038	18.7	35	295	9	HSPMFG2	Homo sapi
AY056047	Homo sapi	9	AY056047	26000	18.7	35	296	9	AY056047	Homo sapi
AL031592	Human DNA	9	HS366B10	26316	18.7	35	297	9	HS366B10	Human DNA
AL336566	Homo sapi	2	AL336566	27103	18.7	35	298	2	AL336566	Homo sapi
249862	Human DNA	9	HS158B6	28142	18.7	35	299	9	HS158B6	Human DNA
AC007059	Homo sapi	9	AC007059	32303	18.7	35	300	9	AC007059	Homo sapi
AF518005	Homo sapi	9	AF518005	33528	18.7	35	301	9	AF518005	Homo sapi
AP002365	Homo sapi	9	AP002365	33615	18.7	35	302	9	AP002365	Homo sapi
AC083896	Homo sapi	2	AC083896	34568	18.7	35	303	2	AC083896	Homo sapi
AC006513	Homo sapi	9	AC006513	34746	18.7	35	304	9	AC006513	Homo sapi
269715	Human tissu	9	HSN74G7	35730	18.7	35	305	9	HSN74G7	Human tissu
K03021	Human tissu	9	HUMTPA	36594	18.7	35	306	9	HUMTPA	Human tissu
AC009003	Homo sapi	9	AC009003	37088	18.7	35	307	9	AC009003	Homo sapi
AC006190	Homo sapi	2	AC006190	38055	18.7	35	308	2	AC006190	Homo sapi
AC000035	Homo sapi	9	AC000035	38429	18.7	35	309	9	AC000035	Homo sapi
AL365437	Human DNA	9	AL365437	39186	18.7	35	310	9	AL365437	Human DNA
AX078379	Sequence	6	AX078379	39198	18.7	35	311	6	AX078379	Sequence
AC004794	Homo sapi	9	AC004794	39854	18.7	35	312	9	AC004794	Homo sapi
AL591670	Human DNA	9	AL591670	40166	18.7	35	313	9	AL591670	Human DNA
AF045450	Homo sapi	9	AF045450	40205	18.7	35	314	9	AF045450	Homo sapi
AC091872	Homo sapi	9	AC091872	40876	18.7	35	315	9	AC091872	Homo sapi
AL078611	Human DNA	9	HSB5E3	40981	18.7	35	316	9	HSB5E3	Human DNA
AC011539	Homo sapi	2	AC011539	41320	18.7	35	317	2	AC011539	Homo sapi
AC107932	Homo sapi	9	AC107932	41319	18.7	35	318	9	AC107932	Homo sapi
AL359082	Human DNA	9	AL359082	41372	18.7	35	319	9	AL359082	Human DNA
AC022159	Homo sapi	9	HS333H9	42098	18.7	35	320	9	HS333H9	Homo sapi
AC074203	Homo sapi	9	AC074203	42479	18.7	35	321	9	AC074203	Homo sapi
AC006277	Homo sapi	9	AC006277	42642	18.7	35	322	9	AC006277	Homo sapi
AL136450	Human DNA	9	AL136450	43480	18.7	35	323	9	AL136450	Human DNA
AL159172	Human DNA	9	AL159172	43958	18.7	35	324	9	AL159172	Human DNA
AC005781	Homo sapi	9	AC005781	44052	18.7	35	325	9	AC005781	Homo sapi
AX008040	Sequence	6	AX008040	44100	18.7	35	326	6	AX008040	Sequence
283308	Human DNA	9	HSRLL1M2	44373	18.7	35	327	9	HSRLL1M2	Human DNA
AL031719	Human DNA	9	HS380F5	44653	18.7	35	328	9	HS380F5	Human DNA
AL136135	Human DNA	9	AC004611	46699	18.7	35	329	9	AC004611	Human DNA
AC004611	Homo sapi	9	AC004611	47055	18.7	35	330	9	AC004611	Homo sapi
AC021101	Homo sapi	9	AC021101	47069	18.7	35	331	9	AC021101	Homo sapi
AC104688	Homo sapi	9	AC104688	47088	18.7	35	332	9	AC104688	Homo sapi
AC003660	Homo sapi	2	AC003660	48000	18.7	35	333	2	AC003660	Homo sapi
AC007945	Homo sapi	9	AC007945	50479	18.7	35	334	9	AC007945	Homo sapi
AC004762	Homo sapi	9	AC004762	50651	18.7	35	335	9	AC004762	Homo sapi
AC118558	Homo sapi	9	AC118558	51825	18.7	35	336	9	AC118558	Homo sapi
AL139251	Human DNA	9	AL139251	52935	18.7	35	337	9	AL139251	Human DNA
AL356535	Human DNA	9	AL356535	53067	18.7	35	338	9	AL356535	Human DNA
AP001415	Homo sapi	9	AP001415	53797	18.7	35	339	9	AP001415	Homo sapi
AC104538	Homo sapi	9	AC104538	54423	18.7	35	340	9	AC104538	Homo sapi
AC084353	Homo sapi	9	AC084353	55448	18.7	35	341	9	AC084353	Homo sapi
AC073841	Homo sapi	9	AC073841	55588	18.7	35	342	9	AC073841	Homo sapi
AX329572	Sequence	6	AX329572	56093	18.7	35	343	6	AX329572	Sequence
AC000064	Human BAC	9	HSAC000064	56093	18.7	35	344	9	HSAC000064	Human BAC
AP002355	Homo sapi	9	AP002355	56331	18.7	35	345	9	AP002355	Homo sapi
AB065501	Homo sapi	9	AB065501	56423	18.7	35	346	9	AB065501	Homo sapi
AC107969	Homo sapi	2	AC107969	57662	18.7	35	347	2	AC107969	Homo sapi
AL513314	Human DNA	9	AL513314	58205	18.7	35	348	9	AL513314	Human DNA
AC021303	Homo sapi	2	AC021303	58546	18.7	35	349	2	AC021303	Homo sapi
AC021303	Homo sapi	9	AC021303	58546	18.7	35	350	9	AC021303	Homo sapi
AC009799	Homo sapi	2	AC009799	59396	18.7	35	351	2	AC009799	Homo sapi
AC074013	Homo sapi	9	AC074013	59657	18.7	35	352	9	AC074013	Homo sapi
AC005179	Homo sapi	9	AC005179	59765	18.7	35	353	9	AC005179	Homo sapi
AC103985	Homo sapi	2	AC103985	60079	18.7	35	354	2	AC103985	Homo sapi
AL139130	Human DNA	9	AL139130	61145	18.7	35	355	9	AL139130	Human DNA
AC090748	Homo sapi	2	AC090748	61309	18.7	35	356	2	AC090748	Homo sapi
AC108469	Homo sapi	9	AC108469	62038	18.7	35	357	9	AC108469	Homo sapi

358	35	18.7	63402	9	AP0000260	Homo sapi	C 431	35	18.7	86165	9	AC107048	Homo sapi
359	35	18.7	63701	9	AL353693	Human DNA	C 432	35	18.7	86203	9	AC017116	Homo sapi
360	35	18.7	64071	2	AC084122	Homo sapi	C 433	35	18.7	86226	2	AC013812	Homo sapi
361	35	18.7	64323	9	AL356976	Human DNA	434	35	18.7	86829	9	AC011382	Homo sapi
362	35	18.7	64529	2	AC108449	Homo sapi	435	35	18.7	86973	9	AC011394	Homo sapi
363	35	18.7	64597	2	AC131571	Homo sapi	436	35	18.7	87201	9	AC007623	Homo sapi
364	35	18.7	64924	2	AC090131	Homo sapi	437	35	18.7	88027	2	AL162401	Homo sapi
365	35	18.7	65541	2	AC021375	Homo sapi	438	35	18.7	88251	2	AC126325	Homo sapi
366	35	18.7	65705	2	AC024394	Homo sapi	C 439	35	18.7	88295	9	AC004612	Homo sapi
367	35	18.7	65752	2	AC011160	Homo sapi	C 440	35	18.7	89211	9	AL669821	Human DNA
368	35	18.7	66092	2	AC125435	Homo sapi	441	35	18.7	89290	9	CNS01DVY	Human chr
369	35	18.7	66188	9	AL391136	Human DNA	442	35	18.7	89448	9	AC005067	Homo sapi
370	35	18.7	66565	9	AC092103	Homo sapi	C 443	35	18.7	90169	9	HS398A12	Human DNA
371	35	18.7	66610	9	AC074386	Homo sapi	444	35	18.7	90171	9	AC095040	Homo sapi
372	35	18.7	67335	9	HS43683	Homo sapi	C 445	35	18.7	90175	9	HS0785886	Human DNA
373	35	18.7	67618	2	AC109634	Homo sapi	C 446	35	18.7	90476	9	AC015910	Homo sapi
374	35	18.7	68764	9	AL389921	Human DNA	C 447	35	18.7	90766	9	AL392166	Human DNA
375	35	18.7	68791	9	AC091961	Homo sapi	C 448	35	18.7	90968	2	AC108722	Homo sapi
376	35	18.7	68808	2	AC022708	Homo sapi	C 449	35	18.7	91071	2	AC022589	Homo sapi
377	35	18.7	68808	2	AC022708	Homo sapi	C 450	35	18.7	91073	2	AC011426	Homo sapi
378	35	18.7	69492	2	AC111157	Homo sapi	C 451	35	18.7	91076	9	AC073892	Homo sapi
379	35	18.7	69587	9	AF146367	Homo sapi	C 452	35	18.7	91099	9	AL139045	Human DNA
380	35	18.7	69778	9	AC022411	Homo sapi	C 453	35	18.7	91388	9	AC005994	Homo sapi
381	35	18.7	70589	2	AC087515	Homo sapi	C 454	35	18.7	92644	2	AF186995	Homo sapi
382	35	18.7	70946	9	AL161614	Human DNA	C 455	35	18.7	92932	9	AC091788	Homo sapi
383	35	18.7	70972	2	AC130332	Homo sapi	C 456	35	18.7	93273	9	AC004084	Homo sapi
384	35	18.7	71382	9	AL590965	Human DNA	C 457	35	18.7	93294	9	AL607144	Human DNA
385	35	18.7	71627	9	AC004851	Homo sapi	458	35	18.7	93778	9	AC016999	Homo sapi
386	35	18.7	71736	9	AC022540	Homo sapi	459	35	18.7	93911	2	HSAC000002	Homo sapi
387	35	18.7	71864	2	AC130372	Homo sapi	C 460	35	18.7	93964	2	AL359456_5	Continuation (6 of
388	35	18.7	73568	2	AC025967	Homo sapi	461	35	18.7	95484	2	AC015854	Homo sapi
389	35	18.7	73643	2	AC018773	Homo sapi	462	35	18.7	96398	9	AL591367	Human DNA
390	35	18.7	74515	9	AL355482	Human DNA	463	35	18.7	96625	9	HSAC000118	Human BAC
391	35	18.7	75525	9	AL391561	Human DNA	C 464	35	18.7	96764	9	AL732325	Human DNA
392	35	18.7	75698	9	AP000228	Homo sapi	C 465	35	18.7	96799	9	AC104647	Homo sapi
393	35	18.7	76241	9	HS07336M4	Human DNA	C 466	35	18.7	97110	9	AL591521	Human DNA
394	35	18.7	76410	2	AC016093	Homo sapi	C 467	35	18.7	97234	9	AL137859	Human DNA
395	35	18.7	76416	9	AC005370	Homo sapi	C 468	35	18.7	97826	9	AL591647	Human DNA
396	35	18.7	76634	2	AC126335	Homo sapi	C 469	35	18.7	97898	9	AL353613	Human DNA
397	35	18.7	76856	2	AC021526	Homo sapi	C 470	35	18.7	97982	9	AP000687	Homo sapi
398	35	18.7	77164	9	AL133514	Human DNA	471	35	18.7	98271	9	AL162590	Human DNA
399	35	18.7	77239	9	AL583844	Human DNA	C 472	35	18.7	98360	9	AL043713	Human DNA
400	35	18.7	78200	9	AP001866	Homo sapi	C 473	35	18.7	98433	9	AC097483	Homo sapi
401	35	18.7	78371	9	HSJ868P24	Human DNA	474	35	18.7	98697	9	AC004854	Homo sapi
402	35	18.7	78386	2	AC015466	Homo sapi	475	35	18.7	99003	2	AL390756	Homo sapi
403	35	18.7	78507	9	AC110743	Homo sapi	476	35	18.7	99011	2	AC004937	Homo sapi
404	35	18.7	79237	9	HS0761M11	Human DNA	477	35	18.7	99227	9	AC114737	Homo sapi
405	35	18.7	79516	9	AC004834	Homo sapi	478	35	18.7	99342	9	HS201D17	Human DNA
406	35	18.7	80421	9	AL663100	Human DNA	479	35	18.7	99411	9	AC005207	Homo sapi
407	35	18.7	80796	9	AC073136	Homo sapi	C 480	35	18.7	99876	9	HS0790108	Human DNA
408	35	18.7	80796	9	AC073136	Homo sapi	481	35	18.7	100000	9	AP000017	Homo sapi
409	35	18.7	80824	9	AL513480	Human DNA	482	35	18.7	100000	9	AP000099	Homo sapi
410	35	18.7	81001	6	AX063464	Sequence	C 483	35	18.7	100000	9	AP000140	Homo sapi
411	35	18.7	81001	6	AX063464	Sequence	484	35	18.7	100000	9	AP000159	Homo sapi
412	35	18.7	81157	9	AC114963	Homo sapi	485	35	18.7	100000	9	AP000175	Homo sapi
413	35	18.7	81364	2	AC021072_3	Continuation (4 of	C 486	35	18.7	100575	9	HS0781P6	Human DNA
414	35	18.7	81759	2	AC023211	Homo sapi	C 487	35	18.7	100919	9	AL359378	Human DNA
415	35	18.7	81759	2	AC023211	Homo sapi	488	35	18.7	100976	9	HS1005F21	Human DNA
416	35	18.7	82183	9	HSJ1037B9	Human DNA	489	35	18.7	100998	9	HS343K2	Human DNA
417	35	18.7	82517	9	HS341D10	Human DNA	C 490	35	18.7	101261	2	AC010628	Homo sapi
418	35	18.7	82921	9	AL356747	Homo sapi	C 491	35	18.7	101269	9	AC005300	Homo sapi
419	35	18.7	83167	9	AL590423	Human DNA	C 492	35	18.7	101584	9	CNS01D55	BAC sequ
420	35	18.7	83175	9	AC110995	Homo sapi	C 493	35	18.7	101744	9	AL512783	Human DNA
421	35	18.7	83684	9	AC105290	Homo sapi	C 494	35	18.7	102259	2	AC015916	Homo sapi
422	35	18.7	83820	9	AL133264	Human DNA	C 495	35	18.7	102282	9	AL158033	Human DNA
423	35	18.7	83888	9	AC008412	Homo sapi	C 496	35	18.7	102326	9	AC087407	Homo sapi
424	35	18.7	84388	9	AL589984	Human DNA	497	35	18.7	102500	2	AC096507	Homo sapi
425	35	18.7	85000	9	AC009772	Homo sapi	498	35	18.7	102663	2	AC008399	Homo sapi
426	35	18.7	85132	9	AC092171	Homo sapi	499	35	18.7	103347	9	AL136086	Human DNA
427	35	18.7	85195	9	AL136093	Human DNA	C 500	35	18.7	103347	9	AC022027	Homo sapi
428	35	18.7	85378	2	AL356577	Homo sapi	C 501	35	18.7	103574	9	HSAC002115	Human DNA
429	35	18.7	85565	9	AL136133	Human DNA	C 502	35	18.7	103727	9	AL136360	Human DNA
430	35	18.7	85946	9	AC004240	Homo sapi	C 503	35	18.7	103875	9	AL136223	Human DNA

504	35	18.7	103926	9	AC093164	AC093164 Homo sapi
505	35	18.7	104228	9	AL135917	AL135917 Human DNA
506	35	18.7	104357	9	AL139213	AL139213 Human DNA
507	35	18.7	104726	9	AC008087	AC008087 Homo sapi
508	35	18.7	104810	9	AC003012	AC003012 Human PAC
509	35	18.7	104844	9	HSJ105707	HSJ105707 Human DNA
510	35	18.7	105702	9	AC034203	AC034203 Homo sapi
511	35	18.7	106265	9	AL133294	AL133294 Human DNA
512	35	18.7	106363	9	AL1662788	AL1662788 Human DNA
513	35	18.7	106427	9	AL356417	AL356417 Human DNA
514	35	18.7	106499	9	AC023271	AC023271 Homo sapi
515	35	18.7	106773	9	AP003097	AP003097 Homo sapi
516	35	18.7	106945	9	AC024337	AC024337 Homo sapi
517	35	18.7	107325	9	AC009189	AC009189 Homo sapi
518	35	18.7	107418	9	HS551E13	HS551E13 Human DNA
519	35	18.7	107480	9	AL596094	AL596094 Human DNA
520	35	18.7	107487	9	AC011483	AC011483 Homo sapi
521	35	18.7	107567	9	AC011481	AC011481 Homo sapi
522	35	18.7	107967	9	AL353701	AL353701 Human DNA
523	35	18.7	108131	9	AL139321	AL139321 Human DNA
524	35	18.7	108765	2	AF216674	AF216674 Homo sapi
525	35	18.7	108969	9	AC004813	AC004813 Homo sapi
526	35	18.7	109056	2	AC074053	AC074053 Homo sapi
527	35	18.7	109609	9	AL138785	AL138785 Human DNA
528	35	18.7	110000	2	AC008576	AC008576 Homo sapi
529	35	18.7	110000	2	AC013391	AC013391 Homo sapi
530	35	18.7	110000	2	AC112773	AC112773 Homo sapi
531	35	18.7	110000	2	AC116301	AC116301 Homo sapi
532	35	18.7	110000	2	AC116301	Continuation (2 of
533	35	18.7	110000	9	AC005079	Continuation (3 of
534	35	18.7	110000	9	AC005079	Continuation (4 of
535	35	18.7	110000	9	AC005079	Continuation (5 of
536	35	18.7	110001	9	AC008480	AC008480 Homo sapi
537	35	18.7	110394	9	AC003086	AC003086 Homo sapi
538	35	18.7	111075	2	AC114337	AC114337 Homo sapi
539	35	18.7	111163	2	AL533214	AL533214 Homo sapi
540	35	18.7	111517	9	AC074366	AC074366 Homo sapi
541	35	18.7	111655	2	AC010239	AC010239 Homo sapi
542	35	18.7	111998	9	AC011509	AC011509 Homo sapi
543	35	18.7	112187	9	AC096749	AC096749 Homo sapi
544	35	18.7	112291	9	AC107067	AC107067 Homo sapi
545	35	18.7	113656	9	AC112253	AC112253 Homo sapi
546	35	18.7	113853	9	AF196971	AF196971 Homo sapi
547	35	18.7	114148	9	AC112655	AC112655 Homo sapi
548	35	18.7	114298	9	HSJ543C6	HSJ543C6 Human DNA
549	35	18.7	114302	9	AL162413	AL162413 Human DNA
550	35	18.7	114411	9	HUAC002551	HUAC002551 Human Chr
551	35	18.7	114596	9	HS1063B2	HS1063B2 Human DNA
552	35	18.7	114624	2	AC099485	AC099485 Homo sapi
553	35	18.7	115027	2	AP001480	AP001480 Homo sapi
554	35	18.7	115289	9	AC011490	AC011490 Homo sapi
555	35	18.7	115292	9	AC120117	AC120117 Homo sapi
556	35	18.7	115626	9	AC103792	AC103792 Homo sapi
557	35	18.7	115663	9	AC093029	AC093029 Homo sapi
558	35	18.7	115793	9	AC025166	AC025166 Homo sapi
559	35	18.7	116106	2	AL162611	AL162611 Homo sapi
560	35	18.7	116370	9	HS569M23	HS569M23 Human DNA
561	35	18.7	116430	9	AL359513	AL359513 Human DNA
562	35	18.7	116671	9	AC087264	AC087264 Pan trogl
563	35	18.7	116879	9	AC106854	AC106854 Homo sapi
564	35	18.7	116911	9	AC093019	AC093019 Homo sapi
565	35	18.7	116948	9	AL357125	AL357125 Human DNA
566	35	18.7	117000	9	AC1117475	AC1117475 Homo sapi
567	35	18.7	117096	9	AC008468	AC008468 Homo sapi
568	35	18.7	117511	2	AC021469	AC021469 Homo sapi
569	35	18.7	117962	9	AF312032	AF312032 Homo sapi
570	35	18.7	117976	9	AL671309	AL671309 Human DNA
571	35	18.7	118022	9	AC114785	AC114785 Homo sapi
572	35	18.7	118234	9	AL355476	AL355476 Human DNA
573	35	18.7	118439	9	AL135905	AL135905 Human DNA
574	35	18.7	118582	2	AC135989	AC135989 Homo sapi
575	35	18.7	118788	9	AC005277	AC005277 Homo sapi
576	35	18.7	118847	9	AC013413	AC013413 Homo sapi
577	35	18.7	119347	9	AC020934	AC020934 Homo sapi
578	35	18.7	119350	9	HS12803	HS12803 Human DNA
579	35	18.7	119386	9	AC079824	AC079824 Homo sapi
580	35	18.7	119453	9	AC004006	AC004006 Homo sapi
581	35	18.7	119460	9	AL590431	AL590431 Human DNA
582	35	18.7	119884	9	AL139814	AL139814 Human DNA
583	35	18.7	119951	2	AC025267	AC025267 Homo sapi
584	35	18.7	120538	9	AC004815	AC004815 Homo sapi
585	35	18.7	120766	9	AC004150	AC004150 Homo sapi
586	35	18.7	121129	9	AL357315	AL357315 Human DNA
587	35	18.7	121348	9	AC106874	AC106874 Homo sapi
588	35	18.7	122073	2	AC090831	AC090831 Homo sapi
589	35	18.7	122289	9	AL389925	AL389925 Human DNA
590	35	18.7	122568	9	AF196972	AF196972 Homo sapi
591	35	18.7	122912	9	AC073182	AC073182 Homo sapi
592	35	18.7	123203	9	AC003036	AC003036 Homo sapi
593	35	18.7	123287	9	AC083807	AC083807 Homo sapi
594	35	18.7	123817	9	AL713980	AL713980 Human DNA
595	35	18.7	124000	2	AC004060	AC004060 Homo sapi
596	35	18.7	124028	9	AC022417	AC022417 Homo sapi
597	35	18.7	124829	9	AC097109	AC097109 Homo sapi
598	35	18.7	125151	9	AC093821	AC093821 Homo sapi
599	35	18.7	125479	9	HSJ244F24	HSJ244F24 Human DNA
600	35	18.7	125495	9	AL359914	AL359914 Human DNA
601	35	18.7	125508	9	AC006345	AC006345 Homo sapi
602	35	18.7	125630	9	HSU91319	HSU91319 Human chrom
603	35	18.7	125644	9	AP004293	AP004293 Homo sapi
604	35	18.7	125798	9	AL390248	AL390248 Human DNA
605	35	18.7	126736	2	AC044788	AC044788 Homo sapi
606	35	18.7	127098	9	AC004050	AC004050 Homo sapi
607	35	18.7	127199	9	AC084262	AC084262 Homo sapi
608	35	18.7	127321	9	AC020903	AC020903 Homo sapi
609	35	18.7	127408	9	AC098828	AC098828 Homo sapi
610	35	18.7	127805	9	AC130271	AC130271 Homo sapi
611	35	18.7	127957	9	AC006122	AC006122 Homo sapi
612	35	18.7	128615	9	AL591051	AL591051 Human DNA
613	35	18.7	128726	9	AL136458	AL136458 Human DNA
614	35	18.7	129338	9	AC016597	AC016597 Homo sapi
615	35	18.7	129517	2	AC016400	AC016400 Homo sapi
616	35	18.7	129559	9	AL731563	AL731563 Human DNA
617	35	18.7	129950	9	HS739H11	HS739H11 Human DNA
618	35	18.7	130030	9	AC004889	AC004889 Homo sapi
619	35	18.7	130195	2	AC090170	AC090170 Homo sapi
620	35	18.7	130318	9	AC026979	AC026979 Homo sapi
621	35	18.7	130445	9	AC116648	AC116648 Homo sapi
622	35	18.7	130607	9	AC004875	AC004875 Homo sapi
623	35	18.7	130647	9	AL157385	AL157385 Human DNA
624	35	18.7	130701	2	AC009889	AC009889 Homo sapi
625	35	18.7	130755	9	AC004253	AC004253 Homo sapi
626	35	18.7	130986	2	AC120597	AC120597 Homo sapi
627	35	18.7	131457	9	AL356600	AL356600 Human DNA
628	35	18.7	131841	9	HSJ881L22	HSJ881L22 Human DNA
629	35	18.7	132281	2	AC089594	AC089594 Homo sapi
630	35	18.7	132710	9	AC093535	AC093535 Homo sapi
631	35	18.7	133401	2	AC079257	AC079257 Homo sapi
632	35	18.7	133541	2	AC027169	AC027169 Homo sapi
633	35	18.7	133641	2	AC097005	AC097005 Pan trogl
634	35	18.7	133893	9	AC005005	AC005005 Homo sapi
635	35	18.7	133925	9	AC011444	AC011444 Homo sapi
636	35	18.7	134010	9	AL353579	AL353579 Human DNA
637	35	18.7	134059	2	AC016284	AC016284 Homo sapi
638	35	18.7	134091	2	AC023349	AC023349 Homo sapi
639	35	18.7	134184	9	AC095044	AC095044 Homo sapi
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641	35	18.7	134210	9	AC005052	AC005052 Homo sapi
642	35	18.7	134339	9	AC114501	AC114501 Homo sapi
643	35	18.7	134725	2	AC091852	AC091852 Homo sapi
644	35	18.7	135062	9	AC026691	AC026691 Homo sapi
645	35	18.7	135405	9	AC000025	AC000025 Homo sapi
646	35	18.7	135672	9	HSAC000113	HSAC000113 Human PAC
647	35	18.7	135693	9	HSJ1167H4	HSJ1167H4 Human DNA
648	35	18.7	135837	9	AC004837	AC004837 Homo sapi
649	35	18.7	136134	9	HS3394P21	HS3394P21 Homo sapi

650	35	18.7	136131	9	AC000360	AC000360 Homo sapi	723	35	18.7	146641	2	AC011140	AC011140 Homo sapi
651	35	18.7	136159	9	AC097475	AC097475 Homo sapi	c 724	35	18.7	146746	9	HS50J22	Z84484 Human DNA s
652	35	18.7	136188	9	AL096819	AL096819 Human DNA	c 725	35	18.7	147109	9	AL591043	AL591043 Human DNA
653	35	18.7	136932	9	AC068035	AC068035 Homo sapi	c 726	35	18.7	147167	9	HS2705	AL033529 Human DNA
654	35	18.7	137101	9	AC016692	AC016692 Homo sapi	c 727	35	18.7	147172	9	AC008688	AC008688 Homo sapi
655	35	18.7	137247	2	AC015865	AC015865 Homo sapi	c 728	35	18.7	147246	2	AC023196	AC023196 Homo sapi
656	35	18.7	137247	9	AC064853	AC064853 Homo sapi	c 729	35	18.7	147246	2	AC023196	AC023196 Homo sapi
657	35	18.7	137345	9	AL669924	AL669924 Human DNA	c 730	35	18.7	147277	2	AC098811	AC098811 Homo sapi
658	35	18.7	137436	9	AL159986	AL159986 Human DNA	c 731	35	18.7	147364	9	AC110998	AC110998 Homo sapi
659	35	18.7	137469	2	AC013370	AC013370 Homo sapi	c 732	35	18.7	147418	9	AC023855	AC023855 Homo sapi
660	35	18.7	138006	9	AL390074	AL390074 Human DNA	c 733	35	18.7	147458	9	AL357832	AL357832 Human DNA
661	35	18.7	138021	9	AC090820	AC090820 Homo sapi	c 734	35	18.7	147520	9	AC117392	AC117392 Homo sapi
662	35	18.7	138215	2	AC023523	AC023523 Homo sapi	c 735	35	18.7	147520	2	AC036186	AC036186 Homo sapi
663	35	18.7	138814	30	AC068997	AC068997 Homo sapi	c 736	35	18.7	147924	2	AC036186	AC036186 Homo sapi
664	35	18.7	138928	9	AC064847	AC064847 Homo sapi	c 737	35	18.7	148049	9	HS300188	AL300188 Homo sapi
665	35	18.7	139086	9	AC025456	AC025456 Homo sapi	c 738	35	18.7	148166	9	CNS07EER	AL445884 Human chr
666	35	18.7	139130	9	AC091504	AC091504 Homo sapi	c 739	35	18.7	148250	9	AL353625	AL353625 Human DNA
667	35	18.7	139144	2	AC124863	AC124863 Homo sapi	c 740	35	18.7	148295	9	AC090510	AC090510 Homo sapi
668	35	18.7	139189	2	AC118553	AC118553 Homo sapi	c 741	35	18.7	148497	9	AL133396	AL133396 Human DNA
669	35	18.7	139476	9	AC010377	AC010377 Homo sapi	c 742	35	18.7	148598	9	HSBA51C14	AL121875 Human DNA
670	35	18.7	139480	9	HUAC002331	AC002331 Homo sapi	c 743	35	18.7	148750	9	AL596225	AL596225 Human DNA
671	35	18.7	139488	9	AC003043	AC003043 Homo sapi	c 744	35	18.7	148824	2	AC025640	AC025640 Homo sapi
672	35	18.7	139737	9	HS228H13	AL031985 Human DNA	c 745	35	18.7	148897	2	AL139034	AL139034 Human DNA
673	35	18.7	139996	9	AL161799	AL161799 Homo sapi	c 746	35	18.7	149002	2	AL445484	AL445484 Homo sapi
674	35	18.7	140330	9	AC026777	AC026777 Homo sapi	c 747	35	18.7	149194	9	AC007566	AC007566 Homo sapi
675	35	18.7	140425	9	AC005479	AC005479 Homo sapi	c 748	35	18.7	149271	9	AC022144	AC022144 Homo sapi
676	35	18.7	140783	9	AC027373	AC027373 Homo sapi	c 749	35	18.7	149308	9	AC005527	AC005527 Homo sapi
677	35	18.7	140856	9	AC002430	AC002430 Homo sapi	c 750	35	18.7	149313	2	AC023548	AC023548 Homo sapi
678	35	18.7	140966	9	AC023058	AC023058 Homo sapi	c 751	35	18.7	149331	2	AC023548	AC023548 Homo sapi
679	35	18.7	141056	9	AL354836	AL354836 Homo sapi	c 752	35	18.7	149445	9	AC013264	AC013264 Homo sapi
680	35	18.7	141266	9	AC004671	AC004671 Homo sapi	c 753	35	18.7	149605	9	AC005522	AC005522 Homo sapi
681	35	18.7	141428	9	AL139415	AL139415 Human DNA	c 754	35	18.7	149745	9	AP000648	AP000648 Homo sapi
682	35	18.7	141442	9	AC108471	AC108471 Homo sapi	c 755	35	18.7	149762	9	AC011270	AC011270 Homo sapi
683	35	18.7	142037	9	AC025171	AC025171 Homo sapi	c 756	35	18.7	149866	9	AC025627	AC025627 Homo sapi
684	35	18.7	142105	9	AC012374	AC012374 Homo sapi	c 757	35	18.7	149977	30	AL355313	AL355313 Human DNA
685	35	18.7	142185	2	AC022656	AC022656 Homo sapi	c 758	35	18.7	150107	2	AC027582	AC027582 Homo sapi
686	35	18.7	142276	9	AC109454	AC109454 Homo sapi	c 759	35	18.7	150114	2	AC074004	AC074004 Homo sapi
687	35	18.7	142640	9	AC006399	AC006399 Homo sapi	c 760	35	18.7	150192	9	AC008686	AC008686 Homo sapi
688	35	18.7	142665	9	HS202121	AL035690 Human DNA	c 761	35	18.7	150199	9	AC087568	AC087568 Pan trogl
689	35	18.7	142667	9	AC125387	AC125387 Homo sapi	c 762	35	18.7	150520	9	AL136305	AL136305 Human DNA
690	35	18.7	142762	2	AL391599	AL391599 Homo sapi	c 763	35	18.7	150541	9	HS072A23	HS072A23 Human DNA
691	35	18.7	142875	2	AC005805	AC005805 Homo sapi	c 764	35	18.7	150541	9	AL590559	AL590559 Human DNA
692	35	18.7	142978	9	AC097717	AC097717 Homo sapi	c 765	35	18.7	150662	9	CNS05TEM	AL592323 Human chr
693	35	18.7	142979	9	AC000029	AC000029 Homo sapi	c 766	35	18.7	150771	9	AL392106	AL392106 Human DNA
694	35	18.7	143084	9	AC034200	AC034200 Homo sapi	c 767	35	18.7	150799	2	AC024402	AC024402 Homo sapi
695	35	18.7	143125	9	AC092338	AC092338 Homo sapi	c 768	35	18.7	150893	2	AC044871	AC044871 Homo sapi
696	35	18.7	143176	2	AC011332	AC011332 Homo sapi	c 769	35	18.7	151517	2	AC031989	AC031989 Homo sapi
697	35	18.7	143444	9	AC007541	AC007541 Homo sapi	c 770	35	18.7	151526	9	AC026636	AC026636 Homo sapi
698	35	18.7	143563	9	HS555C23	AL032821 Human DNA	c 771	35	18.7	151559	9	AL390294	AL390294 Human DNA
699	35	18.7	143585	9	AL176681	AL176681 Homo sapi	c 772	35	18.7	151606	9	AC087441	AC087441 Homo sapi
700	35	18.7	143618	9	AL137856	AL137856 Human DNA	c 773	35	18.7	151796	2	AC096995	AC096995 Homo sapi
701	35	18.7	143673	2	AC087720	AC087720 Homo sapi	c 774	35	18.7	152039	9	AC097489	AC097489 Homo sapi
702	35	18.7	143899	2	AC013606	AC013606 Homo sapi	c 775	35	18.7	152121	2	AP000830	AP000830 Homo sapi
703	35	18.7	143899	6	AX411543	AX411543 Sequence	c 776	35	18.7	152195	2	AC016331	AC016331 Homo sapi
704	35	18.7	144189	9	HS417M14	AL024498 Human DNA	c 777	35	18.7	152322	2	AL357077	AL357077 Homo sapi
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DEFINITION Homo sapiens FEZ1 (FEZ1) gene, complete cds.
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Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
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MEDLINE 10097140
PUBMED
REFERENCE 2 (bases 1 to 5492)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
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AUTHORS 1 (bases 1 to 9108)
          Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
          Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
JOURNAL and its expression is altered in multiple human tumors
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
PUBMED 99199287
REFERENCE 10097140
          2 (bases 1 to 9108)
          Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
          Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
          Institute, 2335 10th street, Philadelphia, PA 19107, USA
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          LQSNMMLKALSPSDGSKLGHNSKADKGPSCVRSPISTDEGSIQLEQKLLERGA
          LQKORSFEKELASSLAVBERPRCRDELGGPEPKGNKLKQASQKRAQOVLHLQ
          VLQQLQKROLROELSLMEQDLLETKLRSYEREKTSFGPALEETQWEYVCQSGEIS
          LLQQLKESQTEYNKASEILGLKQKLDTRGKLEGLRLTQDLEGALRFGKLELVC
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          BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
          ORIGIN

Query Match 100.0%; Score 187; DB 9; Length 9108;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCTAGTCTACTGCGCTCATCTCTGCGGCTCAGCATCTCTGCTGCTCAGCC 60
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Db 6999 ATGATCTAGTCTACTGCGCTCATCTCTGCGGCTCAGCATCTCTGCTGCTCAGCC 7058
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Qy 61 TTCAACTAGTCTGAGTCTAGGTCGCGCCGACCGTCTGCTGCTGCTTTCATTTT 120
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Db 7059 TTCAACTAGTCTGAGTCTAGGTCGCGCCGACCGTCTGCTGCTGCTTTCATTTT 7118
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Qy 121 TGTAGGACGGGTCTCGTTTGTGTGCAAGTGGTCTCAAACTTGTGGCTCAAGCAA 180
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Db 7119 TGTAGGACGGGTCTCGTTTGTGTGCAAGTGGTCTCAAACTTGTGGCTCAAGCAA 7178
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Qy 181 TCCACCT 187
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Db 7179 TCCACCT 7185

RESULT 3
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LOCUS AC025853
DEFINITION Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING

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IN PROGRESS ***, 3 unordered pieces.
AC025853
VERSION GI:21431202
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 173264)
          Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 8, clone RP11-353K12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173264)
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
          Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,
          Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
          Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
          Collymore, A., Cooke, P., DeAvrellano, K., Dewar, K., Diaz, J.S.,
          Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
          Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
          Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
          Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
          Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
          Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
          McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
          Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
          Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
          O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
          Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
          Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
          Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
          Testfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
          Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
          Young, G., Zainoun, J., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 173264)
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
          Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
          Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
          Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
          Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
          Fero, S., Ferreira, P., FitzGerald, M., Fitzhugh, W., Gage, D.,
          Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
          Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
          Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
          Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
          Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
          Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
          Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
          Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
          O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
          Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
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          Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S.,
          Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
          Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
          Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jun 17, 2002 this sequence version replaced gi:21321864.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          ----- Genome Center
          Center: Whitehead Institute/ MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence_submissions@genome.wi.mit.edu
          ----- Project Information

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Center project name: L7454
Center clone name: 353_K_12
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 39461: contig of 39461 bp in length
* 39462 39561: gap of 100 bp
* 39562 108347: contig of 68786 bp in length
* 108348 108447: gap of 100 bp
* 108448 173264: contig of 64817 bp in length.
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/chromosome="8"
/map="8"
/clones="RP11-353K12"
/clone_lib="RPCI-11 Human Male BAC"
47355 a 38861 c 39235 g 47493 t 317 others
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BASE COUNT 47355 a 38861 c 39235 g 47493 t
ORIGIN
Query Match 100.0%; Score 187; DB 2; Length 173264;
Best Local Similarity 100.0%; Pred. NO. 2.2e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGATCATAGCTACTGACGCTCATCTCTGGCTCAGCAATCTCTGCTCAGCC 60
Db 29244 ATGATCATAGCTACTGACGCTCATCTCTGGCTCAGCAATCTCTGCTCAGCC 29303
Qy 61 TTCCAACCTAGCTGGGACTACAGTGGCGGCCGACCGTGGCTGCTTTCATTTT 120
Db 29304 TTCCAACCTAGCTGGGACTACAGTGGCGGCCGACCGTGGCTGCTTTCATTTT 29363
Qy 121 TGTAGGACGGGTCTCGTTTGTGGCAAGCTGGTCTCAAACTTGGCTCAAGCAA 180
Db 29364 TGTAGGACGGGTCTCGTTTGTGGCAAGCTGGTCTCAAACTTGGCTCAAGCAA 29423
Qy 181 TCCACCT 187
Db 29424 TCCACCT 29430
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RESULT 4
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LOCUS Homo sapiens chromosome 17 clone CTD-2291H15 map 17, WORKING DRAFT
DEFINITION AC009449
SEQUENCE 5 unordered pieces.
AC009449
VERSION AC009449.5 GI:15291073
KEYWORDS HTGS, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105051)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeRellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L.,
Karatas, A., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P.,
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misc_feature 718..1791
/notes="assembly_fragment"
misc_feature 1892..11154
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ORIGIN
Query Match 22.5%; Score 42; DB 2; Length 105051;

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Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Testaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
Direct Submission
Submitted (22-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 26, 2001 this sequence version replaced gi:14626922.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Project Information
Center project name: L775
Center clone name: 2291_H_15
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Summary Statistics
Sequencing vector: M13; M77815; 19% of reads
Sequencing vector: Plasmid; n/a; 81% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 102893 bases at least Q40
Consensus quality: 103343 bases at least Q30
Consensus quality: 103573 bases at least Q20
Insert size: 104651; sum-of-contigs
Quality coverage: 16.2 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 617: contig of 617 bp in length
* 618 717: gap of 100 bp
* 718 1791: contig of 1074 bp in length
* 1792 1891: gap of 100 bp
* 1892 11154: contig of 9263 bp in length
* 11155 11254: gap of 100 bp
* 11255 47275: contig of 36021 bp in length
* 47276 47375: gap of 100 bp
* 47376 105051: contig of 57676 bp in length.
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/chromosome="17"
/map="17"
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718..1791
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/notes="assembly_fragment"
11255..47275
/notes="assembly_fragment"
47376..105051
/notes="assembly_fragment"
BASE COUNT 29638 a 22552 c 21751 g 30707 t
ORIGIN
Query Match 22.5%; Score 42; DB 2; Length 105051;

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Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGATCATAGTCTCACTGAGGCTCATATCTCTGGGCTCAAGCA 43  
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RESULT 5  
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LOCUS Homo sapiens chromosome 15, clone RP11-346A8, complete sequence.  
AC011846  
ACCESSION AC011846.16 GI:21389294  
VERSION HTG.  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 147760)  
TITLE Homo sapiens chromosome 15, clone RP11-346A8  
JOURNAL  
REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (15-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 147760)  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 147760)  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (11-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jun 11, 2002 this sequence version replaced gi:14994158.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L2618  
Center clone name: 346\_A\_8  
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Only the last 147.8 kb of this clone are being submitted.  
The remainder overlaps accession number AC105129 [WICGR project L22971].

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/clone\_lib="RPCI-11 Human Male BAC"  
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1666. .1699  
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2049. .2069  
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Query Match      22.5%; Score 42; DB 9; Length 147760;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 47 CTCCTGCTCAGCCCTTCCAACTAGCTGGGACTACAGGTGCGC 88
Db 61532 CTCCTGCTCAGCCCTTCCAACTAGCTGGGACTACAGGTGCGC 61573

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RESULT 6  
 HS97K10/c  
 LOCUS  
 DEFINITION Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSS and CpG island.  
 ACCESSION 281365  
 VERSION 281365.1 GI:16555588  
 KEYWORDS CpG island; X.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 156197)  
 Wray, P.  
 Direct Submission  
 TITLE Submitted (30-OCT-1996) Sanger Centre, Hinxton, Cambridgeshire,  
 JOURNAL CB10 1RQ, UK. E-mail enquires: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 COMMENT IMPORTANT: This sequence is the entire insert of clone 97K10. The true left end of clone 97K10 is at 1 in this sequence. The true right end of clone 97K10 is at 156197.  
 97K10 is from the Human PAC library.  
 FEATURES  
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 /db\_xref="taxon:9606"  
 /chromosome="X"  
 /map="X"  
 /clone="RP1-97K10"  
 /clone\_lib="RPC1-1"  
 548..673  
 /note="MIR repeat: matches 21..147 of consensus"  
 2971..5179  
 /note="Putative CpG island"  
 5673..5771  
 /note="MIR repeat: matches 141..34 of consensus"  
 6281..6384  
 /note="MIR repeat: matches 92..190 of consensus"  
 8048..8192  
 /note="MIR repeat: matches 14..143 of consensus"  
 9008..9304  
 /note="AluSx repeat: matches 298..1 of consensus"  
 9481..9792  
 /note="AluB repeat: matches 11..302 of consensus"  
 9962..10099  
 /note="MIR repeat: matches 118..259 of consensus"  
 10787..10881  
 /note="MIR repeat: matches 52..145 of consensus"  
 11201..11509  
 /note="AluSx repeat: matches 1..299 of consensus"  
 13071..13181  
 /note="MIR repeat: matches 193..80 of consensus"  
 14453..14712  
 /note="AluB repeat: matches 14..288 of consensus"  
 15654..15898  
 /note="MIR repeat: matches 20..262 of consensus"  
 16041..16342  
 /note="AluJo repeat: matches 301..2 of consensus"  
 16343..16477  
 /partial  
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 16775..17028  
 /note="L1ME3A repeat: matches 905..641 of consensus"  
 17018..17320  
 /note="MLTIE repeat: matches 568..256 of consensus"  
 17312..17550  
 /note="MLTID repeat: matches 309..82 of consensus"  
 17652..17887  
 /note="L1ME3 repeat: matches 660..412 of consensus"  
 18334..18480  
 /note="MIR2 repeat: matches 1..143 of consensus"  
 18930..19074

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repeat_region /note="MER3 repeat: matches 1. .148 of consensus"  
19076. .19381  
repeat_region /note="AluSg repeat: matches 301. .2 of consensus"  
19409. .19487  
repeat_region /note="MER3 repeat: matches 131. .209 of consensus"  
20782. .20864  
repeat_region /note="MIR repeat: matches 65. .152 of consensus"  
21630. .21931  
repeat_region /note="AluSx repeat: matches 302. .1 of consensus"  
22185. .22605  
repeat_region /note="MSTA repeat: matches 1. .426 of consensus"  
23148. .23286  
repeat_region /note="MIR repeat: matches 217. .65 of consensus"  
23291. .23709  
repeat_region /note="MSTA repeat: matches 426. .1 of consensus"  
24130. .24419  
repeat_region /note="AluSg repeat: matches 293. .1 of consensus"  
25062. .25350  
repeat_region /note="AluSx repeat: matches 293. .5 of consensus"  
25366. .25649  
repeat_region /note="AluJo repeat: matches 290. .1 of consensus"  
26058. .26093  
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26631. .27157  
repeat_region /note="L1PA12 repeat: matches 369. .902 of consensus"  
27183. .27475  
repeat_region /note="AluJo repeat: matches 1. .301 of consensus"  
27483. .27746  
repeat_region /partial  
repeat_region /note="AluY repeat: matches 301. .38 of consensus"  
30360. .30410  
repeat_region /note="MIR2 repeat: matches 94. .144 of consensus"  
32055. .32239  
repeat_region /note="MIR repeat: matches 61. .262 of consensus"  
32571. .32781  
repeat_region /note="MSTA repeat: matches 216. .425 of consensus"  
33063. .33322  
repeat_region /note="MER42B repeat: matches 1301. .1031 of consensus"  
33684. .33746  
repeat_region /note="MIR repeat: matches 81. .142 of consensus"  
33764. .33879  
repeat_region /note="MERSA repeat: matches 18. .140 of consensus"  
34848. .35013  
repeat_region /note="FRAM repeat: matches 1. .165 of consensus"  
35846. .36152  
repeat_region /note="AluSx repeat: matches 1. .291 of consensus"  
36247. .36428  
repeat_region /note="MIR repeat: matches 17. .214 of consensus"  
37815. .38119  
repeat_region /note="AluJo repeat: matches 1. .302 of consensus"  
39991. .40270  
repeat_region /note="AluJb repeat: matches 290. .1 of consensus"  
40862. .41163  
repeat_region /note="AluSx repeat: matches 302. .1 of consensus"  
42060. .42344  
repeat_region /partial  
repeat_region /note="AluSx repeat: matches 1. .282 of consensus"  
43932. .44218  
repeat_region /note="L1PA1 repeat: matches 762. .1051 of consensus"  
47698. .47929  
repeat_region /partial  
repeat_region /note="AluJb repeat: matches 1. .229 of consensus"  
47940. .48038  
repeat_region /partial  
repeat_region /note="AluJo repeat: matches 200. .294 of consensus"  
49174. .49246  
repeat_region /note="L1PA2 repeat: matches 954. .885 of consensus"  
49266. .49326  
repeat_region /partial  
repeat_region /note="AluSx/g repeat: matches 302. .240 of consensus"  
49339. .49545  
repeat_region /partial  
repeat_region /note="AluJb repeat: matches 98. .300 of consensus"
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repeat_region /note="AluSg repeat: matches 1. .300 of consensus"  
51955. .52996  
repeat_region /note="MLT2 internal repeat: matches 4017. .5042 of  
consensus"  
53263. .53562  
repeat_region /note="AluSx repeat: matches 1. .298 of consensus"  
53772. .54167  
repeat_region /note="MSTA repeat: matches 1. .426 of consensus"  
54416. .54785  
repeat_region /note="MLT1D repeat: matches 505. .119 of consensus"  
54829. .54949  
repeat_region /partial  
repeat_region /note="AluSp repeat: matches 300. .177 of consensus"  
54994. .55100  
repeat_region /note="MLT1D repeat: matches 107. .1 of consensus"  
55707. .56029  
repeat_region /note="MER2 repeat: matches 345. .1 of consensus"  
56258. .61666  
repeat_region /note="L1 repeat: matches 13. .5390 of consensus"  
61517. .62409  
repeat_region /note="L1PA2 repeat: matches 1. .893 of consensus"  
64264. .64323  
repeat_region /note="30 copies of 2 mer 83 % conserved"  
64850. .65196  
repeat_region /note="MLT2FA repeat: matches 1. .358 of consensus"  
65197. .65251  
repeat_region /note="MLT2CA repeat: matches 503. .449 of consensus"  
65197. .65237  
repeat_region /note="MLT2CB repeat: matches 501. .461 of consensus"  
65300. .65629  
repeat_region /note="MLT2CB repeat: matches 462. .145 of consensus"  
65635. .65932  
repeat_region /note="AluSx repeat: matches 298. .1 of consensus"  
65935. .66064  
repeat_region /note="MLT2D repeat: matches 140. .1 of consensus"  
66065. .66180  
repeat_region /note="MLT2FB repeat: matches 318. .414 of consensus"  
66931. .67287  
repeat_region /note="MER39 repeat: matches 80. .460 of consensus"  
68857. .68940  
repeat_region /note="MLT1D repeat: matches 6. .91 of consensus"  
68956. .69258  
repeat_region /note="AluJo repeat: matches 1. .293 of consensus"  
69278. .69653  
repeat_region /note="MLT1D repeat: matches 117. .505 of consensus"  
71353. .71521  
repeat_region /note="MERSA repeat: matches 188. .1 of consensus"  
71538. .71669  
repeat_region /partial  
repeat_region /note="AluJo repeat: matches 49. .171 of consensus"  
71697. .71820  
repeat_region /partial  
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78449. .78752  
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Query Match 22.5%; Score 42; DB 9; Length 156197;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AGCTCACTGCAGCTCATACTCTCTGGGCTCAAGCAATCTCTCC 50  
|||||  
Db 34942 AGCTCACTGCAGCTCATACTCTCTGGGCTCAAGCAATCTCTCC 34901

## RESULT 7

AC105129/c AC105129 198295 bp DNA linear PRI 26-APR-2002  
LOCUS  
DEFINITION Homo sapiens chromosome 15, clone RP11-349G13, complete sequence.  
AC105129  
ACCESSION  
VERSION AC105129.4 GI:20330981



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repeat_region complement(8227..8312)
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repeat_region 9403..9445
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repeat_region 9706..10007
repeat_region /rpt_family="AluJb"
repeat_region complement(10940..11000)
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repeat_region 11001..11284
repeat_region /rpt_family="AluJb"
repeat_region complement(11285..11366)
repeat_region /rpt_family="AluSx"
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repeat_region /rpt_family="AluSg"
repeat_region complement(12071..12294)
repeat_region /rpt_family="AluJb"
repeat_region complement(12410..12697)
repeat_region /rpt_family="AluSx"
repeat_region complement(12708..12998)
repeat_region /rpt_family="AluJb"
repeat_region 13158..13478
repeat_region /rpt_family="AluJb"
repeat_region 13970..14093
repeat_region /rpt_family="FLAM_C"
repeat_region 14108..14412
repeat_region /rpt_family="AluJb"
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repeat_region complement(15130..15432)
repeat_region /rpt_family="AluSg"
repeat_region complement(15532..15841)
repeat_region /rpt_family="AluSx"
repeat_region complement(15906..16077)
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repeat_region complement(16079..16383)
repeat_region /rpt_family="AluSg"
repeat_region 16409..16481
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repeat_region complement(17247..17543)
repeat_region /rpt_family="AluJb"

Query Match 22.5%; Score 42; DB 9; Length 198295;
Best Local Similarity 100.0%; Pred. No. 2-2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 47 CTCCTGCTCAGCTTCCAACTAGCTGGACTACAGTGGCC 88
Db 13355 CTCCTGCTCAGCTTCCAACTAGCTGGACTACAGTGGCC 13314

RESULT 8
AC027220 AC027220 212505 bp DNA linear HTG 22-DEC-2001
LOCUS Homo sapiens chromosome 15 clone RP11-731G9 map 15, *** SEQUENCING
DEFINITION IN PROGRESS ***, 9 unordered pieces.
ACCESSION AC027220
VERSION AC027220.5 GI:17977449
KEYWORDS HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 212505)

```

AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Dec 22, 2001 this sequence version replaced gi:13959268.  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE  
JOURNAL  
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L8347  
Center clone name: 731\_G\_9

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 9 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 32125: contig of 32125 bp in length  
\* 32126 32225: gap of 100 bp  
\* 32226 45347: contig of 13122 bp in length  
\* 45348 45447: gap of 100 bp  
\* 45448 51661: contig of 6214 bp in length  
\* 51662 51761: gap of 100 bp  
\* 51762 59880: contig of 8119 bp in length  
\* 59881 59980: gap of 100 bp  
\* 59981 70993: contig of 11019 bp in length  
\* 71000 71099: gap of 100 bp  
\* 71100 97542: contig of 26443 bp in length  
\* 97543 97642: gap of 100 bp  
\* 97643 176551: contig of 78909 bp in length  
\* 176552 176651: gap of 100 bp  
\* 176652 200765: contig of 24114 bp in length  
\* 200766 200865: gap of 100 bp  
\* 200866 212505: contig of 11640 bp in length.

FEATURES  
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BASE COUNT 63128 a 43850 c 45173 g 59473 t 881 others
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Query Match 22.5%; Score 42; DB 2; Length 212505;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 CTCCTGCTCAGCTTCCAACTAGCTGGGACTACAGTGGCG 88
Db 306 CTCCTGCTCAGCTTCCAACTAGCTGGGACTACAGTGGCG 347

FEATURES
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-46B3"
/clone.lib="RPCI human BAC library 11"
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Best Local Similarity 100.0%; Pred. No. 8.3e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCATAGCTCAGCTGCGCTCCTACTCTCTGGGCTCAAG 41
Db 58322 ATGATCATAGCTCAGCTGCGCTCCTACTCTCTGGGCTCAAG 58282

RESULT 10
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LOCUS AP001184 120186 bp DNA linear PRI 27-APR-2002
DEFINITION Homo sapiens genomic DNA, chromosome.11q clone:RP11-715F10,
complete sequences.
ACCESSION AP001184
VERSION AP001184.4 GI:203334320
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens DNA, clone:RP11-715F10.

REFERENCE
1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2000)
REFERENCE 2 (bases 1 to 120186)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
TITLE Submitted (16-FEB-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba-shi, Ibaraki, Japan 305-8565, Japan
(E-mail:hattori@gscc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:11320825.
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-715F10"
BASE COUNT 28902 a 30130 c 31345 g 29809 t
ORIGIN

Query Match 21.9%; Score 41; DB 9; Length 120186;
Best Local Similarity 100.0%; Pred. No. 8.2e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAGCAATCTCTGCTGCTGCTTCCAAAC 67
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Db      84093 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAAC 84053
RESULT 11
AC073631/c
LOCUS   AC073631
DEFINITION Homo sapiens chromosome 3 clone RP11-195H14, *** SEQUENCING IN
AC073631
AC073631.1 GI:8748850
VERSION HTG; HTGS PHASE1.
KEYWORDS Homo sapiens.
SOURCE  Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 155877)
AUTHORS   Waterston,R.H.
TITLE     The sequence of Homo sapiens clone
JOURNAL   Unpublished
AUTHORS   2 (bases 1 to 155877)
REFERENCE Waterston,R.H.
TITLE     Direct Submission
JOURNAL   Submitted (27-JUN-2000) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA

COMMENT
----- Genome Center -----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1086: contig of 1086 bp in length
* 1087 1186: gap of unknown length
* 1187 2446: contig of 1260 bp in length
* 2447 2546: gap of unknown length
* 2547 5563: contig of 3017 bp in length
* 5564 5663: gap of unknown length
* 5664 9561: contig of 3898 bp in length
* 9562 9661: gap of unknown length
* 9662 18553: contig of 8892 bp in length
* 18554 18653: gap of unknown length
* 18654 29773: contig of 11120 bp in length
* 29774 29874: gap of unknown length
* 29874 42605: contig of 12732 bp in length
* 42606 42705: gap of unknown length
* 42706 56734: contig of 14029 bp in length
* 56735 56833: gap of unknown length
* 56833 70734: contig of 13900 bp in length
* 70735 70834: gap of unknown length
* 70835 83357: contig of 14523 bp in length
* 83358 85458: gap of unknown length
* 85458 101145: contig of 15688 bp in length
* 101146 101245: gap of unknown length
* 101246 121898: contig of 20653 bp in length
* 121899 121998: gap of unknown length
* 121999 155877: contig of 33879 bp in length.
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*   /db_xref="taxon:9606"
*   /chromosome="3"
*   /clone="RP11-195H14"
BASE COUNT 49091 a 27354 c 27491 g 50736 t 1205 others
ORIGIN
Query Match          21.9%; Score 41; DB 2; Length 155877;
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 CCTCATACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
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Db      154908 CCTCATACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 154868

RESULT 12
AC009930/c
LOCUS   AC009930
DEFINITION Homo sapiens chromosome 8, clone RP11-11408, complete sequence.
AC009930
AC009930.7 GI:15983558
VERSION HTG.
KEYWORDS human.
SOURCE  Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 165662)
AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
TITLE     Homo sapiens chromosome 8, clone RP11-11408
JOURNAL   Unpublished
AUTHORS   2 (bases 1 to 165662)
REFERENCE Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
          Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
          Castle,A., Cerry,J., Colangelo,M., Collins,S., Collymore,A.,
          Cooke,P., DeArelano,K., Depayre,E., Devon,K., Dewar,K.,
          Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
          Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
          Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
          Karatas,A., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P.,
          Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
          Meldrum,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
          Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
          Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
          Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
          Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
          Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE     Direct Submission
JOURNAL   Submitted (08-SEP-1999) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 165662)
AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
          Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgaiter,B.,
          Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
          Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
          Fero,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
          Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
          Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A.,
          Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
          Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
          McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mienga,V.,
          Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
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          Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
          Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
          Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
          Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
          Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
          Zembek,L., Zimmer,A. and Zody,M.
TITLE     Direct Submission
JOURNAL   Submitted (13-JUL-2002) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On Oct 8, 2001 this sequence version replaced gi:15421962.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          ----- Genome Center
          Center: Whitehead Institute/ MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence.submissions@genome.wi.mit.edu
          ----- Project Information
          Center project name: L1961
          Center clone name: 114_O_8

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repeat_region		/clone_lib="RPC1-11 Human Male BAC"
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repeat_region		19808. .20107
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repeat_region		20108. .20276
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 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 166098)  
 AUTHORS Smith,D.R.  
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome  
 Sequence Data  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 166098)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JAN-2000) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 REFERENCE 3 (bases 1 to 166098)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2001) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 REFERENCE 4 (bases 1 to 166098)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-MAY-2002) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 COMMENT On May 17, 2002 this sequence version replaced gi:17149359.  
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 /clone\_lib="RPCI-11"  
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 Best Local Similarity 100.0%; Pred. No. 7.9e-12;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 105935 ATGATCATAGCTACTGCAGCCTCATCTCTGGGCTCAAG 105895  
 RESULT 14  
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 LOCUS AC012152 180423 bp DNA linear PRI 31-DEC-1999  
 DEFINITION Homo sapiens 3 BAC RP11-552C10 (Roswell Park Cancer Institute Human  
 BAC library) complete sequence.  
 ACCESSION AC012152  
 VERSION AC012152.12 GI:6649262  
 KEYWORDS HTG.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 180423)  
 AUTHORS Muzny,D.M., Adams,C., Bailey,M., Barabara,J., Blankenburg,K.,  
 Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,  
 Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,  
 David,R., Delgado,O., Deshazo,D., Ding,Y., Donah-Rashid,N.,  
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 Gorrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J.,  
 Hodgson,A., Hughes,M., Holloway,C., Hosak,H., Jackson,L.E.,  
 Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y.,  
 Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O.,  
 Lozado,R.J., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P.,

Mei,G., Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S.,  
 Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Osawa,G., Parish,B.,  
 Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D.,  
 Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H.,  
 Simon,M., Sparks,A., Stamps,A., Sucgang,R., Tabor,P., Taylor,T.,  
 Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S., Wren,J.,  
 Wrenstorf,G., Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 180423)  
 Worley,K.C.  
 Direct Submission  
 Submitted (21-OCT-1999) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 180423)  
 Worley,K.C.  
 Direct Submission  
 Submitted (31-DEC-1999) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Dec 31, 1999 this sequence version replaced gi:6646737.  
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
[gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)  
 CLONE LENGTH: This sequence does not necessarily represent the  
 entire insert of this clone. Overlapping regions of clones are only  
 sequenced and submitted once, so the sequence for the remainder of  
 the insert may be found in the record for the adjacent clones.  
 Overlapping clones are noted at the beginning and end of the  
 Features listing.  
 ANNOTATION OF FEATURES:  
 STSS are identified using ePCR (Genome Res. 7:541-550) searches  
 of a local database that includes entries from dbSTS, GDB, and  
 local mapping efforts.  
 Repeats are identified using RepeatMasker (A. Smit and P. Green,  
 unpublished.) for Human and Mouse sequences.  
 Genes and Region of sequence similarity are identified by BLAST  
 (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the  
 EST and cDNA sequences. Genes demonstrate at least two exons  
 flanked by consensus splice sites that maintained sequence  
 continuity across the splice junctions. Sequences that are not  
 identical matches are annotated as similar.  
 SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
 standard of double strand coverage with a minimum of 2 clones and 2  
 reads with no ambiguities or 2 chemistries with a minimum of 2  
 clones and 3 reads with no ambiguities. If the sequence quality for  
 a region does not meet this standard, it will be indicated in the  
 annotation as Low Coverage.  
 QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
 standards - estimated error rate less than 1 per 10,000 bases.  
 Reports of lowest quality individual bases and measures of base  
 quality are listed below. Description of the metrics can be found  
 at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.  
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44309..44339

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Query Match 21.9%; Score 41; DB 9; Length 180423;
Best Local Similarity 100.0%; Pred.No. 7.8e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCTCATCTCTCTGGGCTCAAGCAATCTCTGCTGCTCAGCCT 61
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Db 108235 CCTCATCTCTCTGGGCTCAAGCAATCTCTGCTGCTCAGCCT 108275

RESULT 15
AC073984 187266 bp DNA linear HTG 02-SEP-2000
LOCUS Homo sapiens chromosome 3 clone RP11-394K18, WORKING DRAFT
DEFINITION SEQUENCE, 9 unordered pieces.
ACCESSION AC073984
VERSION AC073984.4 GI:9965004
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 187266)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Waterston,R.H.
JOURNAL The sequence of Homo sapiens clone
REFERENCE 2 (bases 1 to 187266)
AUTHORS Waterston,R.H.
JOURNAL Direct Submission
TITLE Submitted (08-JUL-2000) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Sep 2, 2000 this sequence version replaced gi:9739341.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0394K18
----- Summary Statistics -----
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Sequencing vector: M13; 100%  
 Chemistry: Dye-terminator Big Dye; 0% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 181863 bases at least Q40  
 Consensus quality: 183568 bases at least Q30  
 Consensus quality: 184222 bases at least Q20  
 Insert size: 196000; agarose-fp  
 Quality coverage: 6.15 in Q20 bases; agarose-fp  
 Quality coverage: 6.52 in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 9 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1735: contig of 1735 bp in length  
 \* 1736 1835: gap of unknown length  
 \* 1836 9195: contig of 7360 bp in length  
 \* 9196 9295: gap of unknown length  
 \* 9296 16758: contig of 7463 bp in length  
 \* 16759 16858: gap of unknown length  
 \* 16859 27746: contig of 10888 bp in length  
 \* 27747 27846: gap of unknown length  
 \* 27847 41286: contig of 13440 bp in length  
 \* 41287 41386: gap of unknown length  
 \* 41387 64712: contig of 23326 bp in length  
 \* 64713 100745: contig of 35933 bp in length  
 \* 100746 100845: gap of unknown length  
 \* 100846 141830: contig of 40985 bp in length  
 \* 141831 141931 187266: contig of 45336 bp in length.

# FEATURES Location/Qualifiers

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 misc\_feature  
 27847..41286  
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 41387..64712  
 /note="assembly\_name:Contig22"  
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 64813..100745  
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 141931..187266  
 /note="assembly\_name:Contig25" 803 others

## BASE COUNT

60278 a 32312 c 33080 g 60793 t

## Query Match

Best Local Similarity 21.9%; Score 41; DB 2; Length 187266;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CCTCATACTCCTGGGCTCAAGCAATCCTCCTGCCTCAGCCT 61  
 |||||  
 Db 107131 CCTCATACTCCTGGGCTCAAGCAATCCTCCTGCCTCAGCCT 107171

Search completed: June 17, 2003, 03:58:43  
 Job time : 391.575 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 33.0127 Seconds  
(without alignments)

Title: US-09-513-888C-1\_COPY\_6939\_7125

Perfect score: 187  
Sequence: 1 atgatacatgctcactgcag.....tggcctcaagcaatccacct 187

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_101002.\*

- 1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*
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- 15: /SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*
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- 18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	187	100.0	5492	21	AAA64508
2	187	100.0	9048	21	AAA64507
3	40	21.4	12767	22	ABAI7068
4	40	21.4	18997	24	AAD36072
5	40	21.4	84495	24	AAS20588
6	40	21.4	160552	22	AAD02687
7	38	20.3	24843	24	AAS17764
8	37	19.8	328	22	ABAI5496
9	36	19.3	831	22	AAI96106
CDNA sequence of t					
Nucleotide sequenc					
Human nervous syst					
Human POLD2 genom					
Human methionine a					
Human glycosyl sul					
Human Genomic DNA					
Human nervous syst					
Human neuroblastom					

Human musculoskele  
Human reproductive  
Human ovarian canc  
Human polynucleoti  
Human polynucleoti  
Novel human polynu  
Human polynucleoti  
Human polynucleoti  
Human breast cance  
Human immune/haema  
Human cDNA clone  
Human cancer relat  
Human immune/haema  
Human reproductive  
Human breast cance  
Human breast cance  
Human LNXp80 homol  
Human breast cance  
DNA encoding novel  
Human immune/haema  
Human immune/haema  
Human immune/haema  
Human immune/haema  
Human PRO1722 homo  
Human cancer suppr  
cDNA sequence #425  
Human cDNA sequenc  
Human immunoglobul  
Human cDNA SEQ ID  
cDNA encoding huma  
Human secreted pro  
Human low adenosin  
Human adenosine re  
CD25 T cell activa  
Human TANGO 364 al  
Human secreted pro  
Human cDNA sequenc  
Human cDNA sequenc  
Human TANGO 364 CD  
Human prostate exp  
Human prostate exp  
Human glucose 6-ph  
Human immune/haema  
Human cDNA sequenc  
Genomic sequence #  
Genomic sequence #  
DNA encoding human  
Human excretory re  
Human kidney relat  
Human IL-1ra BAC c  
Human immune/haema  
Genomic sequence #  
Human low adenosin  
Human adenosine re  
Human pancreatic c  
Human genomic DNA  
Human genomic DNA  
Human cardiovascular  
Human DNA for a no  
Human DNA for a no  
Genomic DNA encodi  
Human polynucleoti  
Human polynucleoti  
Genomic sequence #  
Human nervous syst  
Human immune/haema  
Human polyamine-mo  
Human reticovital s  
Human immune/haema  
Human immune/haema  
Colon adenocarcino  
Human nibrin DNA  
Human apolipoprote

83	35	18.7	143899	24	AAL38336	Genomic sequence e	32	17.1	814	21	AACT5898
C 84	35	18.7	144460	21	AAZ93815	Olfactory receptor	32	17.1	5516	22	AAK90637
C 85	34	18.2	51	22	AAHA0296	Human SNP flanking	32	17.1	5553	22	ABAI4823
C 86	34	18.2	411	22	AAI86466	Human polynucleoti	32	17.1	7983	22	AAK73139
C 87	34	18.2	441	22	AAS35908	Human cardiovascular	32	17.1	13646	22	AAK97857
C 88	34	18.2	441	22	AAS35910	Human cardiovascular	32	17.1	24884	22	AAK67892
C 89	34	18.2	473	22	AAS44700	Human full-length	32	17.1	34878	22	AAK66167
C 90	34	18.2	514	24	ABL83540	Human ovarian canc	32	17.1	34878	22	AAK80088
C 91	34	18.2	558	24	ABQ56499	Human colon cancer	32	17.1	4100	21	ABN97975
C 92	34	18.2	797	21	AACT7141	Human OREF ORF2696	32	17.1	172570	24	ABQ88207
C 93	34	18.2	876	22	AAS40689	DNA encoding human	31	16.6	364	21	AAK13155
C 94	34	18.2	876	22	AAL06592	Human reproductive	31	16.6	476	23	ABV01550
C 95	34	18.2	1531	22	ABA20466	Human nervous syst	31	16.6	477	22	ABAI4998
C 96	34	18.2	2589	20	AAZ28760	Human cyclophilin	31	16.6	514	23	ABV31884
C 97	34	18.2	2813	22	AAK95585	Human immune/haema	31	16.6	514	23	ABV40843
C 98	34	18.2	2814	22	AAK95584	Human immune/haema	31	16.6	540	23	ABV60384
C 99	34	18.2	3133	22	AAK756612	Human immune/haema	31	16.6	546	23	ABV58627
C 100	34	18.2	3164	22	AAH18730	Human cDNA sequenc	31	16.6	555	22	AAH16899
C 101	34	18.2	3350	17	AAT08553	Oncogene R-ras mut	31	16.6	608	23	ABV10719
C 102	34	18.2	5071	22	ABAI5499	Human nervous syst	31	16.6	629	24	ABN64320
C 103	34	18.2	5686	24	ABK14231	Human related RAS	31	16.6	1258	22	AAK75907
C 104	34	18.2	5686	24	ABK14233	Human related RAS	31	16.6	1259	22	AAK75908
C 105	34	18.2	6554	22	ABAI7685	Human nervous syst	31	16.6	1259	22	AAK65689
C 106	34	18.2	9324	22	AAK756610	Human immune/haema	31	16.6	1607	21	AAC59256
C 107	34	18.2	15734	22	AAS36442	Human cardiovascular	31	16.6	1779	24	ABK34995
C 108	34	18.2	17146	22	AAL37485	Human musculocele	31	16.6	2164	22	AAH17265
C 109	34	18.2	26928	22	ABA82620	Human HBM gene reg	31	16.6	2703	22	AAI65263
C 110	34	18.2	28928	24	ABK22779	Human high bone ma	31	16.6	6302	22	AAK65687
C 111	34	18.2	30568	22	AAL37486	Human musculocele	31	16.6	13138	22	AAK65690
C 112	34	18.2	32196	22	ABAI18857	Human nervous syst	31	16.6	15848	20	AAZ32190
C 113	34	18.2	32199	22	AAK90296	Human digestive sy	31	16.6	15849	24	ABN95864
C 114	34	18.2	32199	22	AAI57673	Human colorectal c	31	16.6	18664	24	ABK65421
C 115	34	18.2	35959	22	AAK78275	Human immune/haema	31	16.6	18664	22	AAK84438
C 116	34	18.2	41765	22	AAK76675	Human immune/haema	31	16.6	22791	22	AAK69857
C 117	34	18.2	41772	22	AAK76676	Human immune/haema	31	16.6	22791	22	AAK69857
C 118	34	18.2	112460	24	ABK33567	Human cDNA differe	31	16.6	25975	22	AAK49955
C 119	33	17.6	252	22	ABAI7318	Human nervous syst	31	16.6	25975	23	ABL97849
C 120	33	17.6	276	24	ABK80265	Bacillus clausii g	31	16.6	32174	22	ABAI5665
C 121	33	17.6	347	24	ABL83445	Human ovarian canc	31	16.6	32174	22	ABAI9477
C 122	33	17.6	380	22	AAI86608	Human polynucleoti	31	16.6	32174	22	ABA20359
C 123	33	17.6	393	22	AAI80381	Human polynucleoti	31	16.6	32174	22	ABA21505
C 124	33	17.6	410	22	AAI86660	Human polynucleoti	31	16.6	32174	22	AAK36280
C 125	33	17.6	566	24	ABL62267	Colon adenocarcino	31	16.6	32174	22	AAK32655
C 126	33	17.6	566	24	ABL63618	Breast cancer rela	31	16.6	32174	22	AAS34394
C 127	33	17.6	566	24	ABL64029	Breast cancer rela	31	16.6	32174	22	AAS30638
C 128	33	17.6	589	23	ABV50429	Human prostate exp	31	16.6	32174	22	AAK03792
C 129	33	17.6	2133	22	AAH15667	Human cDNA sequenc	31	16.6	32174	22	AAK07491
C 130	33	17.6	2207	21	AAC59284	Human secreted pro	31	16.6	32174	22	AAK28700
C 131	33	17.6	2634	24	ABK35089	Human cDNA encodin	31	16.6	32174	22	AAI62606
C 132	33	17.6	2664	24	ABK51251	Human cDNA encodin	31	16.6	32174	22	AAS34394
C 133	33	17.6	6281	23	ABK42480	DNA encoding novel	31	16.6	32174	22	AAK30638
C 134	33	17.6	11646	22	AAK70925	Human immune/haema	31	16.6	32174	22	AAK03792
C 135	33	17.6	14148	22	AAK70926	Human immune/haema	31	16.6	32174	22	AAK07491
C 136	33	17.6	16183	22	AAK74819	Human immune/haema	31	16.6	32220	22	AAK37568
C 137	33	17.6	16281	22	AAK70314	Human immune/haema	31	16.6	38771	22	AAK66361
C 138	33	17.6	16281	23	ABK42480	Genomic sequence #	31	16.6	38771	22	AAK68883
C 139	33	17.6	16285	22	AAK70315	Human immune/haema	31	16.6	38771	22	AAK69604
C 140	33	17.6	16285	22	AAK70316	Human immune/haema	31	16.6	38771	22	AAK71499
C 141	33	17.6	16285	23	ABK42481	Genomic sequence #	31	16.6	38771	22	AAK72925
C 142	33	17.6	16285	23	ABK42482	Genomic sequence #	31	16.6	38771	22	AAK75870
C 143	33	17.6	17150	22	AAK92982	Human DNA methyltr	31	16.6	38771	22	AAK80325
C 144	33	17.6	17595	22	AAK71154	Human immune/haema	31	16.6	109906	24	AAK83538
C 145	33	17.6	17792	22	AAS32727	Human genomic DNA	31	16.6	121162	21	ABK94411
C 146	33	17.6	17792	22	AAS36099	Human cardiovascular	31	16.6	222930	24	ABK84349
C 147	33	17.6	21693	22	AAK79930	Human immune/haema	31	16.6	227968	24	ABK83497
C 148	33	17.6	24079	22	AAK71153	Human immune/haema	31	16.6	325791	22	AAS43104
C 149	33	17.6	30115	21	AAAS9651	Modified adenovira	30	16.0	122	22	AAK86623
C 150	33	17.6	65608	24	ABL62910	Breast cancer rela	30	16.0	122	22	AAK86624
C 151	33	17.6	65608	24	ABL64414	Stomach cancer rel	30	16.0	278	23	ABV53552
C 152	33	17.6	65608	24	ABL67668	Oesophagus cancer	30	16.0	289	21	ABV53552
C 153	33	17.6	84495	24	AAS20588	Human methionine a	30	16.0	338	22	AAK75949
C 154	33	17.6	172570	24	ABQ88207	Human osteoblast d	30	16.0	338	22	AAK75950
C 155	32	17.1	403	21	AAH30457	Human colon cancer	30	16.0	345	22	AAI86872



229	30	16.0	387	23	ABV43001	Human prostate exp	302	29	15.5	338	14	AAQ59619	Human brain expres
230	30	16.0	388	23	ABV03849	Human prostate exp	c 303	29	15.5	348	22	AAF65880	Novel human polynu
231	30	16.0	406	23	AAI85057	Human polynucleoti	c 304	29	15.5	364	22	AAI88966	Human polynucleoti
232	30	16.0	409	23	ABV04720	Human prostate exp	c 305	29	15.5	366	22	AAS27779	DNA encoding novel
233	30	16.0	421	20	AAV87192	EST clone BN139.	c 306	29	15.5	373	22	AAI85901	Human polynucleoti
234	30	16.0	434	22	AAI93309	Human polynucleoti	c 307	29	15.5	398	22	AAI86942	Human polynucleoti
235	30	16.0	436	23	ABV34139	Human prostate exp	c 308	29	15.5	408	24	ABQ58163	Human colon cancer
236	30	16.0	438	23	ABV13889	Human prostate exp	c 309	29	15.5	410	22	ABA17229	Human nervous syst
237	30	16.0	459	23	ABV35001	Human prostate exp	c 310	29	15.5	411	22	AAF64900	Novel human polynu
238	30	16.0	459	23	ABV43849	Human prostate exp	c 311	29	15.5	412	22	AAI83800	Human polynucleoti
239	30	16.0	471	23	ABV13018	Human prostate exp	c 312	29	15.5	416	22	ABA17230	Human nervous syst
240	30	16.0	490	22	AAI86033	Human polynucleoti	c 313	29	15.5	443	22	ABL87836	Human ovarian canc
241	30	16.0	492	22	AAH71568	Human cervical can	c 314	29	15.5	495	22	AAS60582	Human cancer agent
242	30	16.0	540	22	AAH70143	Human cervical can	c 315	29	15.5	496	22	AAI12047	Human breast cancer
243	30	16.0	589	24	ABN64952	Human cancer relat	c 316	29	15.5	496	24	ABN65848	Human cancer relat
244	30	16.0	620	22	AAI07458	Human reproductive	c 317	29	15.5	504	22	AAI60340	Human cancer agent
245	30	16.0	637	22	AAH33384	Human colon cancer	c 318	29	15.5	524	22	AAI93453	Human polynucleoti
246	30	16.0	674	21	AAZ79992	Human colon cancer	c 319	29	15.5	543	22	ABA60844	Human foetal liver
247	30	16.0	1069	23	AAS80995	DNA encoding novel	c 320	29	15.5	543	22	ABA28851	Human genome-deriv
248	30	16.0	1610	22	AAH15274	Human CDNA sequenc	c 321	29	15.5	554	22	AAK09131	Human immune/haema
249	30	16.0	1746	22	AAK70288	Human immune/haema	c 322	29	15.5	569	22	AAK62069	Human immune/haema
250	30	16.0	1746	22	AAK70289	Human immune/haema	c 323	29	15.5	571	24	ABN63980	Human cancer relat
251	30	16.0	1757	22	ABA15128	Human nervous syst	c 324	29	15.5	590	22	AAI82752	Human polynucleoti
252	30	16.0	1990	22	AAK87390	Human immune/haema	c 325	29	15.5	600	22	AAI20932	Human breast cancer
253	30	16.0	1990	22	AAK87391	Human immune/haema	c 326	29	15.5	605	22	AAS35625	Human cardiovascular
254	30	16.0	2006	22	AAK87389	Human immune/haema	c 327	29	15.5	623	23	AAV48087	Human prostate exp
255	30	16.0	2044	22	AAK65721	Human immune/haema	c 328	29	15.5	684	24	ABN60127	Human cancer relat
256	30	16.0	2044	22	AAK65722	Human immune/haema	c 329	29	15.5	725	22	AAH03539	Human CDNA clone
257	30	16.0	2044	22	AAK69117	Human immune/haema	c 330	29	15.5	795	22	AAK82472	Human immune/haema
258	30	16.0	2044	22	AAK69118	Human immune/haema	c 331	29	15.5	795	22	AAK82473	Human immune/haema
259	30	16.0	2045	22	AAK65720	Human immune/haema	c 332	29	15.5	950	23	ABK42761	Genomic sequence #
260	30	16.0	2045	22	AAK65725	Human immune/haema	c 333	29	15.5	950	23	ABK42762	Genomic sequence #
261	30	16.0	2045	22	AAK69116	Human immune/haema	c 334	29	15.5	1031	23	ABK42763	Genomic sequence #
262	30	16.0	2045	22	AAK69119	Human immune/haema	c 335	29	15.5	1040	22	AAK69263	Human prostate exp
263	30	16.0	2607	22	AAK97848	Human neuroblastom	c 336	29	15.5	1233	22	AAI36111	Human immune/haema
264	30	16.0	4066	19	AAV59181	Human bak gene pro	c 337	29	15.5	1254	22	AAI36110	Human musculoskele
265	30	16.0	4156	22	AAK83412	Human immune/haema	c 338	29	15.5	1254	22	AAI36110	Human musculoskele
266	30	16.0	7640	22	AAK91239	Human digestive sy	c 339	29	15.5	1726	20	AAI206248	Human secreted pro
267	30	16.0	7703	22	AAK91239	Human digestive sy	c 340	29	15.5	2160	22	AAI36895	Human musculoskele
268	30	16.0	7703	22	AAK90945	Human digestive sy	c 341	29	15.5	2218	14	AAO47929	Paired basic amino
269	30	16.0	7703	22	AAK91939	Human liver associ	c 342	29	15.5	2268	22	AAI42150	Genomic sequence #
270	30	16.0	7703	22	AAK91980	Human liver associ	c 343	29	15.5	2270	22	AAI42152	Genomic sequence #
271	30	16.0	7703	24	ABN90294	Human liver antige	c 344	29	15.5	2465	24	AAI47848	Human basic helix-
272	30	16.0	7703	24	ABN90335	Human liver antige	c 345	29	15.5	2465	24	AAI47848	Insert of lambda 3
273	30	16.0	8764	22	AAK91240	Human digestive sy	c 346	29	15.5	2971	22	AAI02843	Human reproductive
274	30	16.0	10195	22	AAS26626	Human genomic DNA	c 347	29	15.5	2971	22	AAI02843	Human reproductive
275	30	16.0	15366	22	AAS28623	Genomic sequence #	c 348	29	15.5	5092	22	AAS61001	Human cancer agent
276	30	16.0	15843	22	AAS36896	Human cardiovascular	c 349	29	15.5	5514	21	AAS55313	Human activation-i
277	30	16.0	15843	22	AAK67635	Human immune/haema	c 350	29	15.5	5573	22	AAH18243	Human CDNA sequenc
278	30	16.0	16774	22	AAS36895	Human cardiovascular	c 351	29	15.5	5955	22	ABA20275	Human tumour-associ
279	30	16.0	16774	22	AAS36898	Human cardiovascular	c 352	29	15.5	5955	22	ABA20275	Human nervous syst
280	30	16.0	16774	22	AAK67634	Human immune/haema	c 353	29	15.5	6163	24	ABA20274	Human tumour-associ
281	30	16.0	16774	22	AAK67637	Human immune/haema	c 354	29	15.5	6428	22	AAK78562	Human immune/haema
282	30	16.0	21721	22	ABA06775	Human genomic DNA	c 355	29	15.5	6517	22	AAK78562	Human immune/haema
283	30	16.0	21721	22	AAS41719	Genomic sequence #	c 356	29	15.5	7152	22	AAK84144	Human immune/haema
284	30	16.0	21721	22	AAK69459	Human immune/haema	c 357	29	15.5	7683	23	ABK42286	Genomic sequence #
285	30	16.0	33795	24	ABN95686	Gene #2184 used to	c 358	29	15.5	10097	22	AAI97856	Human neuroblastom
286	30	16.0	47090	22	AAK68725	Human immune/haema	c 359	29	15.5	10302	22	ABA16133	Human nervous syst
287	30	16.0	47090	22	AAK78219	Human immune/haema	c 360	29	15.5	10437	22	AAS41709	Genomic sequence #
288	30	16.0	48727	22	AAK67375	Human immune/haema	c 361	29	15.5	11204	21	AAS55339	Human activation-i
289	30	16.0	54863	22	AAK66025	Human immune/haema	c 362	29	15.5	12339	22	AAK81687	Human immune/haema
290	30	16.0	54877	22	AAK66026	Human immune/haema	c 363	29	15.5	12339	22	AAK81691	Human immune/haema
291	30	16.0	90220	24	ABK831576	Human CDNA differe	c 364	29	15.5	12392	22	ABA15896	Human nervous syst
292	30	16.0	106746	21	AAI10225	Human PCTA-1 genom	c 365	29	15.5	12620	22	ABA16891	Human nervous syst
293	30	16.0	110096	24	ABN95044	Gene #1542 used to	c 366	29	15.5	13608	22	AAK87529	Human immune/haema
294	30	16.0	145831	24	ABL62309	Colon adenocarcino	c 367	29	15.5	13934	22	AAK81690	Human immune/haema
295	30	16.0	145831	24	ABL66806	Lung cancer relate	c 368	29	15.5	17104	22	AAS30249	DNA encoding rena
296	30	16.0	145831	24	ABL68588	Kidney cancer rela	c 369	29	15.5				
297	30	16.0	145831	24	ABL69213	Prostate cancer re	c 370	29	15.5				
298	30	16.0	167343	24	ABL64403	Stomach cancer rel	c 371	29	15.5				
299	30	16.0	167343	24	ABL67239	Thyroid cancer rel	c 372	29	15.5				
300	29	15.5	51	22	AAH89505	Human coding sequ	c 373	29	15.5				
301	29	15.5	246	21	AAC16539	Human secreted pro	c 374	29	15.5				

C 375	29	15.5	17104	22	AAS26973	Human genomic DNA
C 376	29	15.5	17104	22	AAS33484	DNA encoding human
C 377	29	15.5	17107	22	AAS30248	DNA encoding rena
C 378	29	15.5	17107	22	AAS26972	Human genomic DNA
C 379	29	15.5	21107	22	AAS33483	DNA encoding human
C 380	29	15.5	21129	22	AAS36234	Human cardiovascular
C 381	29	15.5	21936	22	ABA15865	Human nervous syst
C 382	29	15.5	21936	22	AA106119	Human reproductive
C 383	29	15.5	21936	22	AA106758	Human reproductive
C 384	29	15.5	21936	22	AA162664	Human breast or ov
C 385	29	15.5	21936	23	ABL98684	Human testicular a
C 386	29	15.5	22700	22	AAK70746	Human immune/haema
C 387	29	15.5	22700	22	AAK66230	Human immune/haema
C 388	29	15.5	23580	22	AAK93578	Human immune/haema
C 389	29	15.5	24000	21	AAK88551	Human dual-specifi
C 390	29	15.5	24977	22	AA103263	Human reproductive
C 391	29	15.5	24977	22	AA105788	Human reproductive
C 392	29	15.5	24977	23	ABL98352	Human testicular a
C 393	29	15.5	24983	22	AA103262	Human reproductive
C 394	29	15.5	24983	22	AA105787	Human reproductive
C 395	29	15.5	24983	23	ABL98351	Human testicular a
C 396	29	15.5	27148	22	AAS28612	Genomic sequence #
C 397	29	15.5	29329	22	ABA18026	Human nervous syst
C 398	29	15.5	29329	22	ABA20511	Human nervous syst
C 399	29	15.5	29329	22	AAK70791	Human immune/haema
C 400	29	15.5	29329	22	AAK78512	Human immune/haema
C 401	29	15.5	32134	22	AA199172	Human excretory re
C 402	29	15.5	32134	22	AA163522	Human kidney relat
C 403	29	15.5	32184	22	ABA20589	Human nervous syst
C 404	29	15.5	32184	22	ABA20590	Human nervous syst
C 405	29	15.5	32192	22	AA199173	Human excretory re
C 406	29	15.5	32192	22	AA163523	Human kidney relat
C 407	29	15.5	32199	22	AAK90296	Human digestive sy
C 408	29	15.5	32199	22	AA157673	Human colorectal c
C 409	29	15.5	35100	22	AAK65700	Human immune/haema
C 410	29	15.5	35100	22	AAK69767	Human immune/haema
C 411	29	15.5	35115	22	AAK65699	Human immune/haema
C 412	29	15.5	35115	22	AAK69766	Human immune/haema
C 413	29	15.5	35871	22	AAK84974	Human immune/haema
C 414	29	15.5	38272	22	AAK84952	Human immune/haema
C 415	29	15.5	38348	22	AAK84953	Human immune/haema
C 416	29	15.5	43599	24	ABK84242	Human cDNA differe
C 417	29	15.5	48037	22	AAK84729	Human immune/haema
C 418	29	15.5	48037	22	AAK85983	Human immune/haema
C 419	29	15.5	48045	22	AAK84730	Human immune/haema
C 420	29	15.5	48045	22	AAK85984	Human immune/haema
C 421	29	15.5	110096	24	ABN95044	Gene #1542 used to
C 422	29	15.5	110608	24	ABK83572	Human cDNA differe
C 423	29	15.5	117574	24	AA145288	Human KCNB1 Gene.
C 424	29	15.5	121162	21	AAK66548	Human kinesin-like
C 425	28	15.0	196	21	AAK12258	Human secreted pro
C 426	28	15.0	347	22	ABA19979	Human nervous syst
C 427	28	15.0	348	22	ABA19978	Human nervous syst
C 428	28	15.0	351	22	AA183981	Human polynucleoti
C 429	28	15.0	353	22	AA186190	Human polynucleoti
C 430	28	15.0	390	23	ABV50386	Human prostate exp
C 431	28	15.0	401	22	AAK36414	Human neuregulin g
C 432	28	15.0	401	22	AAK97907	Human neuregulin g
C 433	28	15.0	404	22	AA186627	Human polynucleoti
C 434	28	15.0	407	22	AA193349	Human polynucleoti
C 435	28	15.0	416	22	AAK76092	Human immune/haema
C 436	28	15.0	417	22	AAK76091	Human immune/haema
C 437	28	15.0	417	24	ABL83801	Human ovarian canc
C 438	28	15.0	449	22	AA186596	Human polynucleoti
C 439	28	15.0	478	21	AAK19773	Human secreted pro
C 440	28	15.0	514	24	ABN63452	Human cancer relat
C 441	28	15.0	544	23	ABV53170	Human prostate exp
C 442	28	15.0	555	23	ABV54906	Human prostate exp
C 443	28	15.0	592	23	AAK58987	Human prostate exp
C 444	28	15.0	593	23	AAK67044	Human immune/haema
C 445	28	15.0	617	23	ABV51224	Human prostate exp
C 446	28	15.0	827	22	ABA20530	Human nervous syst
C 447	28	15.0	1631	22	AAS01475	Human secreted pro
C 448	28	15.0	1644	24	ABK35053	Human cDNA encodin
C 449	28	15.0	1738	21	AAZ65086	Membrane-bound pro
C 450	28	15.0	1738	22	AAZ46044	Human DNA encoding
C 451	28	15.0	1738	22	AAZ46044	Human PRO156 (UNQ
C 452	28	15.0	1776	22	AAZ44232	Human full-length
C 453	28	15.0	4748	22	ABA07182	Human pancreatic c
C 454	28	15.0	4748	22	AAK89814	Human digestive sy
C 455	28	15.0	5139	22	AAZ36394	Human cardiovascular
C 456	28	15.0	5366	22	ABA20542	Human nervous syst
C 457	28	15.0	5366	22	AAK87126	Human immune/haema
C 458	28	15.0	6519	22	AAZ97859	Human neuroblastom
C 459	28	15.0	6928	22	ABA21109	Human nervous syst
C 460	28	15.0	10093	22	ABA07184	Human pancreatic c
C 461	28	15.0	10093	22	AAZ35890	Human cardiovascular
C 462	28	15.0	10093	22	AAK89816	Human digestive sy
C 463	28	15.0	10538	22	AAK71513	Human immune/haema
C 464	28	15.0	11186	24	AAZ36213	Human cytochrome p
C 465	28	15.0	11216	22	AAZ39593	Genomic sequence #
C 466	28	15.0	11216	22	AAK88992	Human digestive sy
C 467	28	15.0	11811	20	AAV83943	Bacterial artifici
C 468	28	15.0	12891	22	AAK85953	Human immune/haema
C 469	28	15.0	13608	22	AAK87529	Human immune/haema
C 470	28	15.0	13864	22	AAZ97861	Human neuroblastom
C 471	28	15.0	17947	22	AAK77679	Human immune/haema
C 472	28	15.0	19012	14	AAQ36952	HSA gene. Homo sa
C 473	28	15.0	22756	22	AAZ40321	DNA encoding human
C 474	28	15.0	22756	22	AA103921	Human reproductive
C 475	28	15.0	32195	22	AAZ36517	Human cardiovascular
C 476	28	15.0	32219	22	AAZ36516	Human cardiovascular
C 477	28	15.0	32249	22	AAZ36814	Human cardiovascular
C 478	28	15.0	35973	24	ABK13076	Human amyloid beta
C 479	28	15.0	36651	24	AAZ28072	Human kinase genom
C 480	28	15.0	53552	22	AAZ13655	Genomic DNA sequen
C 481	28	15.0	59065	24	AB142416	Human serine/threo
C 482	28	15.0	59747	24	ABQ88209	Human osteoblast d
C 483	28	15.0	123219	23	AAH88703	Human DNA sequence
C 484	28	15.0	128978	24	AAK83459	Human cDNA differe
C 485	28	15.0	143306	24	ABK49586	Human transporter
C 486	28	15.0	143899	24	AAZ13836	Genomic sequence e
C 487	28	15.0	1503900	22	AAK95240	Human neuregulin-1
C 488	28	15.0	1503900	22	AAK95240	Human neuregulin-1
C 489	28	15.0	1503900	22	AAK96733	Human neuregulin-1
C 490	28	15.0	1503900	22	AAK96733	Human neuregulin-1
C 491	27	14.4	239	14	AAQ60227	Human brain Expres
C 492	27	14.4	285	21	AAZ26514	Human secreted pro
C 493	27	14.4	286	21	AAK77171	Human immune/haema
C 494	27	14.4	291	21	AAZ01150	Human colon cancer
C 495	27	14.4	294	22	AAZ22271	Human breast canc
C 496	27	14.4	300	20	AAZ14874	Human gene express
C 497	27	14.4	300	20	AAZ14219	Human gene express
C 498	27	14.4	301	21	AAZ27970	Human secreted pro
C 499	27	14.4	320	22	AAZ13401	Human breast canc
C 500	27	14.4	357	22	AAZ26671	Human genomic DNA
C 501	27	14.4	372	24	ABL77513	Human ovarian canc
C 502	27	14.4	382	24	AAZ87908	Human polynucleoti
C 503	27	14.4	402	24	ABN96275	Gene #2773 used to
C 504	27	14.4	442	22	AAK67377	Human immune/haema
C 505	27	14.4	487	22	AAH10346	Human cDNA clone (
C 506	27	14.4	493	23	ABV18906	Human prostate exp
C 507	27	14.4	542	22	AAH12053	Human cDNA clone (
C 508	27	14.4	544	23	ABV48686	Human prostate exp
C 509	27	14.4	558	22	AAK92557	Human cDNA 3'-end
C 510	27	14.4	616	22	AAK78123	Human immune/haema
C 511	27	14.4	627	24	ABN62667	Human cancer relat
C 512	27	14.4	700	22	AAH92467	Human inflammatory
C 513	27	14.4	731	22	AAI95571	Human neuroblastom
C 514	27	14.4	741	20	AAZ16697	Human gene express
C 515	27	14.4	758	20	AAZ17480	Human gene express
C 516	27	14.4	759	20	AAZ16373	Human gene express
C 517	27	14.4	760	21	AAZ69550	Human secreted pro
C 518	27	14.4	808	20	AAK89617	Human cDNA encodin
C 519	27	14.4	808	22	AAS59248	Human cDNA encodin
C 520	27	14.4	808	24	ABA90917	Human polynucleoti

c 521	27	14.4	820	22	AAK75851	Human immune/haema	594	27	14.4	36305	24	ABK22783	Human high bone ma
c 522	27	14.4	951	22	AAI86541	Human polynucleoti	595	27	14.4	36933	22	AAK66362	Human immune/haema
c 523	27	14.4	1055	22	AAK64168	Human immune/haema	c 596	27	14.4	52562	22	AAK86669	Human immune/haema
c 524	27	14.4	1068	22	AAK86818	Human immune/haema	c 597	27	14.4	53075	22	AAK86671	Human immune/haema
c 525	27	14.4	1081	22	AAK68843	Human immune/haema	c 598	27	14.4	54108	24	ABK22782	Human high bone ma
c 526	27	14.4	1276	22	ABA16339	Human nervous syst	c 599	27	14.4	72049	22	ABA82823	Human HBM gene reg
c 527	27	14.4	1466	22	ABA08564	Human Grb7 effecto	c 600	27	14.4	97662	22	ABF83908	Genomic sequence o
c 528	27	14.4	1675	24	ABQ78825	Human Mch2 protein	c 601	27	14.4	97835	24	ABR84796	Human cDNA differe
c 529	27	14.4	1763	22	AAK94891	Human full-length	c 602	27	14.4	110000	22	ABF84800	Nucleotide sequenc
c 530	27	14.4	1852	22	AAH18681	Human cDNA sequenc	c 603	27	14.4	149480	22	ABL61947	Colon adenocarcino
c 531	27	14.4	1886	22	AAH17946	Human cDNA sequenc	c 604	27	14.4	149480	24	ABL61948	Colon adenocarcino
c 532	27	14.4	1923	22	AAK89342	Human S-HT3-B DNA..	c 605	27	14.4	149480	24	ABL68365	Kidney cancer rela
c 533	27	14.4	2027	22	AAH17405	Human cDNA sequenc	c 606	27	14.4	149671	24	ABK84797	Human cDNA differe
c 534	27	14.4	2040	23	AAK85019	DNA encoding novel	c 607	27	14.4	159400	24	ABQ88126	Human osteoblast d
c 535	27	14.4	2151	24	ABK34851	Human cDNA for nov	c 608	27	14.4	174424	24	ABL68122	Ovary cancer relat
c 536	27	14.4	2154	22	AAH17497	Human cDNA sequenc	c 609	27	14.4	174424	24	ABL68122	Ovary cancer relat
c 537	27	14.4	2277	22	AAK68770	Human immune/haema	c 610	27	14.4	235033	19	AAV57926	Hereditary haemoch
c 538	27	14.4	2399	24	ABK34922	Human cDNA encodin	c 611	26	13.9	129	20	AAH85825	Human single nucle
c 539	27	14.4	2449	22	AAK32585	Human genomic DNA	c 612	26	13.9	182	24	ABL87181	Human ovarian canc
c 540	27	14.4	2903	24	AAI44608	Human muscle creat	c 613	26	13.9	225	21	AAK25960	Human secreted pro
c 541	27	14.4	3408	22	AAK05598	Human secreted pro	c 614	26	13.9	239	21	AAK11964	Human secreted pro
c 542	27	14.4	4054	22	AAK74209	Human immune/haema	c 615	26	13.9	248	21	AAK20340	Human secreted pro
c 543	27	14.4	4461	22	AAK72635	Human immune/haema	c 616	26	13.9	258	20	AAV88716	EST clone HH404
c 544	27	14.4	4553	22	AAK85916	Human immune/haema	c 617	26	13.9	279	24	AAI69101	Activated T-cell d
c 545	27	14.4	4976	24	ABN83973	Human gene sequenc	c 618	26	13.9	319	22	AAK62615	Human immune/haema
c 546	27	14.4	6111	22	AAK36193	Human cardiovascular	c 619	26	13.9	319	22	AAK82895	Human immune/haema
c 547	27	14.4	6111	22	AAK78300	Human immune/haema	c 620	26	13.9	319	22	AAK82896	Human immune/haema
c 548	27	14.4	7282	22	AAK72425	Human immune/haema	c 621	26	13.9	333	21	AAK41492	Human secreted exp
c 549	27	14.4	7379	19	AAK49653	Human SCL DNA, HO	c 622	26	13.9	336	22	AAI81940	Human polynucleoti
c 550	27	14.4	7491	22	AAK78292	Human immune/haema	c 623	26	13.9	335	22	AAI80295	Human polynucleoti
c 551	27	14.4	8276	22	AAK70800	Human immune/haema	c 624	26	13.9	346	24	ABL64216	Stomach cancer rel
c 552	27	14.4	8705	22	ABA82624	Human HBM gene reg	c 625	26	13.9	351	23	ABV49084	Human prostate exp
c 553	27	14.4	9496	22	AAI16328	Human nervous syst	c 626	26	13.9	354	22	AAK64027	Human immune/haema
c 554	27	14.4	9591	22	AAI03355	Human reproductive	c 627	26	13.9	356	21	AAK280255	Human colon cancer
c 555	27	14.4	9591	22	AAK28906	Human immunoglobul	c 628	26	13.9	370	21	AAK02846	Human secreted pro
c 556	27	14.4	9968	22	AAK32240	Human DNA repair a	c 629	26	13.9	372	22	ABAI8488	Human nervous syst
c 557	27	14.4	10448	22	AAI999191	Human excretory re	c 630	26	13.9	386	21	AAH30469	Human colon cancer
c 558	27	14.4	10448	22	AAI63541	Human kidney relat	c 631	26	13.9	398	22	AAK58627	Human immune/haema
c 559	27	14.4	12415	22	AAI03356	Human reproductive	c 632	26	13.9	401	22	AAK96108	Human neuroregulin g
c 560	27	14.4	12415	22	AAK28907	Human immunoglobul	c 633	26	13.9	401	22	AAK96109	Human neuroregulin g
c 561	27	14.4	13585	17	AAI11549	Tumour rejection a	c 634	26	13.9	401	22	AAK97601	Human neuroregulin g
c 562	27	14.4	15261	22	AAU07498	Human reproductive	c 635	26	13.9	401	22	AAK97602	Human neuroregulin g
c 563	27	14.4	15399	22	ABAI8197	Human nervous syst	c 636	26	13.9	412	24	ABL78970	Human ovarian canc
c 564	27	14.4	15399	22	ABAI8198	Human nervous syst	c 637	26	13.9	423	24	ABL77253	Human ovarian canc
c 565	27	14.4	17979	22	AAK64964	Human immune/haema	c 638	26	13.9	431	23	ABV16978	Human prostate exp
c 566	27	14.4	17979	22	AAK71664	Human immune/haema	c 639	26	13.9	436	24	ABL81158	Human ovarian canc
c 567	27	14.4	20565	22	AAI03357	Human reproductive	c 640	26	13.9	438	22	AAK70880	Human immune/haema
c 568	27	14.4	20565	22	AAK28908	Human immunoglobul	c 641	26	13.9	442	22	AAI83526	Human polynucleoti
c 569	27	14.4	20565	22	AAK89083	Human digestive sy	c 642	26	13.9	461	24	ABQ54456	Human ovarian anti
c 570	27	14.4	23164	22	AAK79678	Human immune/haema	c 643	26	13.9	475	23	ABV13017	Human prostate exp
c 571	27	14.4	27359	22	ABAI19957	Human nervous syst	c 644	26	13.9	476	23	ABV03848	Human prostate exp
c 572	27	14.4	27371	22	ABAI19958	Human nervous syst	c 645	26	13.9	478	22	AAI86439	Human polynucleoti
c 573	27	14.4	28818	22	AAI35901	Human musculoskele	c 646	26	13.9	478	22	ABV46773	Human prostate exp
c 574	27	14.4	29329	22	ABAI8026	Human nervous syst	c 647	26	13.9	507	22	AAK70049	Human immune/haema
c 575	27	14.4	29329	22	ABAI8026	Human nervous syst	c 648	26	13.9	507	22	AAK70050	Human immune/haema
c 576	27	14.4	29329	22	AAK70791	Human immune/haema	c 649	26	13.9	508	23	ABV21474	Human prostate exp
c 577	27	14.4	29329	22	AAK78512	Human immune/haema	c 650	26	13.9	508	23	ABV27292	Human prostate exp
c 578	27	14.4	30037	22	AAK20038	Human nervous syst	c 651	26	13.9	508	23	ABV60406	Human prostate exp
c 579	27	14.4	31949	22	AAI05410	Human reproductive	c 652	26	13.9	513	23	ABV34138	Human prostate exp
c 580	27	14.4	31949	23	ABU98289	Human testicular a	c 653	26	13.9	513	23	ABV43000	Human prostate exp
c 581	27	14.4	32152	22	AAK39621	Genomic sequence #	c 654	26	13.9	522	24	ABL77779	Human ovarian canc
c 582	27	14.4	32152	22	AAK89020	Human digestive sy	c 655	26	13.9	533	20	AAH10131	Human cDNA clone (
c 583	27	14.4	32152	22	AAK91534	Human digestive sy	c 656	26	13.9	537	20	AAI217754	Human gene express
c 584	27	14.4	32152	22	AAI57791	Human colorectal c	c 657	26	13.9	538	22	AAH10203	Human cDNA clone (
c 585	27	14.4	32186	22	ABAI6117	Human nervous syst	c 658	26	13.9	538	23	ABV41555	Human prostate exp
c 586	27	14.4	32186	22	AAI05411	Human reproductive	c 659	26	13.9	542	23	ABV19310	Human prostate exp
c 587	27	14.4	32186	23	ABU98270	Human testicular a	c 660	26	13.9	548	22	AAH10712	Human cDNA clone (
c 588	27	14.4	32186	22	AAK32249	Human DNA repair a	c 661	26	13.9	558	24	ABN64455	Human cancer relat
c 589	27	14.4	32188	22	AAK28365	Genomic sequence #	c 662	26	13.9	561	22	AAH12647	Human cDNA clone (
c 590	27	14.4	32204	22	AAK39620	Genomic sequence #	c 663	26	13.9	571	22	AAK69674	Human immune/haema
c 591	27	14.4	32204	22	AAK89019	Human digestive sy	c 664	26	13.9	574	22	AAK69673	Human immune/haema
c 592	27	14.4	32204	22	AAK91533	Human digestive sy	c 665	26	13.9	574	22	AAK69675	Human immune/haema
c 593	27	14.4	32204	22	AAI57790	Human colorectal c	c 666	26	13.9	609	22	AAH09405	Human cDNA clone (

C 667	26	13.9	614	24	ABN61386	Human cancer relat
C 668	26	13.9	628	22	AAS22853	Human cDNA encodin
C 669	26	13.9	628	23	ABV54668	Human prostate exp
C 670	26	13.9	629	22	AAK57858	Human immune/haema
C 671	26	13.9	634	24	ABN60146	Human cancer relat
C 672	26	13.9	634	24	ABN61981	Human cancer relat
C 673	26	13.9	644	24	ABN61351	Human cancer relat
C 674	26	13.9	663	24	ABQ57171	Human colon cancer
C 675	26	13.9	795	24	ABN59620	Novel human coding
C 676	26	13.9	934	21	AAC59515	Human secreted pro
C 677	26	13.9	978	20	AAK51732	DNA encoding a hum
C 678	26	13.9	988	22	AAI93555	Human polynucleoti
C 679	26	13.9	988	22	AAI93557	Human secreted pro
C 680	26	13.9	1458	21	AAC59929	Human secreted pro
C 681	26	13.9	1554	20	AAZ10643	CNA encoding a hu
C 682	26	13.9	1596	22	AAH17127	Human cDNA sequenc
C 683	26	13.9	1688	24	ABL68589	Kidney cancer rela
C 684	26	13.9	1753	22	AAH18420	Human cDNA sequenc
C 685	26	13.9	1753	22	AAH18445	Human cDNA sequenc
C 686	26	13.9	1767	22	AAH15897	Human cDNA sequenc
C 687	26	13.9	1821	22	AAH17442	Human cDNA sequenc
C 688	26	13.9	1899	22	AAH14906	Human cDNA sequenc
C 689	26	13.9	2081	24	ABK11363	Human cDNA encodin
C 690	26	13.9	2391	22	AAI92576	Human polynucleoti
C 691	26	13.9	2575	22	AAK82973	Human immune/haema
C 692	26	13.9	2588	24	AAS62260	CNA sequence #47
C 693	26	13.9	2750	22	AAH16544	Human cDNA sequenc
C 694	26	13.9	2752	21	AAC69119	Human secreted pro
C 695	26	13.9	2789	22	AAK67124	Human immune/haema
C 696	26	13.9	2810	19	AAV17099	Human brain derive
C 697	26	13.9	2990	22	AAS60842	Human cancer agent
C 698	26	13.9	3121	20	AAS70307	Human IL-1ra BAC C
C 699	26	13.9	3127	23	AAK576376	DNA encoding novel
C 700	26	13.9	3144	22	AAH13942	Human cDNA sequenc
C 701	26	13.9	3361	22	AAK81871	Human immune/haema
C 702	26	13.9	3566	23	AAS76905	DNA encoding novel
C 703	26	13.9	3648	24	ABA95675	Human interleukin-
C 704	26	13.9	3729	22	AAI03253	Human reproductive
C 705	26	13.9	3809	24	AAI45769	Human acid phospho
C 706	26	13.9	4837	22	AAI36474	Human musculoskele
C 707	26	13.9	4932	22	AAK82980	Human immune/haema
C 708	26	13.9	4933	22	AAK82972	Human cDNA differe
C 709	26	13.9	5204	24	ABK83946	Human immune/haema
C 710	26	13.9	5331	22	AAK76629	Human immune/haema
C 711	26	13.9	5332	22	AAS32735	Human genomic DNA
C 712	26	13.9	5670	24	ABL65836	Lung cancer relate
C 713	26	13.9	5690	22	AAI99536	Human polynucleoti
C 714	26	13.9	6149	22	AAK90925	Human digestive sy
C 715	26	13.9	6149	22	AAK90926	Human digestive sy
C 716	26	13.9	6149	22	AAS31960	Human liver associ
C 717	26	13.9	6149	22	AAS31961	Human liver associ
C 718	26	13.9	6149	24	ABN90315	Human liver antige
C 719	26	13.9	6149	24	ABN90316	Human liver antige
C 720	26	13.9	6259	22	AAK93975	Human immune/haema
C 721	26	13.9	6389	22	ABA17557	Human nervous syst
C 722	26	13.9	6744	20	AAS238125	Human FATP genomic
C 723	26	13.9	7099	22	AAI04882	Human reproductive
C 724	26	13.9	7099	23	ABL97776	Human testicular a
C 725	26	13.9	12192	22	AAS28195	Genomic sequence #
C 726	26	13.9	12729	22	AAK97873	Human neuroblastom
C 727	26	13.9	12842	22	ABA20815	Human nervous syst
C 728	26	13.9	13001	22	AAK92979	Human immune/haema
C 729	26	13.9	13294	22	AAK85255	Human immune/haema
C 730	26	13.9	14796	19	AAV27941	Survivin gene. Ho
C 731	26	13.9	14796	22	AAS21523	DNA encoding human
C 732	26	13.9	14796	22	AAH47531	Human Her-3 genomi
C 733	26	13.9	14796	24	ABN96924	Gene #3422 used to
C 734	26	13.9	14796	24	ABL65663	Lung cancer relate
C 735	26	13.9	14796	24	ABL66326	Lung cancer relate
C 736	26	13.9	14796	24	ABL68655	Kidney cancer rela
C 737	26	13.9	15054	22	AAS40425	DNA encoding human
C 738	26	13.9	15054	22	AAI04033	Human reproductive
C 739	26	13.9	15295	22	AAI37039	Human musculoskele
C 740	26	13.9	15914	22	AAK73222	Human immune/haema
C 741	26	13.9	16146	20	AAK84529	Human immune/haema
C 742	26	13.9	16891	22	AAK37084	MEFV gene sequence
C 743	26	13.9	16939	22	AAI04817	Human reproductive
C 744	26	13.9	16939	23	ABL97711	Human testicular a
C 745	26	13.9	17327	14	AAQ44278	Serglycin - proteo
C 746	26	13.9	17327	14	AAQ44278	Human cytoskeletal
C 747	26	13.9	17730	22	AAS29826	Human immune/haema
C 748	26	13.9	19243	22	AAK71662	Human reproductive
C 749	26	13.9	22689	22	AAI04819	Human testicular a
C 750	26	13.9	22689	23	ABL97713	Human ion3 coding
C 751	26	13.9	22735	20	AAK87198	Human prothrombin
C 752	26	13.9	26928	20	AAZ32184	Gene #2278 used to
C 753	26	13.9	27841	22	AAS29820	Human cytoskeletal
C 754	26	13.9	27841	22	AAS29827	Human cytoskeletal
C 755	26	13.9	31952	22	AAK89370	Human digestive sy
C 756	26	13.9	32192	22	AAK89452	Human digestive sy
C 757	26	13.9	32217	22	AAK841738	Genomic sequence #
C 758	26	13.9	33718	22	AAK65257	Human immune/haema
C 759	26	13.9	33718	22	AAK86411	Human immune/haema
C 760	26	13.9	35959	22	AAK78275	Human immune/haema
C 761	26	13.9	37783	22	AAK70780	Human immune/haema
C 762	26	13.9	37783	22	AAK76625	Human immune/haema
C 763	26	13.9	37783	22	AAK80913	Human immune/haema
C 764	26	13.9	40308	22	AAK68184	Human immune/haema
C 765	26	13.9	57248	24	ABK83553	Human cDNA differe
C 766	26	13.9	76798	24	ABN97454	Gene #3952 used to
C 767	26	13.9	81800	24	ABK84756	Human cDNA differe
C 768	26	13.9	89328	24	ABL61995	Colon adenocarcino
C 769	26	13.9	107820	22	AAI16230	Human ATP-binding
C 770	26	13.9	126512	24	ABN83429	Human transporter
C 771	26	13.9	175737	24	ABK83571	Human cDNA differe
C 772	26	13.9	178896	24	ABQ88146	Human osteoblast d
C 773	26	13.9	220895	22	ABK84798	Human cDNA differe
C 774	26	13.9	240825	22	AAK24497	Human PG-3 gene.
C 775	26	13.9	325791	22	AAS43104	Human oestrogen re
C 776	26	13.9	452327	24	ABQ87681	Human oestrogen re
C 777	26	13.9	452327	24	ABA90193	Human oestrogen re
C 778	25	13.4	108	21	AAK21941	Human secreted pro
C 779	25	13.4	117	22	AAK78904	Human immune/haema
C 780	25	13.4	145	21	AAI14944	Human secreted pro
C 781	25	13.4	152	21	AAK65545	Human immune/haema
C 782	25	13.4	158	21	AAC04856	Human secreted pro
C 783	25	13.4	176	21	AAI13110	Human secreted pro
C 784	25	13.4	178	22	AAK65541	Human immune/haema
C 785	25	13.4	191	22	AAA11380	Human secreted exp
C 786	25	13.4	210	22	AAI80988	Human polynucleoti
C 787	25	13.4	229	22	AAI89884	Human polynucleoti
C 788	25	13.4	239	22	AAK65273	Human immune/haema
C 789	25	13.4	239	22	AAK69836	Human immune/haema
C 790	25	13.4	243	22	AAI80854	Human polynucleoti
C 791	25	13.4	243	24	ABL85663	Human ovarian canc
C 792	25	13.4	252	24	ABL86044	Human ovarian canc
C 793	25	13.4	257	21	AAC03720	Human secreted pro
C 794	25	13.4	289	21	AAC21549	Human secreted pro
C 795	25	13.4	294	21	AAC25334	Human secreted pro
C 796	25	13.4	307	22	ABA20816	Human nervous syst
C 797	25	13.4	307	22	AAI90896	Human polynucleoti
C 798	25	13.4	313	21	AAC29140	Human secreted pro
C 799	25	13.4	320	22	AAI86771	Human polynucleoti
C 800	25	13.4	338	24	ABL85243	Human ovarian canc
C 801	25	13.4	340	22	AAI05529	Human reproductive
C 802	25	13.4	340	22	AAK70517	Human immune/haema
C 803	25	13.4	343	21	AAI12745	Human secreted pro
C 804	25	13.4	344	22	AAI01608	Human reproductive
C 805	25	13.4	344	22	AAK55080	Human immune/haema
C 806	25	13.4	346	21	AAI10697	Human secreted pro
C 807	25	13.4	350	22	ABA11527	Human nervous syst
C 808	25	13.4	353	22	AAI80926	Human polynucleoti
C 809	25	13.4	355	22	ABA18242	Human nervous syst
C 810	25	13.4	355	22	ABA18242	Human breast cance
C 811	25	13.4	365	21	AAK28473	Human secreted pro
C 812	25	13.4	371	22	AAI15140	Human breast cance

C 813	25	13.4	373	22	AA186899	Human polynucleoti
C 814	25	13.4	377	22	AA183591	Human polynucleoti
C 815	25	13.4	377	22	AAK86977	Human immune/haema
C 816	25	13.4	377	22	AAK86978	Human immune/haema
C 817	25	13.4	377	22	AAK86979	Human immune/haema
C 818	25	13.4	383	22	AAK81123	Human immune/haema
C 819	25	13.4	406	22	AA181312	Human polynucleoti
C 820	25	13.4	409	24	ABU83510	Human ovarian canc
C 821	25	13.4	415	22	AA186972	Human polynucleoti
C 822	25	13.4	421	22	ABAI11360	Human nervous syst
C 823	25	13.4	421	23	ABV18008	Human prostate exp
C 824	25	13.4	430	22	AAK65031	Human immune/haema
C 825	25	13.4	434	22	AAK65751	Human immune/haema
C 826	25	13.4	434	22	AAK73893	Human immune/haema
C 827	25	13.4	443	21	AAK26202	Human secreted pro
C 828	25	13.4	453	22	AA187017	Human polynucleoti
C 829	25	13.4	465	24	ABU85335	Human ovarian canc
C 830	25	13.4	467	22	AAK24798	Human ovarian PCR-
C 831	25	13.4	475	22	ABU43814	Human breast cell
C 832	25	13.4	475	22	ABU54269	Human foetal liver
C 833	25	13.4	475	22	ABU24024	Probe #2490 for ge
C 834	25	13.4	475	22	AAK02547	Human brain expres
C 835	25	13.4	475	22	AAK27986	Human bone marrow
C 836	25	13.4	475	22	AA112568	Probe #2501 for ge
C 837	25	13.4	475	22	AA133915	Probe #2601 used t
C 838	25	13.4	475	22	AA102475	Probe #2466 used t
C 839	25	13.4	475	24	ABSO2452	Human genome-deriv
C 840	25	13.4	477	22	ABU06379	Human CDNA SEQ ID
C 841	25	13.4	477	22	AAK57097	CDNA encoding nove
C 842	25	13.4	477	22	AAK86955	Human immune/haema
C 843	25	13.4	489	21	AAK28371	Human immune/haema
C 844	25	13.4	513	22	AA186094	Human secreted pro
C 845	25	13.4	513	22	AAH12118	Human polynucleoti
C 846	25	13.4	513	22	AAH10417	Human CDNA clone (
C 847	25	13.4	523	23	ABU47797	Human prostate exp
C 848	25	13.4	527	22	AAK83169	Human immune/haema
C 849	25	13.4	544	23	ABV18300	Human prostate exp
C 850	25	13.4	553	22	AAH09954	Human CDNA clone (
C 851	25	13.4	556	22	AAH83432	Human ovarian tumo
C 852	25	13.4	556	22	AAH10417	Human CDNA clone (
C 853	25	13.4	557	22	AAH10283	Human CDNA clone (
C 854	25	13.4	562	21	AAK99969	Human secreted pro
C 855	25	13.4	565	24	ABN64837	Human cancer relat
C 856	25	13.4	566	23	ABV56854	Human prostate exp
C 857	25	13.4	574	22	ABU07578	Human ovarian and
C 858	25	13.4	574	22	AAU00647	Human reproductive
C 859	25	13.4	574	22	AAH09363	Human CDNA clone (
C 860	25	13.4	629	23	ABV58132	Human prostate exp
C 861	25	13.4	655	24	ABN62513	Human cancer relat
C 862	25	13.4	679	21	AAK02065	Human colon cancer
C 863	25	13.4	682	22	AAK64694	Human immune/haema
C 864	25	13.4	687	22	ABU16476	Human nervous syst
C 865	25	13.4	692	21	AAK02064	Human colon cancer
C 866	25	13.4	694	22	AAK64203	Human immune/haema
C 867	25	13.4	700	22	AAH92688	Human inflammatory
C 868	25	13.4	728	21	AAK99894	Human secreted pro
C 869	25	13.4	738	20	AAK27431	Human CDNA clone (
C 870	25	13.4	765	22	AAH08429	Human prostate exp
C 871	25	13.4	773	24	ABQ89708	Human immune/haema
C 872	25	13.4	775	24	ABQ89633	Human immune/haema
C 873	25	13.4	781	20	AA215116	Human immune/haema
C 874	25	13.4	806	22	AAH04371	Human secreted pro
C 875	25	13.4	938	24	ABQ88881	Human CDNA sequenc
C 876	25	13.4	1032	22	AAK83157	Human immune/haema
C 877	25	13.4	1032	22	AAK83478	Human immune/haema
C 878	25	13.4	1034	22	AAK83479	Human immune/haema
C 879	25	13.4	1241	21	AAK79745	Human secreted pro
C 880	25	13.4	1242	22	AAH15609	Human CDNA sequenc
C 881	25	13.4	1317	22	AAK84446	Human immune/haema
C 882	25	13.4	1381	15	AAQ77883	Neural thread prot
C 883	25	13.4	1381	17	AAI27765	AD 10-7 human neur
C 884	25	13.4	1400	22	AAH24242	Human oxidoreducta
C 885	25	13.4	1433	24	ABK34834	Human CDNA for nov
C 886	25	13.4	1457	22	AAK77700	Human immune/haema
C 887	25	13.4	1473	20	AAF45097	Human secreted pro
C 888	25	13.4	1588	20	AAK98019	Human secreted pro
C 889	25	13.4	1625	22	AAK83155	Human immune/haema
C 890	25	13.4	1625	22	AAK83171	Human immune/haema
C 891	25	13.4	1650	24	ABU55368	Human leucine zipp
C 892	25	13.4	1706	22	AAK94092	Human full-length
C 893	25	13.4	1730	24	ABU50929	Human CDNA sequenc
C 894	25	13.4	1780	22	AAH15367	Human CDNA sequenc
C 895	25	13.4	1833	22	AAK22596	Human cDNA encodin
C 896	25	13.4	1833	22	AAK22832	Human cDNA encodin
C 897	25	13.4	1873	22	AAH17314	Human CDNA sequenc
C 898	25	13.4	1954	22	AAH17332	Human CDNA sequenc
C 899	25	13.4	1964	22	AAU05791	Human reproductive
C 900	25	13.4	1964	23	ABU98355	Human testicular a
C 901	25	13.4	1970	24	ABQ77574	Human cyclophilin-
C 902	25	13.4	1984	22	ABU44109	Human breast cell
C 903	25	13.4	1984	22	ABU45462	Human foetal liver
C 904	25	13.4	1984	22	ABA24345	Probe #2811 for ge
C 905	25	13.4	1984	22	AAK02855	Human brain expres
C 906	25	13.4	1984	22	AAK28297	Human bone marrow
C 907	25	13.4	1984	22	AAI12861	Probe #2794 for ge
C 908	25	13.4	1984	22	AAI14218	Probe #2904 used t
C 909	25	13.4	1984	22	AAI02777	Probe #2768 used t
C 910	25	13.4	1984	24	ABSO2806	Human genome-deriv
C 911	25	13.4	2071	24	AAH98877	CDNA encoding an e
C 912	25	13.4	2225	22	AAH16675	Human CDNA sequenc
C 913	25	13.4	2236	22	ABU07878	Human ovarian and
C 914	25	13.4	2236	22	AAU03695	Human reproductive
C 915	25	13.4	2236	22	AAK66847	Human immune/haema
C 916	25	13.4	2236	22	AAK69056	Human immune/haema
C 917	25	13.4	2236	22	AAK72813	Human immune/haema
C 918	25	13.4	2236	22	AAH13864	Human CDNA sequenc
C 919	25	13.4	2373	22	AAH17310	Human CDNA sequenc
C 920	25	13.4	2583	22	AAK81358	Human immune/haema
C 921	25	13.4	2627	22	AAH17965	Human CDNA sequenc
C 922	25	13.4	2656	22	AAK87660	Human immune/haema
C 923	25	13.4	2854	22	AAK83164	Human immune/haema
C 924	25	13.4	2901	24	ABU01040	Human uterine glob
C 925	25	13.4	3116	22	AAK39688	Genomic sequence #
C 926	25	13.4	3116	22	AAK90031	Human digestive sy
C 927	25	13.4	3304	22	ABU18014	Human nervous syst
C 928	25	13.4	3396	22	AAK27756	DNA encoding novel
C 929	25	13.4	3585	22	AAK27755	DNA encoding novel
C 930	25	13.4	3622	22	AAK86394	Human immune/haema
C 931	25	13.4	3666	24	ABN96799	Gene #3297 used to
C 932	25	13.4	3760	22	AAK72031	Human immune/haema
C 933	25	13.4	4283	22	AAK83180	Human immune/haema
C 934	25	13.4	4340	24	ABN95734	Gene #2232 used to
C 935	25	13.4	4412	22	ABU16083	Human nervous syst
C 936	25	13.4	4678	22	AAK87310	Human immune/haema
C 937	25	13.4	5025	22	AAK84573	Human immune/haema
C 938	25	13.4	5029	22	AAK84574	Human immune/haema
C 939	25	13.4	5054	22	AAK83477	Human immune/haema
C 940	25	13.4	5216	22	AAK28261	Genomic sequence #
C 941	25	13.4	5216	22	AAK31528	Human DNA for a no
C 942	25	13.4	5216	24	ABO66852	Human polynucleoti
C 943	25	13.4	5441	22	AAI98937	Human kidney relat
C 944	25	13.4	5441	22	AAI63287	Human excretory re
C 945	25	13.4	5814	22	AAK83448	Human immune/haema
C 946	25	13.4	5932	22	AAU03052	Human reproductive
C 947	25	13.4	5932	23	ABU97388	Human testicular a
C 948	25	13.4	5966	22	ABU07890	Human ovarian and
C 949	25	13.4	5966	22	AAU03707	Human reproductive
C 950	25	13.4	6071	22	AAK27758	DNA encoding novel
C 951	25	13.4	6440	22	AAK68762	Human immune/haema
C 952	25	13.4	6440	22	AAK68763	Human immune/haema
C 953	25	13.4	6440	22	AAK68764	Human immune/haema
C 954	25	13.4	6512	22	AAK27757	DNA encoding novel
C 955	25	13.4	6686	22	AAK81545	Human immune/haema
C 956	25	13.4	6751	22	AAK83163	Human immune/haema
C 957	25	13.4	6767	22	AAK83147	Human immune/haema
C 958	25	13.4	6945	22	AAK88968	Human digestive sy

c 959 25 13.4 6945 22 AAK88969 Human digestive sy  
c 960 25 13.4 6945 22 AAS31837 Human liver associ  
c 961 25 13.4 6945 22 AAS31838 Human liver associ  
c 962 25 13.4 6945 24 ABN90192 Human liver antige  
c 963 25 13.4 6945 24 ABN90193 Human liver antige  
c 964 25 13.4 7042 21 AAV84785 Apoptosis inducer  
c 965 25 13.4 7042 21 AAZ46656 Human full-length  
c 966 25 13.4 7042 21 AAZ46656 Wild type Apaf-1 c  
c 967 25 13.4 7042 24 ABK93574 Human apoptotic pr  
c 968 25 13.4 7075 20 AAV84798 Apoptosis inducer  
c 969 25 13.4 7166 22 AAS32736 Human genomic DNA  
c 970 25 13.4 7301 24 ABA98878 Genomic DNA encodi  
c 971 25 13.4 7633 22 AAK83159 Human immune/haema  
c 972 25 13.4 7725 22 AAK87157 Human immune/haema  
c 973 25 13.4 7858 22 AAK67290 Human immune/haema  
c 974 25 13.4 8003 22 AAK83149 Human immune/haema  
c 975 25 13.4 8021 22 AAK85877 Human immune/haema  
c 976 25 13.4 8121 22 AAS36189 Human cardiovascular  
c 977 25 13.4 8190 22 ABA18373 Human nervous syst  
c 978 25 13.4 8253 22 AAS40470 DNA encoding human  
c 979 25 13.4 8253 22 AAL04087 Human reproductive  
c 980 25 13.4 8794 22 AAS30465 DNA encoding novel  
c 981 25 13.4 8794 22 AAL06245 Human reproductive  
c 982 25 13.4 8846 22 ABA15292 Human nervous syst  
c 983 25 13.4 9133 22 AAK83165 Human immune/haema  
c 984 25 13.4 9192 22 AAL35853 Human musculoskele  
c 985 25 13.4 9192 23 ABK42359 Genomic sequence #  
c 986 25 13.4 9217 22 AAK83151 Human immune/haema  
c 987 25 13.4 9337 22 AAK76038 Human immune/haema  
c 988 25 13.4 9337 22 AAK78564 Human immune/haema  
c 989 25 13.4 9837 18 AAT96851 Intron 21 of human  
c 990 25 13.4 10102 22 AAK83072 Human immune/haema  
c 991 25 13.4 10497 22 AAK67302 Human immune/haema  
c 992 25 13.4 10497 22 AAK83166 Human immune/haema  
c 993 25 13.4 10899 22 ABA15344 Human nervous syst  
c 994 25 13.4 11079 22 AAK90954 Human digestive sy  
c 995 25 13.4 11079 22 AAK31989 Human liver associ  
c 996 25 13.4 11079 24 ABN90344 Human liver antige  
c 997 25 13.4 11244 22 AAK74606 Human immune/haema  
c 998 25 13.4 11266 24 AAL43028 Human P2X7 gene in  
c 999 25 13.4 11298 23 ABK42456 Genomic sequence #  
c1000 25 13.4 11655 22 AAK87506 Human immune/haema

## ALIGNMENTS

RESULT 1  
AAA64508  
ID ARA64508 standard; cDNA; 5492 BP.  
XX  
AC AAA64508;  
XX  
DT 02-JAN-2001 (first entry)  
XX  
DE cDNA sequence of the wild type human FEZ1 gene.  
XX  
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200050565-A2.  
XX  
XX 31-AUG-2000.  
XX  
XX 25-FEB-2000; 2000WO-US04950.  
XX  
XX 25-FEB-1999; 99US-0121537.  
XX  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Croce CM, Ishii H;  
XX  
XX WPI; 2000-558396/51.  
XX  
DR New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -  
XX  
XX Example 2; Fig 5B; 255pp; English.  
PS  
XX  
XX The present sequence represents the cDNA sequence of the human FEZ1 gene.  
CC FEZ1 is a tumour suppressor gene, located at chromosome location 8p22.  
CC Decreased or no expression of FEZ1 is detected in a variety of cancer  
CC cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
CC also interacts with tubulin, with microtubules, and with protein  
CC Efi-gamma. Post-translational phosphorylation and dephosphorylation  
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
CC expression are useful for inducing cells to proliferate. Compounds  
CC which modulate FEZ1 association with tubulin are useful for alleviating  
CC tubulin hyper- or hypo- polymerisation disorders, such as those  
CC associated with aberrant initiation of mitosis, modulation of the  
CC initiation and rate of cell proliferation and cell growth, modulation of  
CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
CC DNA replication, intracellular distribution of organelles, metastatic  
CC potential of cell and cellular transformation from a non-cancerous to  
CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
CC phosphorylation are also useful for alleviating a disorder, such as  
CC tumorigenesis, tumour survival, growth and metastasis.  
XX  
SQ Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;  
Query Match 100.0%; Score 187; DB 21; Length 5492;  
Best Local Similarity 100.0%; Pred. No. 1.3e-82;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATCATATAGTCTCAGCTGCGCTCTACTCTCTGGCTCAAGCAATCTCTGCTCAGCC 60  
Db 3348 ATCATATAGTCTCAGCTGCGCTCTACTCTCTGGCTCAAGCAATCTCTGCTCAGCC 3407  
QY 61 TTCCAACATAGCTGGGACTCAGGTGCGCGCCACCGTGGCTGCTTCAATTTT 120  
Db 3408 TTCCAACATAGCTGGGACTCAGGTGCGCGCCACCGTGGCTGCTTCAATTTT 3467  
QY 121 TGTAGGACGGGTCTCGTTTGTGTCGAAGCTGCTCTCAAACTTGTGCGCTCAAGCAA 180  
Db 3468 TGTAGGACGGGTCTCGTTTGTGTCGAAGCTGCTCTCAAACTTGTGCGCTCAAGCAA 3527  
QY 181 TCCACCT 187  
Db 3528 TCCACCT 3534  
RESULT 2  
AAA64507  
ID ARA64507 standard; DNA; 9048 BP.  
XX  
AC AAA64507;  
XX  
XX 02-JAN-2001 (first entry)  
XX  
XX Nucleotide sequence comprising the human FEZ1 gene.  
XX  
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein Efi-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200050565-A2.

XX 31-AUG-2000.  
XX 25-FEB-2000; 2000WO-US04950.  
XX 25-FEB-1999; 99US-0121537.  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX Croce CM, Ishii H;  
XX WPI; 2000-558396/51.  
XX New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -  
XX Claim 2; Fig 5A; 255pp; English.  
XX The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour  
CC suppressor gene, located at chromosome location 8p22. Decreased or no  
CC expression of FEZ1 is detected in a variety of cancer cells. Expression  
CC of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts  
CC with tubulin, with microtubules, and with protein ERF1-gamma.  
CC Post-translational phosphorylation and dephosphorylation modulates the  
CC effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are  
CC useful for inducing cells to proliferate. Compounds which modulate FEZ1  
CC association with tubulin are useful for alleviating tubulin hyper- or  
CC hypo- polymerisation disorders, such as those associated with aberrant  
CC initiation of mitosis, modulation of the initiation and rate of cell  
CC proliferation and cell growth, modulation of cell shape, cell rigidity,  
CC cell motility, rate and stage of cellular DNA replication, intracellular  
CC distribution of organelles, metastatic potential of cell and cellular  
CC transformation from a non-cancerous to cancerous phenotype. Compounds  
CC which modulate FEZ1 binding and phosphorylation are also useful for  
CC alleviating a disorder, such as tumorigenesis, tumour survival, growth  
CC and metastasis.  
XX SQ Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;  
Query Match 100.0%; Score 187; DB 21; Length 9048;  
Best Local Similarity 100.0%; Pred. No. 1.3e-82;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGATCATAGCTACTGCGCTCATCTCTGGGCTCAAGCAATCTCTGCTGCTCAGCC 60  
Db 6939 ATGATCATAGCTACTGCGCTCATCTCTGGGCTCAAGCAATCTCTGCTGCTCAGCC 6998  
Qy 61 TTCAACTAGCTGGGCTCGTTTGTGTCGAAGCTGGTCTCAAACTTGTGGCTCAGCAA 120  
Db 6999 TTCAACTAGCTGGGCTCGTTTGTGTCGAAGCTGGTCTCAAACTTGTGGCTCAGCAA 7058  
Qy 121 TGTAGGACGGGCTCGTTTGTGTCGAAGCTGGTCTCAAACTTGTGGCTCAGCAA 180  
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Qy 181 TCACCT 187  
Db 7119 TCACCT 7125  
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ID ABAL7068 standard; DNA; 12767 BP.  
XX AC ABAL7068;  
XX 23-JAN-2002 (first entry)  
XX Human nervous system related polynucleotide SEQ ID NO 9399.  
XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW

KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebrotective; antiinflammatory;  
KW antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
XX Homo sapiens.  
OS WO200159063-A2.  
XX 16-AUG-2001.  
PD 17-JAN-2001; 2001WO-US01334.  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184564.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 27-JUN-2000; 2000US-0209467.  
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PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.







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FT FT 11534..15656
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FT FT 18885..18890
FT FT /*tag= u
XX XX WO200224741-A2.
XX XX 28-MAR-2002.
XX XX 21-SEP-2001; 2001WO-US29454.
XX XX 21-SEP-2000; 2000US-234422P.
XX XX (RYAN/) RYAN J W.
XX XX Ryan JW;
```

```
XX WPI; 2002-394128/42.
DR P-PSDB; AAE22740.
XX
XX Novel genomic polynucleotide from human chromosome-7 encoding snare
PT YKT6, liver glucokinase, adipocyte enhancer binding protein (AEBP1) and DNA
PT delta small subunit useful in gene therapy for treating e.g. diabetes,
PT cancer -
XX
XX Claim 1; Page 54-63; 94pp; English.
XX
XX The present invention relates to novel genomic polynucleotide from human
CC chromosome 7 encoding human snare YKT6, liver glucokinase (ATP: D-hexose
CC 6-phosphotransferase), adipocyte enhancer binding protein (AEBP1) and DNA
CC directed 50 kDa regulatory subunit (POLD2). Sequences of the invention
CC are used to prevent, treat or ameliorate a medical condition. Antisense
CC oligonucleotides specific for snare YKT6 are useful for inhibiting cell
CC growth and in particular to treat or prevent tumour growth. Glucokinase
CC and AEBP are useful for treating hyperglycaemia. Genomic sequences of
CC the invention are useful for gene therapy e.g., SNARE YKT6 is useful to
CC modulate or prevent cell apoptosis and treat disorder such as virus-
CC induced lymphocyte depletion (AIDS-acquired immune deficiency syndrome),
CC cell death in neurodegenerative disorders (e.g., Alzheimer's disease,
CC Parkinson's disease, ALS (amyotrophic lateral sclerosis), retinitis
CC pigmentosa, spinal muscular atrophy and various forms of cerebellar
CC degeneration), cell death in blood cell disorders resulting from the
CC deprivation of growth factors (anaemia associated with chronic disease,
CC aplastic anaemia, chronic neutropenia and myelodysplastic syndromes)
CC and disorders arising from acute loss of blood flow such as stroke and
CC myocardial infarctions. Glucokinase gene is useful for treating diabetes
CC mellitus. AEBP is useful in modulating or inhibiting adipogenesis and
CC in treating obesity, diabetes mellitus or osteopenic disorders. POLD2 is
CC useful in treating defects in DNA repair such as xeroderma pigmentosum,
CC progeria and ataxia telangiectasia. The present sequence is human POLD2
CC genomic DNA.
XX
XX SQ Sequence 18997 BP; 4650 A; 4852 C; 5028 G; 4467 T; 0 other;
XX
XX Query Match 21.4%; Score 40; DB 24; Length 18997;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-10;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 66
Db 6339 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 6300
XX
XX RESULT 5
XX AAS20588
XX ID AAS20588 standard; DNA; 84495 BP.
XX AC AAS20588;
XX XX
XX 23-APR-2002 (first entry)
XX
XX Human methionine aminopeptidase protease genomic DNA.
XX
XX Human; methionine aminopeptidase; protease; adrenal cortico adenoma; ds;
KW Cushing's syndrome; prostate embryonal carcinoma; colon tumour; brain;
KW hepatocellular carcinoma; foetal lung; testis; b cell; kidney; prostate;
KW gene.
XX
XX Homo sapiens.
XX
XX US6329188-B1.
XX
XX 11-DEC-2001.
XX
XX 05-MAR-2001; 2001US-0797906.
XX
XX 02-MAR-2001; 2001US-0797000.
XX
XX (PEKE ) PE CORP NY.
XX
XX PA
```



CC DNA encoding GST-4alpha and GST-4beta. GST-4 gene is found on  
CC chromosome 16q23.1.  
CC GST is a type 2 membrane protein useful for inhibiting a binding event  
CC between a selectin and a selectin ligand, which comprises contacting the  
CC selectin with a non-sulphated selectin ligand. GST and a small molecular  
CC agent that inhibits the sulphation activity of GST. GST is also useful  
CC in inhibiting a selectin mediated binding event. GST is useful in gene  
CC therapy to treat disorders such as acute or chronic inflammation,  
CC systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis  
CC nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes,  
CC glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's  
CC disease, Grave's disease, adrenailitis, hypoparathyroidism, pernicious  
CC anaemia, demyelinating diseases, cirrhosis, ulcerative colitis,  
CC dermatitis, myocarditis, regional enteritis, adult respiratory distress  
CC syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis,  
CC bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection  
CC during transplantation.

XX Sequence 160552 BP; 40281 A; 37573 C; 38015 G; 44564 T; 119 other;

Query Match 21.4%; Score 40; DB 22; Length 160552;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 27 ACTCCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 66  
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Db 24529 ACTCCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 24490

#### RESULT 7

AAS17764  
ID AAS17764 standard; DNA; 24843 BP.

XX AAS17764;

DT 12-MAR-2002 (first entry)

XX Human Genomic DNA for CRYBB1.

XX Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmological;  
KW cataract; allele specific oligonucleotide; ASO; ds; haplotype;  
KW genotyping; transgenic animal.

OS Homo sapiens.

XX Key Location/Qualifiers  
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FT /product= "CRYBB1"  
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FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism"  
FT /note= "Polymorphic site 1"  
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XX WO200185998-A1.

XX 15-NOV-2001.

XX 07-MAY-2001; 2001WO-US14715.

XX 05-MAY-2000; 2000US-202253P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Kazemi A, Kliem SE, Koshy B, Rounds E;

XX WPI; 2002-0622253/08.  
XX P-PSDB; AAU11447.

XX Novel polymorphic variants of crystallin, beta B1 useful in studying  
FT expression and function of the protein, useful for screening candidate  
FT drugs to treat diseases e.g. cataract

XX Claim 19; Fig 1; 94pp; English.

XX The invention relates to an isolated polynucleotide comprising a  
CC sequence which is a polymorphic variant of a reference sequence for  
CC crystallin, beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their  
CC fragment, where the polymorphic variant comprises a CRYBB1 isogene  
CC defined by a haplotype from haplotypes 1-16 as given in the  
CC specification. Also included are a transgenic non-human animal  
CC transformed or transfected with the polymorphic variant, a computer  
CC system for storing and analysing polymorphism data for CRYBB1 gene, a  
CC genome anthology for the CRYBB1 gene which comprises the defined CRYBB1  
CC isogenes, methods of determining an individual's haplotype or  
CC genotype as well as methods of determining the association of a  
CC particular haplotype with a disease or trait and a composition comprising  
CC at least one genotyping oligonucleotide (especially allele-specific  
CC oligonucleotides (ASO)) for detecting a polymorphism in the CRYBB1.  
CC The isogenes or haplotypes are useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with CRYBB1 activity, e.g. cataract.  
CC and can also be used by the pharmaceutical research scientist to  
CC validate CRYBB1 as a candidate target for, and in design of clinical  
CC trials of candidate drugs for, treating a specific condition or  
CC disease predicted to be associated with CRYBB1 activity. The ASOs are  
CC useful as probes and primers, and for assaying a polymorphism in the  
CC target region. The present sequence is the genomic DNA encoding  
CC CRYBB1.

XX Sequence 24843 BP; 6532 A; 6034 C; 5997 G; 6280 T; 0 other;

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Query Match          20.3%; Score 38; DB 24; Length 24843;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      29 TCCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 66
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RESULT 8
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ID   ABAI5496 standard; DNA; 328 BP.
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AC   ABAI5496;
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DT   23-JAN-2002 (first entry)
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DE   Human nervous system related polynucleotide SEQ ID NO 7827.
XX
KW   Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW   antiparkinsonian; antieckling; antianemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antilulcer; anticonvulsant; antifungal;
KW   antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
XX   WO200159063-A2.
XX
PD   16-AUG-2001.
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XX   17-JAN-2001; 2001WO-US01334.
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PR   31-JAN-2000; 2000US-0179065.
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PR   17-NOV-2000; 2000US-0249213.
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PR 05-DEC-2000; 2000US-0251030.
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PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 03-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure; SEQ ID NO 7827; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABAI1004-ABA21534) and proteins
XX (ABBI4678-ABBI18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful
XX in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 328 BP; 86 A; 78 C; 75 G; 89 T; 0 other;
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XX Query Match 19.8%; Score 37; DB 22; Length 328;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-08;
XX Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTC 63
XX
XX 109 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTC 73
XX
XX
XX RESULT 9
XX AAI96106
XX ID AAI96106 standard; cDNA; 831 BP.
XX
XX AC AAI96106;
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```
XX
XX 13-NOV-2001 (first entry)
XX
XX Human neuroblastoma expressed polynucleotide SEQ ID NO 2181.
XX
XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
XX
XX Homo sapiens.
XX
XX WO2001.66719-A1.
XX
XX 13-SEP-2001.
XX
XX 02-MAR-2001; 2001WO-JP01629.
XX
XX 07-MAR-2000; 2000JP-0159195.
XX
XX (CHIB-) CHIBA PREFECTURE.
XX (HISM) HISAMITSU PHARM CO LTD.
XX
XX Nakagawara A;
XX
XX WPI; 2001-565584/63.
XX
XX Nucleic acids originating in gene expressed in human neuroblastoma,
XX useful as probe or primer in diagnosing prognosis of human
XX neuroblastoma, malignancy and susceptibility indicator or tumour marker
XX for anti-cancer agents -
XX
XX Claim 1; Page 1608-1609; 2979pp; Japanese.
XX
XX The invention relates to novel genes (AAI93926-AAI97963) expressed in
XX human neuroblastoma. The nucleic acids are applicable as a probe or
XX primer in diagnosing the prognosis of human neuroblastoma, malignancy and
XX susceptibility indicators or tumour markers for anti-cancer agents. The
XX gene information for diagnosing prognosis is related to factors similar
XX to that for N-myc and TrkA genes.
XX
XX Sequence 831 BP; 220 A; 156 C; 166 G; 256 T; 33 other;
XX
XX Query Match 19.3%; Score 36; DB 22; Length 831;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-08;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 31 CTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCTCAA 66
XX
XX 222 CTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCTCAA 257
XX
XX
XX RESULT 10
XX AAL36563
XX ID AAL36563 standard; DNA; 27483 BP.
XX
XX AAL36563;
XX
XX 08-JAN-2002 (first entry)
XX
XX Human musculoskeletal system related polynucleotide SEQ ID NO 2928.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;
XX musculoskeletal system; ds.
XX
XX Homo sapiens.
XX
XX WO2001.55367-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01338.
XX
XX PF
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XX PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 13-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
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PR 11-JUL-2000; 2000US-0217487.  
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PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
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PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
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PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
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PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
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PR 14-SEP-2000; 2000US-0232401.  
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PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
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PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-024617.  
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PR 08-NOV-2000; 2000US-0246523.  
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PR 08-NOV-2000; 2000US-0246613.  
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PR 17-NOV-2000; 2000US-0249213.  
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PR 17-NOV-2000; 2000US-0249215.  
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PR 17-NOV-2000; 2000US-0249245.  
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PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249267.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
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PR 06-DEC-2000; 2000US-0251479.  
PR 06-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-451937/48.

XX Isolated polypeptide for treating, preventing and/ or prognosing  
PT disorders related to the musculoskeletal system including

PT musculoskeletal cancers and also for testing and detection e.g.  
XX diagnosis -  
PS Example 2; SEQ ID NO 2928; 781pp + Sequence Listing; English.  
PX  
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins  
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful  
CC for preventing, treating or ameliorating medical conditions e.g. by  
CC protein or gene therapy. The genes are isolated from a range of human  
CC tissues disclosed in the specification. The nucleic acids, proteins,  
CC antibodies and (ant)agonists are useful in the diagnosis, treatment  
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and  
CC other cancers of the adrenal gland, bone, bone marrow, breast,  
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound  
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
CC and (f) infectious diseases such as viral, bacterial, fungal and  
CC parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 27483 BP; 6854 A; 6529 C; 6936 G; 7164 T; 0 other;  
Query Match 19.3%; Score 36; DB 22; Length 27483;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 27 ACTCTGGGTCAGCAATCTCTGCTCAGCCCTT 62  
Db 25969 ACTCTGGGTCAGCAATCTCTGCTCAGCCCTT 26004  
RESULT 11  
AAL06975/c  
ID AAL06975 standard; DNA; 32250 BP.  
XX  
AC AAL06975;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
XX Human reproductive system related antigen DNA SEQ ID NO: 9663.  
DE Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
XX W0200155320-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01339.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
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PR 14-JUL-2000; 2000US-0218290.  
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PR 02-OCT-2000; 2000US-0237039.  
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PR 02-OCT-2000; 2000US-0237040.  
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PR 17-NOV-2000; 2000US-0249214.  
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PR 17-NOV-2000; 2000US-0249216.  
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PR 17-NOV-2000; 2000US-0249287.  
PR 17-NOV-2000; 2000US-0249299.  
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PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
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PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-465570/50.  
XX Isolated nucleic acid molecule encoding a reproductive system antigen -  
PT is used in preventing, treating or ameliorating a medical condition -  
XX Disclosure; SEQ ID NO 9663; 1297pp + Sequence Listing; English.  
XX The present invention provides the protein and coding sequences of a  
CC number of human reproductive system related antigens. These can be used  
CC in the prevention and treatment of reproductive system disorders,  
CC including cancer. The present sequence is a genomic sequence encoding a  
CC protein of the invention.  
XX  
SQ Sequence 32250 BP; 9497 A; 6491 C; 6656 G; 9606 T; 0 other;  
Query Match 19.3%; Score 36; DB 22; Length 32250;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 TACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCT 61  
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Db 1584 TACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCT 1549  
RESULT 12  
ABL84298/c  
ID ABL84298 standard; cDNA; 359 BP.  
XX  
AC ABL84298;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human ovarian cancer related cDNA clone SEQ ID NO:7276.  
XX  
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192581-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 29-MAY-2001; 2001WO-US17756.  
XX  
PR 26-MAY-2000; 2000US-207484P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Algate PA, Harlocker SL, Jones R;  
XX  
DR WPI; 2002-122075/16.  
XX  
PT Composition for therapy and diagnosis of ovarian cancer comprising  
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
PT polypeptide, antibody specific to polypeptide or T cell expressing  
XX polypeptide  
PS Claim 1; SEQ ID 7276; 489pp; English.  
XX  
CC The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL87934. (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (S1) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.  
XX  
SQ Sequence 359 BP; 116 A; 57 C; 69 G; 117 T; 0 other;  
Query Match 18.7%; Score 35; DB 24; Length 359;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCT 61  
|||||  
Db 335 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCT 301  
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RESULT 13  
AAI86984/c



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ID  AAI85984 standard; cDNA; 406 BP.
XX
AC  AAI86984;
XX
DT
XX  06-NOV-2001 (first entry)
XX
DE  Human polynucleotide SEQ ID NO 7044.
XX
XX  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorders; arthritis; inflammation; ss.
XX
OS  Homo sapiens.
XX
PN  WO200164835-A2.
XX
PD  07-SEP-2001.
XX
PF  26-FEB-2001; 2001WO-US04927.
XX
PR  28-FEB-2000; 2000US-0515126.
XX  18-MAY-2000; 2000US-0577409.
XX  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Drmanac RT;
XX  WPI; 2001-514838/56.
XX  P-PSDB; AAO07053.
XX
PT  Isolated nucleic acids and polypeptides, useful for preventing
PT  diagnosing and treating e.g. leukaemia, inflammation and immune
PT  disorders -
XX
XX  Claim 1; SEQ ID NO 7044; 1399pp + Sequence Listing; English.
XX
CC  The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC  the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC  cytokine, cell proliferation or cell differentiation or which may induce
CC  production of other cytokines in other cell populations. The
CC  polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC  peptide therapy. The polypeptides have various cytokine-like activities,
CC  e.g. stem cell growth factor activity, haematopoiesis regulating
CC  activity, tissue growth factor activity, immunomodulatory activity and
CC  activin/inhibin activity and may be useful in the diagnosis and/or
CC  treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC  inflammation.
CC  Note: The sequence data for this patent did not form part of the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 406 BP; 138 A; 64 C; 90 G; 114 T; 0 other;

Query Match      18.7%; Score 35; DB 22; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC  AAI88863;
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DT  06-NOV-2001 (first entry)
XX
DE  Human polynucleotide SEQ ID NO 8923.
XX
XX  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorders; arthritis; inflammation; ss.
XX
OS  Homo sapiens.
XX
PN  WO200164835-A2.
XX
PD  07-SEP-2001.
XX
PF  26-FEB-2001; 2001WO-US04927.
XX
PR  28-FEB-2000; 2000US-0515126.
XX  18-MAY-2000; 2000US-0577409.
XX  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Drmanac RT;
XX  WPI; 2001-514838/56.
XX  P-PSDB; AAO07053.
XX
PT  Isolated nucleic acids and polypeptides, useful for preventing
PT  diagnosing and treating e.g. leukaemia, inflammation and immune
PT  disorders -
XX
XX  Claim 1; SEQ ID NO 8923; 1399pp + Sequence Listing; English.
XX
CC  The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC  the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC  cytokine, cell proliferation or cell differentiation or which may induce
CC  production of other cytokines in other cell populations. The
CC  polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC  peptide therapy. The polypeptides have various cytokine-like activities,
CC  e.g. stem cell growth factor activity, haematopoiesis regulating
CC  activity, tissue growth factor activity, immunomodulatory activity and
CC  activin/inhibin activity and may be useful in the diagnosis and/or
CC  treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC  inflammation.
CC  Note: The sequence data for this patent did not form part of the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 414 BP; 91 A; 96 C; 81 G; 146 T; 0 other;

Query Match      18.7%; Score 35; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT  09-APR-2001 (first entry)
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KW  Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KW  breast cancer; lung cancer; cancer detection; ss.
XX
XX  Homo sapiens.
XX
PN  WO200102568-A2.
XX
PD  11-JAN-2001.
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XX 30-JUN-2000; 2000WO-US18374.  
XX  
XX  
XX 02-JUL-1999; 99US-0142310.  
XX 02-JUL-1999; 99US-0142311.  
XX  
XX (CHIR ) CHIRON CORP.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;  
XX Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;  
XX Crkenjakov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;  
XX Kita D, Garcia V, Jones LW, Strache-Crain B;  
XX  
XX WPI; 2001-091805/10.  
XX  
XX Library of polynucleotides for diagnosing a cancerous state of a  
XX mammalian cell and detecting cancer, particularly of the colon or  
XX prostate, comprises 3351 human polynucleotide sequences -  
XX  
XX Claim 9; Page 981; 1046pp; English.  
XX  
XX The present sequence is one of 3351 sequences in a library of human  
XX polynucleotides. The library is used to detect differentially expressed  
XX genes correlated with a cancerous state of a mammalian cell and can  
XX detect colon, prostate, breast and lung cancer. The library can be used  
XX to produce probes for detection of mRNA and to produce additional copies  
XX of the polynucleotides. The probes can be used for chromosome mapping of  
XX the polynucleotide and for detection of transcription levels. Ribozymes  
XX or antisense oligonucleotides can be generated. The polynucleotides and  
XX their gene products are used as genetic or biochemical markers (e.g. in  
XX blood or tissues) that will detect the earliest changes along the  
XX carcinogenesis pathway and/or monitor the efficacy of therapies and  
XX preventive interventions. The polynucleotides, polypeptides and  
XX antibodies against them can be used in pharmaceutical compositions to  
XX treat the cancers and proliferative disorders such as neoplasia,  
XX dysplasia and hyperplasia.  
XX  
XX SQ Sequence 417 BP; 152 A; 91 C; 102 G; 72 T; 0 other;

Query Match 18.7%; Score 35; DB 22; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size :

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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16	28	15.0	11811	4	US-09-078-294-7	Sequence 7, Appli	
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c 104	23	12.3	35100	5	PCT-US93-06251-19	Sequence 19, Appl	c 177	21	11.2	3741	4	US-09-723-820-9	Sequence 9, Appl
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c 139	22	11.8	10898	3	US-08-787-739-5	Sequence 5, Appl	c 212	20	10.7	347	4	US-09-127-480-44	Sequence 44, Appl
c 140	22	11.8	10898	3	US-08-487-077A-5	Sequence 5, Appl	c 213	20	10.7	347	4	US-08-496-841C-44	Sequence 44, Appl
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c 144	22	11.8	10898	4	US-09-177-776-5	Sequence 5, Appl	c 217	20	10.7	693	4	US-09-712-016-12	Sequence 12, Appl
c 145	22	11.8	17425	4	US-09-511-625B-5	Sequence 5, Appl	c 218	20	10.7	950	4	US-08-991-789A-6	Sequence 6, Appl
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C 248	20	10.7	2562	1	US-08-146-421-4	Sequence 4, Appli	321	19	10.2	4016	1	US-08-410-540-3	Sequence 3, Appli
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C 399	19	10.2	70000	4	US-08-851-896-3	Sequence 3, Appl	C 472	18	9.6	1361	4	US-09-119-264-1	Sequence 1, Appl
C 400	19	10.2	70000	4	US-08-268-992-7	Sequence 7, Appl	C 473	18	9.6	1371	3	US-08-884-324-11	Sequence 11, Appl
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C 441	18	9.6	500	4	US-08-496-841C-86	Sequence 86, Appl	514	18	9.6	3117	4	US-09-146-580-6	Sequence 6, Appl
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C 454	18	9.6	512	4	US-09-177-776-45	Sequence 45, Appl	C 527	18	9.6	5092	4	PCT-US96-01314-39	Sequence 39, Appl
C 455	18	9.6	548	4	US-08-991-789A-15	Sequence 15, Appl	C 528	18	9.6	5137	5	PCT-US96-01314-39	Sequence 39, Appl
C 456	18	9.6	548	4	US-09-062-451-15	Sequence 15, Appl	C 529	18	9.6	5138	2	US-08-476-062A-39	Sequence 39, Appl
C 457	18	9.6	548	4	US-09-598-326-15	Sequence 15, Appl	C 530	18	9.6	5262	4	US-08-520-373D-5	Sequence 5, Appl
C 458	18	9.6	553	4	US-09-227-357-94	Sequence 94, Appl	531	18	9.6	6669	3	US-09-212-971-5	Sequence 5, Appl
C 459	18	9.6	602	4	US-09-078-294-27	Sequence 27, Appl	532	18	9.6	6669	3	US-08-800-929A-5	Sequence 5, Appl
C 460	18	9.6	624	4	US-09-385-982-414	Sequence 414, App	533	18	9.6	6669	4	US-09-617-053A-5	Sequence 5, Appl
C 461	18	9.6	685	4	US-09-227-357-100	Sequence 100, App	534	18	9.6	8133	4	US-09-659-791A-10	Sequence 10, Appl
C 462	18	9.6	690	4	US-08-328-111-74	Sequence 74, Appl	C 535	18	9.6	8353	3	US-08-611-587-1	Sequence 1, Appl
C 463	18	9.6	817	1	US-08-672-569-2	Sequence 2, Appl	C 536	18	9.6	8982	3	US-08-976-255-5	Sequence 5, Appl
C 464	18	9.6	949	4	US-09-247-155-148	Sequence 148, App	C 537	18	9.6	9704	4	US-09-814-951A-3	Sequence 3, Appl
C 465	18	9.6	1000	4	US-09-018-584A-33	Sequence 33, Appl	538	18	9.6	9734	4	US-09-347-114A-80	Sequence 80, Appl

C 539	18	9.6	10684	3	US-08-618-100B-3	Sequence 3, Appli	c 612	17	9.1	1043	4	US-09-165-868-4	Sequence 4, Appli
C 540	18	9.6	10898	2	US-08-481-658B-5	Sequence 5, Appli	613	17	9.1	1048	4	US-09-227-357-145	Sequence 145, App
C 541	18	9.6	10898	2	US-08-477-504A-5	Sequence 5, Appli	614	17	9.1	1247	4	US-09-178-115-110	Sequence 110, App
C 542	18	9.6	10898	2	US-08-486-756A-5	Sequence 5, Appli	615	17	9.1	1247	4	US-09-177-776-110	Sequence 110, App
C 543	18	9.6	10898	2	US-08-485-862B-5	Sequence 5, Appli	616	17	9.1	1287	4	US-09-564-805-217	Sequence 217, App
C 544	18	9.6	10898	3	US-08-787-739-5	Sequence 5, Appli	617	17	9.1	1320	1	US-08-599-252-84	Sequence 84, Appl
C 545	18	9.6	10898	3	US-08-487-077A-5	Sequence 5, Appli	618	17	9.1	1320	1	US-08-436-074-57	Sequence 57, Appl
C 546	18	9.6	10898	3	US-08-485-863A-5	Sequence 5, Appli	619	17	9.1	1320	1	PCT-US96-06352-84	Sequence 84, Appl
C 547	18	9.6	10898	4	US-08-485-049D-5	Sequence 5, Appli	620	17	9.1	1320	5	PCT-US96-06583-84	Sequence 84, Appl
C 548	18	9.6	10898	4	US-09-178-115-5	Sequence 5, Appli	621	17	9.1	1407	1	US-09-153-804-6	Sequence 6, Appli
C 549	18	9.6	10898	4	US-08-177-776-5	Sequence 5, Appli	622	17	9.1	1526	1	US-08-694-915-3	Sequence 3, Appli
C 550	18	9.6	10952	1	US-08-602-036A-1	Sequence 1, Appli	623	17	9.1	1600	2	US-08-487-113B-117	Sequence 117, App
C 551	18	9.6	10952	2	US-08-602-374A-1	Sequence 1, Appli	624	17	9.1	1600	2	US-08-720-420A-117	Sequence 117, App
C 552	18	9.6	10952	2	US-08-642-407A-1	Sequence 1, Appli	625	17	9.1	1640	1	US-08-068-945A-32	Sequence 32, Appl
C 553	18	9.6	11298	2	US-07-869-933-31	Sequence 31, Appl	626	17	9.1	1640	1	US-08-442-806-32	Sequence 32, Appl
C 554	18	9.6	11298	1	US-08-201-879A-2	Sequence 2, Appli	627	17	9.1	2178	3	US-08-781-891-72	Sequence 72, Appl
C 555	18	9.6	11298	4	US-09-103-663-31	Sequence 31, Appl	628	17	9.1	2201	1	US-08-580-401-1	Sequence 1, Appli
C 556	18	9.6	12565	4	US-08-345-217-3	Sequence 3, Appli	629	17	9.1	2316	1	US-08-135-511-34	Sequence 34, Appl
C 557	18	9.6	12847	1	US-08-550-715-1	Sequence 1, Appli	630	17	9.1	2316	1	US-08-483-852-11	Sequence 11, Appl
C 558	18	9.6	13158	2	US-08-687-080-105	Sequence 105, App	631	17	9.1	2316	1	US-08-361-458-6	Sequence 6, Appli
C 559	18	9.6	14581	4	US-08-520-373D-4	Sequence 4, Appli	632	17	9.1	2316	1	US-08-477-953-11	Sequence 11, Appl
C 560	18	9.6	15297	4	US-09-817-180-3	Sequence 3, Appli	633	17	9.1	2316	1	US-08-187-453-34	Sequence 34, Appl
C 561	18	9.6	15977	4	US-09-608-285A-59	Sequence 59, Appl	634	17	9.1	2316	2	US-08-477-952-11	Sequence 11, Appl
C 562	18	9.6	18073	4	US-08-078-294-12	Sequence 12, Appl	635	17	9.1	2501	3	US-08-787-739-58	Sequence 58, Appl
C 563	18	9.6	20674	4	US-09-641-638-651	Sequence 651, App	636	17	9.1	2501	4	US-09-178-115-58	Sequence 58, Appl
C 564	18	9.6	22481	4	US-08-367-841A-43	Sequence 43, Appl	637	17	9.1	2501	4	US-09-177-776-58	Sequence 58, Appl
C 565	18	9.6	22481	5	PCT-US95-07201-43	Sequence 43, Appl	638	17	9.1	2688	2	US-08-909-965C-1	Sequence 1, Appli
C 566	18	9.6	22484	4	US-09-875-223-2	Sequence 2, Appli	639	17	9.1	2964	2	US-08-846-790A-2	Sequence 2, Appli
C 567	18	9.6	28001	4	US-09-819-993-3	Sequence 3, Appli	640	17	9.1	2964	3	US-08-935-333-2	Sequence 2, Appli
C 568	18	9.6	35060	3	US-08-814-095-7	Sequence 7, Appli	641	17	9.1	3373	1	US-08-273-411-2	Sequence 2, Appli
C 569	18	9.6	35828	4	US-09-449-218D-17	Sequence 17, Appl	642	17	9.1	3532	3	US-08-787-739-90	Sequence 90, Appl
C 570	18	9.6	40328	3	US-08-742-185-102	Sequence 102, App	643	17	9.1	3532	4	US-09-178-115-90	Sequence 90, Appl
C 571	18	9.6	43795	3	US-08-742-185-101	Sequence 101, App	644	17	9.1	3532	4	US-09-177-776-90	Sequence 90, Appl
C 572	18	9.6	45546	4	US-09-146-053-6	Sequence 6, Appli	645	17	9.1	3601	3	US-09-017-631-23	Sequence 23, Appl
C 573	18	9.6	45716	4	US-08-965-048-5	Sequence 5, Appli	646	17	9.1	3602	2	US-08-883-795A-33	Sequence 33, Appl
C 574	18	9.6	45989	4	US-08-965-048-6	Sequence 6, Appli	647	17	9.1	3602	4	US-09-018-138-1	Sequence 1, Appli
C 575	18	9.6	55827	4	US-08-813-133A-3	Sequence 3, Appli	648	17	9.1	3609	4	US-09-705-299-11	Sequence 11, Appl
C 576	18	9.6	98844	4	US-09-791-211-30	Sequence 10, Appl	649	17	9.1	3683	4	US-08-450-962-1	Sequence 1, Appli
C 577	18	9.6	111282	4	US-09-754-250-3	Sequence 3, Appli	650	17	9.1	3848	4	US-09-112-096-28	Sequence 28, Appl
C 578	18	9.6	169998	4	US-09-676-610B-24	Sequence 24, Appl	651	17	9.1	3865	1	US-08-832-883-48	Sequence 48, Appl
C 579	17	9.1	98	4	US-08-991-789A-282	Sequence 282, App	652	17	9.1	3865	2	US-08-832-877-48	Sequence 48, Appl
C 580	17	9.1	98	4	US-09-062-451-282	Sequence 282, App	653	17	9.1	4233	4	US-09-056-105-27	Sequence 27, Appl
C 581	17	9.1	191	4	US-09-276-531-36	Sequence 36, Appl	654	17	9.1	4550	4	US-09-103-663-35	Sequence 35, Appl
C 582	17	9.1	211	2	US-08-332-766A-34	Sequence 34, Appl	655	17	9.1	4793	4	US-09-561-497-10	Sequence 10, Appl
C 583	17	9.1	262	2	US-08-481-658B-57	Sequence 57, Appl	656	17	9.1	5037	4	US-09-705-299-13	Sequence 13, Appl
C 584	17	9.1	262	2	US-08-481-658B-60	Sequence 60, Appl	657	17	9.1	5543	2	US-08-687-080-101	Sequence 101, App
C 585	17	9.1	262	2	US-08-477-504A-57	Sequence 57, Appl	658	17	9.1	5668	4	US-09-112-096-14	Sequence 14, Appl
C 586	17	9.1	262	2	US-08-477-504A-60	Sequence 60, Appl	659	17	9.1	5668	4	US-09-605-785-777	Sequence 777, App
C 587	17	9.1	262	2	US-08-486-756A-57	Sequence 57, Appl	660	17	9.1	5892	3	US-08-755-587-27	Sequence 27, Appl
C 588	17	9.1	262	2	US-08-486-756A-60	Sequence 60, Appl	661	17	9.1	6769	1	US-08-480-784-20	Sequence 20, Appl
C 589	17	9.1	262	2	US-08-485-862B-57	Sequence 57, Appl	662	17	9.1	6769	1	US-08-483-553-20	Sequence 20, Appl
C 590	17	9.1	262	2	US-08-485-862B-60	Sequence 60, Appl	663	17	9.1	6769	1	US-08-487-002-20	Sequence 20, Appl
C 591	17	9.1	262	3	US-08-787-739-57	Sequence 57, Appl	664	17	9.1	6769	1	US-08-483-554B-20	Sequence 20, Appl
C 592	17	9.1	262	3	US-08-787-739-60	Sequence 60, Appl	665	17	9.1	6769	1	US-08-488-011B-20	Sequence 20, Appl
C 593	17	9.1	262	3	US-08-487-077A-57	Sequence 57, Appl	666	17	9.1	6769	4	US-08-850-727-20	Sequence 20, Appl
C 594	17	9.1	262	3	US-08-487-077A-60	Sequence 60, Appl	667	17	9.1	6769	5	PCT-US95-10203-20	Sequence 20, Appl
C 595	17	9.1	262	3	US-08-485-863A-57	Sequence 57, Appl	668	17	9.1	6769	5	PCT-US95-10203-20	Sequence 20, Appl
C 596	17	9.1	262	3	US-08-485-863A-60	Sequence 60, Appl	669	17	9.1	6769	5	PCT-US95-10220-20	Sequence 20, Appl
C 597	17	9.1	262	4	US-08-485-049D-60	Sequence 60, Appl	670	17	9.1	7152	4	US-09-167-681-29	Sequence 29, Appl
C 598	17	9.1	262	4	US-09-178-115-57	Sequence 57, Appl	671	17	9.1	8174	1	US-07-914-241-5	Sequence 5, Appli
C 599	17	9.1	262	4	US-09-178-115-60	Sequence 60, Appl	672	17	9.1	8174	1	US-08-393-246-5	Sequence 5, Appli
C 600	17	9.1	262	4	US-09-177-776-57	Sequence 57, Appl	673	17	9.1	8174	2	US-08-525-058A-5	Sequence 5, Appli
C 601	17	9.1	262	4	US-09-177-776-60	Sequence 60, Appl	674	17	9.1	8174	2	US-08-696-731-5	Sequence 5, Appli
C 602	17	9.1	461	4	US-09-404-879A-47	Sequence 47, Appl	675	17	9.1	8174	4	US-09-042-531-5	Sequence 5, Appli
C 603	17	9.1	490	4	US-09-328-111-41	Sequence 41, Appl	676	17	9.1	8174	5	PCT-US91-00899-3	Sequence 3, Appli
C 604	17	9.1	529	4	US-09-232-575-100	Sequence 100, App	677	17	9.1	8396	4	US-09-328-174A-1	Sequence 1, Appli
C 605	17	9.1	688	6	5498694-3	Patent No. 5498694	678	17	9.1	8409	4	US-09-167-681-37	Sequence 37, Appl
C 606	17	9.1	799	4	US-09-166-350-11	Sequence 11, Appl	679	17	9.1	8453	3	US-09-167-681-45	Sequence 45, Appl
C 607	17	9.1	1000	4	US-09-018-584A-30	Sequence 30, Appl	680	17	9.1	8835	3	US-08-884-324-10	Sequence 10, Appl
C 608	17	9.1	1000	4	US-09-018-584A-31	Sequence 31, Appl	681	17	9.1	9365	4	US-09-608-285A-8	Sequence 8, Appli
C 609	17	9.1	1000	4	US-09-641-638-647	Sequence 647, App	682	17	9.1	9365	4	US-09-350-836B-8	Sequence 8, Appli
C 610	17	9.1	1001	4	US-09-641-638-113	Sequence 113, App	683	17	9.1	9365	4	US-09-370-265-8	Sequence 8, Appli
C 611	17	9.1	1001	4	US-09-641-638-381	Sequence 381, App	684	17	9.1	10642	4	US-09-934-551-3	Sequence 3, Appli

c 685	17	9.1	11531	1	US-08-068-945A-1	Sequence 1, Appli	c 758	16	8.6	411	4	US-09-385-982-5	Sequence 5, Appli
c 686	17	9.1	11531	1	US-08-442-806-1	Sequence 1, Appli	759	16	8.6	418	4	US-08-642-274D-46	Sequence 46, Appl
c 687	17	9.1	14747	4	US-09-608-285A-42	Sequence 42, Appl	760	16	8.6	418	4	US-08-952-014C-46	Sequence 46, Appl
c 688	17	9.1	14753	4	US-09-821-736-3	Sequence 3, Appli	c 761	16	8.6	443	4	US-09-385-982-28	Sequence 28, Appl
c 689	17	9.1	15328	2	US-08-888-497-33	Sequence 33, Appl	c 762	16	8.6	456	4	US-09-427-357-110	Sequence 110, App
c 690	17	9.1	15328	4	US-09-362-230-33	Sequence 33, Appl	c 763	16	8.6	471	4	US-09-018-584A-6	Sequence 6, Appli
c 691	17	9.1	15328	5	PCT-US94-07926-33	Sequence 33, Appl	764	16	8.6	476	4	US-09-020-956-80	Sequence 80, Appl
c 692	17	9.1	15581	3	US-08-646-538-35	Sequence 35, Appl	765	16	8.6	476	4	US-09-030-607-80	Sequence 80, Appl
c 693	17	9.1	15581	4	US-09-503-222-35	Sequence 35, Appl	766	16	8.6	476	4	US-09-605-785-80	Sequence 80, Appl
c 694	17	9.1	17949	4	US-09-087-465-3	Sequence 3, Appli	767	16	8.6	476	4	US-09-439-313-80	Sequence 80, Appl
c 695	17	9.1	32042	4	US-09-245-281-44	Sequence 44, Appl	768	16	8.6	476	4	US-09-352-616A-80	Sequence 80, Appl
c 696	17	9.1	40000	4	US-09-780-049-18	Sequence 18, Appl	769	16	8.6	476	4	US-09-232-149A-80	Sequence 80, Appl
c 697	17	9.1	56516	2	US-08-996-306-1	Sequence 1, Appli	770	16	8.6	479	4	US-09-030-607-182	Sequence 182, App
c 698	17	9.1	56516	4	US-09-338-907-1	Sequence 1, Appli	771	16	8.6	479	4	US-09-605-785-182	Sequence 182, App
c 699	17	9.1	56516	4	US-09-218-207-1	Sequence 1, Appli	772	16	8.6	479	4	US-09-439-313-182	Sequence 182, App
c 700	17	9.1	56520	4	US-09-338-907-179	Sequence 179, App	773	16	8.6	479	4	US-09-352-616A-182	Sequence 182, App
c 701	17	9.1	56520	4	US-09-218-207-179	Sequence 179, App	774	16	8.6	479	4	US-09-232-149A-182	Sequence 182, App
c 702	17	9.1	90050	4	US-09-245-041-5	Sequence 5, Appli	c 775	16	8.6	485	2	US-08-332-766A-18	Sequence 18, Appl
c 703	17	9.1	168575	4	US-09-426-290-1	Sequence 1, Appli	c 776	16	8.6	492	4	US-09-280-116-208	Sequence 208, App
c 704	17	8.6	20	4	US-08-286-959B-12	Sequence 12, Appl	777	16	8.6	504	4	US-09-328-111-123	Sequence 123, App
c 705	16	8.6	60	3	US-08-545-860D-71	Sequence 71, Appl	c 778	16	8.6	520	4	US-08-642-274D-57	Sequence 57, Appl
c 706	16	8.6	60	3	US-08-545-860D-72	Sequence 72, Appl	c 779	16	8.6	520	4	US-08-952-014C-57	Sequence 57, Appl
c 707	16	8.6	60	5	PCT-US94-04496-71	Sequence 71, Appl	c 780	16	8.6	534	1	US-08-599-252-101	Sequence 101, App
c 708	16	8.6	66	2	PCT-US94-04496-72	Sequence 72, Appl	c 781	16	8.6	534	5	PCT-US96-06583-101	Sequence 101, App
c 709	16	8.6	66	2	US-08-454-557C-67	Sequence 67, Appl	c 782	16	8.6	534	5	PCT-US96-06583-101	Sequence 101, App
c 710	16	8.6	66	2	US-08-340-426D-67	Sequence 67, Appl	c 783	16	8.6	542	4	US-09-305-639-5	Sequence 5, Appli
c 711	16	8.6	66	2	US-08-450-673C-67	Sequence 67, Appl	c 784	16	8.6	578	4	US-09-385-982-11	Sequence 11, Appl
c 712	16	8.6	66	5	PCT-US95-17111A-67	Sequence 67, Appl	c 785	16	8.6	585	4	US-08-991-789A-39	Sequence 39, Appl
c 713	16	8.6	141	4	US-09-404-879A-58	Sequence 58, Appl	c 786	16	8.6	585	4	US-09-062-451-39	Sequence 39, Appl
c 714	16	8.6	167	2	US-08-454-557C-90	Sequence 90, Appl	c 787	16	8.6	585	4	US-09-598-326-39	Sequence 39, Appl
c 715	16	8.6	167	2	US-08-340-426D-90	Sequence 90, Appl	c 788	16	8.6	588	4	US-09-385-982-128	Sequence 128, App
c 716	16	8.6	167	2	US-08-450-673C-90	Sequence 90, Appl	c 789	16	8.6	610	1	US-08-661-168-5	Sequence 5, Appli
c 717	16	8.6	167	5	PCT-US95-17111A-90	Sequence 90, Appl	c 790	16	8.6	618	4	US-09-385-982-373	Sequence 373, App
c 718	16	8.6	200	1	US-08-438-500-1	Sequence 1, Appli	c 791	16	8.6	629	4	US-09-385-982-204	Sequence 204, App
c 719	16	8.6	200	1	US-08-477-442-1	Sequence 1, Appli	c 792	16	8.6	633	4	US-09-328-111-358	Sequence 2, Appli
c 720	16	8.6	200	5	PCT-US94-05910-1	Sequence 1, Appli	793	16	8.6	640	4	US-09-385-982-2	Sequence 2, Appli
c 721	16	8.6	201	2	US-08-849-701-5	Sequence 5, Appli	794	16	8.6	657	4	US-09-385-982-326	Sequence 326, App
c 722	16	8.6	231	4	US-09-605-785-464	Sequence 464, App	c 795	16	8.6	719	4	US-09-227-357-74	Sequence 74, Appl
c 723	16	8.6	231	4	US-09-439-313-464	Sequence 464, App	c 796	16	8.6	722	4	US-09-288-143-63	Sequence 63, Appl
c 724	16	8.6	231	4	US-09-352-616A-464	Sequence 464, App	c 797	16	8.6	774	3	US-08-755-587-20	Sequence 20, Appl
c 725	16	8.6	292	2	US-08-481-658B-56	Sequence 56, Appl	c 798	16	8.6	798	4	US-09-288-143-21	Sequence 21, Appl
c 726	16	8.6	292	2	US-08-481-658B-59	Sequence 59, Appl	c 799	16	8.6	811	4	US-09-404-879A-55	Sequence 55, Appl
c 727	16	8.6	292	2	US-08-477-504A-56	Sequence 56, Appl	c 800	16	8.6	856	4	US-09-288-143-47	Sequence 47, Appl
c 728	16	8.6	292	2	US-08-477-504A-59	Sequence 59, Appl	c 801	16	8.6	859	4	US-09-535-008-58	Sequence 58, Appl
c 729	16	8.6	292	2	US-08-486-756A-56	Sequence 56, Appl	c 802	16	8.6	922	1	US-08-480-784-27	Sequence 27, Appl
c 730	16	8.6	292	2	US-08-486-756A-59	Sequence 59, Appl	c 803	16	8.6	922	1	US-08-483-553-27	Sequence 27, Appl
c 731	16	8.6	292	2	US-08-485-862B-56	Sequence 56, Appl	c 804	16	8.6	922	1	US-08-487-002-27	Sequence 27, Appl
c 732	16	8.6	292	2	US-08-485-862B-59	Sequence 59, Appl	c 805	16	8.6	922	1	US-08-483-554B-27	Sequence 27, Appl
c 733	16	8.6	292	2	US-08-787-739-59	Sequence 59, Appl	c 806	16	8.6	922	1	US-08-488-011B-27	Sequence 27, Appl
c 734	16	8.6	292	3	US-08-787-739-59	Sequence 59, Appl	c 807	16	8.6	922	4	US-08-850-727-27	Sequence 27, Appl
c 735	16	8.6	292	3	US-08-487-077A-56	Sequence 56, Appl	c 808	16	8.6	922	5	PCT-US95-10202-27	Sequence 27, Appl
c 736	16	8.6	292	3	US-08-487-077A-59	Sequence 59, Appl	c 809	16	8.6	922	5	PCT-US95-10203-27	Sequence 27, Appl
c 737	16	8.6	292	3	US-08-485-863A-56	Sequence 56, Appl	c 810	16	8.6	922	5	PCT-US95-10202-27	Sequence 27, Appl
c 738	16	8.6	292	3	US-08-485-863A-59	Sequence 59, Appl	c 811	16	8.6	940	4	US-09-659-791A-11	Sequence 11, Appl
c 739	16	8.6	292	4	US-08-485-049D-59	Sequence 59, Appl	c 812	16	8.6	951	4	US-09-605-785-570	Sequence 570, App
c 740	16	8.6	292	4	US-09-178-115-56	Sequence 56, Appl	c 813	16	8.6	955	4	US-09-641-638-4	Sequence 4, Appli
c 741	16	8.6	292	4	US-09-178-115-59	Sequence 59, Appl	c 814	16	8.6	955	4	US-09-641-638-5	Sequence 5, Appli
c 742	16	8.6	292	4	US-09-177-776-56	Sequence 56, Appl	c 815	16	8.6	955	4	US-09-641-638-7	Sequence 7, Appli
c 743	16	8.6	292	4	US-09-177-776-59	Sequence 59, Appl	c 816	16	8.6	956	4	US-09-641-638-41	Sequence 41, Appl
c 744	16	8.6	295	2	US-08-849-701-8	Sequence 8, Appli	c 817	16	8.6	1000	2	US-08-747-121-20	Sequence 20, Appl
c 745	16	8.6	301	4	US-09-605-785-233	Sequence 233, App	c 818	16	8.6	1000	4	US-09-018-584A-32	Sequence 32, Appl
c 746	16	8.6	301	4	US-09-439-313-233	Sequence 233, App	c 819	16	8.6	1000	4	US-09-641-638-590	Sequence 590, App
c 747	16	8.6	301	4	US-09-352-616A-233	Sequence 233, App	c 820	16	8.6	1000	4	US-09-641-638-650	Sequence 650, App
c 748	16	8.6	301	4	US-09-232-149A-233	Sequence 233, App	c 821	16	8.6	1001	4	US-09-641-638-319	Sequence 319, App
c 749	16	8.6	308	4	US-09-222-575-88	Sequence 88, Appl	c 822	16	8.6	1001	4	US-09-641-638-365	Sequence 365, App
c 750	16	8.6	320	1	US-08-629-939-5	Sequence 5, Appli	c 823	16	8.6	1001	4	US-09-641-638-366	Sequence 366, App
c 751	16	8.6	320	1	US-08-759-873-5	Sequence 5, Appli	c 824	16	8.6	1001	4	US-09-641-638-376	Sequence 376, App
c 752	16	8.6	321	4	US-09-385-982-366	Sequence 366, App	c 825	16	8.6	1001	4	US-09-641-638-448	Sequence 448, App
c 753	16	8.6	371	4	US-09-221-298-96	Sequence 96, Appl	c 826	16	8.6	1002	4	US-09-641-638-581	Sequence 581, App
c 754	16	8.6	374	4	US-09-385-982-135	Sequence 135, App	c 827	16	8.6	1014	4	US-09-257-179-32	Sequence 32, Appl
c 755	16	8.6	380	1	US-08-126-587C-5	Sequence 5, Appli	c 828	16	8.6	1037	4	US-09-257-179-16	Sequence 16, Appl
c 756	16	8.6	410	2	US-08-475-844-16	Sequence 16, Appl	c 829	16	8.6	1050	3	US-08-755-587-21	Sequence 21, Appl
c 757	16	8.6	410	5	PCT-US95-08429-16	Sequence 16, Appl	830	16	8.6	1078	2	US-08-728-521-2	Sequence 2, Appli





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977 16 8.6 4421 4 US-08-367-841A-9
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980 16 8.6 4441 4 US-09-641-999-2
981 16 8.6 4460 4 US-09-103-875-4
982 16 8.6 4543 2 US-08-519-547A-5
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984 16 8.6 4576 1 US-08-832-883-49
985 16 8.6 4576 2 US-08-832-877-49
986 16 8.6 4668 4 US-09-045-301-1
987 16 8.6 4698 4 US-09-439-261-34
988 16 8.6 4698 4 US-09-227-613-33
989 16 8.6 4704 2 US-08-476-062A-52
990 16 8.6 4741 1 US-07-695-472B-4
991 16 8.6 4742 1 US-08-250-740-35
992 16 8.6 4895 3 US-09-053-866-1
993 16 8.6 4895 4 US-09-479-130-1
994 16 8.6 4905 1 US-07-978-895-3
995 16 8.6 4905 1 US-08-473-119-3
996 16 8.6 4905 2 US-08-475-352-3
997 16 8.6 4922 2 US-08-330-272-5
998 16 8.6 4922 5 PCT-US95-13663-5
999 16 8.6 4975 4 US-09-630-706-3
1000 16 8.6 5035 2 US-08-616-392C-3

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## ALIGNMENTS

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RESULT 1
US-09-797-906-3
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO015ICIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

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Query Match 21.4%; Score 40; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 27 ACTCTGGCTCAAGCAATCTCTGCTCAGCCTTCAA 66
Db 9295 ACTCTGGCTCAAGCAATCTCTGCTCAGCCTTCAA 9334

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RESULT 2
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihaian, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric

```

```

; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89.US2.CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; NAME/KEY: primer_bind
; LOCATION: 12029..12050
; OTHER INFORMATION: 17-42.pu
; NAME/KEY: primer_bind
; LOCATION: 12581..12603

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OTHER INFORMATION: 17-42.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 1492..15012  
OTHER INFORMATION: 17-41.pu  
NAME/KEY: primer\_bind  
LOCATION: 15460..15482  
OTHER INFORMATION: 17-41.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 42070..42090  
OTHER INFORMATION: 20-841.pu  
NAME/KEY: primer\_bind  
LOCATION: 42572..42591  
OTHER INFORMATION: 20-841.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 45328..45347  
OTHER INFORMATION: 20-842.pu  
NAME/KEY: primer\_bind  
LOCATION: 45863..45883  
OTHER INFORMATION: 20-842.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 76644..76664  
OTHER INFORMATION: 20-853.pu  
NAME/KEY: primer\_bind  
LOCATION: 77166..77185  
OTHER INFORMATION: 20-853.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 1220..1238  
OTHER INFORMATION: 20-828-311.mis  
NAME/KEY: primer\_bind  
LOCATION: 1240..1258  
OTHER INFORMATION: 20-828-311.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 12328..12346  
OTHER INFORMATION: 17-42-319.mis  
NAME/KEY: primer\_bind  
LOCATION: 12348..12366  
OTHER INFORMATION: 17-42-319.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 15222..15240  
OTHER INFORMATION: 17-41-250.mis  
NAME/KEY: primer\_bind  
LOCATION: 15242..15260  
OTHER INFORMATION: 17-41-250.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 42199..42217  
OTHER INFORMATION: 20-841-149.mis  
NAME/KEY: primer\_bind  
LOCATION: 42219..42237  
OTHER INFORMATION: 20-841-149.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 45423..45441  
OTHER INFORMATION: 20-842-115.mis  
NAME/KEY: primer\_bind  
LOCATION: 45443..45461  
OTHER INFORMATION: 20-842-115.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 77039..77057  
OTHER INFORMATION: 20-853-415.mis  
NAME/KEY: primer\_bind  
LOCATION: 77059..77077  
OTHER INFORMATION: 20-853-415.mis complement  
NAME/KEY: misc binding  
LOCATION: 1227..1251  
OTHER INFORMATION: 20-828-311.probe  
NAME/KEY: misc binding  
LOCATION: 12335..12359  
OTHER INFORMATION: 17-42-319.probe  
NAME/KEY: misc binding  
LOCATION: 15225..15253  
OTHER INFORMATION: 17-41-250.probe  
NAME/KEY: misc binding  
LOCATION: 42206..42230  
OTHER INFORMATION: 20-841-149.probe

NAME/KEY: misc binding  
LOCATION: 45430..45454  
OTHER INFORMATION: 20-842-115.probe  
NAME/KEY: misc binding  
LOCATION: 77046..77070  
OTHER INFORMATION: 20-853-415.probe  
US-09-750-580-1  
Query Match 18.7%; Score 35; DB 4; Length 81001;  
Best Local Similarity 100.0%; Pred. No. 2.3e-08;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61  
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Db 3410 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 3376  
RESULT 3  
US-09-128-155-17  
Sequence 17, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 176373  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(176373)  
OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-17  
Query Match 18.7%; Score 35; DB 3; Length 176373;  
Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61  
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Db 86219 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 86253  
RESULT 4  
US-08-482-728A-3  
Sequence 3, Application US/08482728A  
Patent No. 5968802  
GENERAL INFORMATION:  
APPLICANT: Wang, Bruce  
APPLICANT: Fisher, Joseph  
APPLICANT: Payan, Donald  
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton  
ADDRESSEE: & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,728A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 36,304  
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2589 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93..1652  
US-08-482-728A-3

Query Match 18.2%; Score 34; DB 2; Length 2589;  
Best Local Similarity 100.0%; Pred. No. 7.9e-08;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCCTGGGCTCAAGCAATCTCTGCTCAGCCT 61  
Db 2075 CTCCTGGGCTCAAGCAATCTCTGCTCAGCCT 2108

RESULT 5  
US-08-247-946A-2/c  
Sequence 2, Application US/08247946A  
Patent No. 5792838  
GENERAL INFORMATION:  
APPLICANT: AARONSON, S.A.; CHAN, A.;  
APPLICANT: MIKI, T.  
TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED  
TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA  
TITLE OF INVENTION: CLONING  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/247,946A  
FILING DATE: 24-MAY-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY R. AUTH  
REGISTRATION NUMBER: 36,434  
REFERENCE/DOCKET NUMBER: 2026-4150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3350  
TYPE: Nucleic acid

LENGTH: 3350  
TYPE: Nucleic acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: No  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
FEATURE:  
NAME/KEY: Human R-ras gene  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: exons 2-6.  
US-08-247-946A-2

Query Match 18.2%; Score 34; DB 1; Length 3350;  
Best Local Similarity 100.0%; Pred. No. 7.7e-08;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCCTGGGCTCAAGCAATCTCTGCTCAGCCT 61  
Db 2764 CTCCTGGGCTCAAGCAATCTCTGCTCAGCCT 2731

RESULT 6  
PCT-US95-06420-2/c  
Sequence 2, Application PC/TUS9506420  
GENERAL INFORMATION:  
APPLICANT: AARONSON, S.A.; CHAN, A.;  
APPLICANT: MIKI, T.  
TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED  
TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA  
TITLE OF INVENTION: CLONING  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06420  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/247,946  
FILING DATE: 24-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY R. AUTH  
REGISTRATION NUMBER: 36,434  
REFERENCE/DOCKET NUMBER: 2026-4150PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3350  
TYPE: Nucleic acid

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; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY: Human R-ras gene
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: exons 2-6.
PCT-US95-06420-2

Query Match      18.2%; Score 34; DB 5; Length 3350;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db 2764 CTCTGGGCTCAAGCAATCTCTGCTCAGCCT 2731

RESULT 7
US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match      17.6%; Score 33; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGC 59
Db 35591 ACTCTGGGCTCAAGCAATCTCTGCTCAGC 35559

RESULT 8
US-09-797-906-3/c
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US97906
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match      17.6%; Score 33; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 TCCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db 45348 TCCTGGGCTCAAGCAATCTCTGCTCAGCCT 45316

RESULT 9
US-09-328-111-76
; Sequence 76, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(674)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-76

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTC 56
Db 93 ACTCTGGGCTCAAGCAATCTCTGCTC 122

RESULT 10
US-09-367-750-1
; Sequence 1, Application US/09367750
; Patent No. 6436639
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Ossina, Natalya K.
; TITLE OF INVENTION: BAK PROMOTER EXPRESSION SYSTEM
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; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAR BIOTECHNOLOGY INC.
; STREET: 3095 Richmond Parkway, Suite 213
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/367,750
; FILING DATE: 07-DEC-1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-14-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4066 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4022..4066
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 4022
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; US-09-367-750-1
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; Query Match 16.0%; Score 30; DB 4; Length 4066;
; Best Local Similarity 100.0%; Pred. No. 6.7e-06;
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; QY 47 CTCCTGCTCAGCTTCCAACTAGCTGGGA 76
; DB 955 CTCCTGCTCAGCTTCCAACTAGCTGGGA 984
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; RESULT 11
; US-08-284-941-3/c
; Sequence 3, Application US/08284941
; Patent No. 5863756
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,941
; FILING DATE: 2 August 1994
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; US-08-284-941-3
; Sequence 3, Application US/08447642
; Patent No. 5989890
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,642
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,941
; FILING DATE: 2 August 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..58
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; US-08-284-941-3
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; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 29 TCCTGGGCTCAAGCAATCCTCTGCCTCA 57
; DB 414 TCCTGGGCTCAAGCAATCCTCTGCCTCA 386
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; RESULT 12
; US-08-447-642-3/c
; Sequence 3, Application US/08447642
; Patent No. 5989890
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,642
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,941
; FILING DATE: 2 August 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..58
US-08-447-642-3

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Best Local Similarity 100.0%; Pred. No. 2.2e-05;
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QY 29 TCCTGGGCTCAAGCAATCCTCTCGCTCA 57
Db 414 TCCTGGGCTCAAGCAATCCTCTCGCTCA 386

RESULT 13
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; Sequence 3, Application US/09236503
; Patent No. 6277590
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael J
; TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
; FILE REFERENCE: Polypeptides in Cells
; CURRENT APPLICATION NUMBER: US/09/236.503
; EARLIER FILING DATE: 1999-01-25
; EARLIER APPLICATION NUMBER: 08/447,642
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: 08/284,941
; EARLIER FILING DATE: 1994-08-02
; EARLIER APPLICATION NUMBER: 07/848,629
; EARLIER FILING DATE: 1992-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 636
; TYPE: DNA
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US-09-236-503-3

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RESULT 14
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; Sequence 3, Application PC/TUS9302147A
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; APPLICANT: KIEFER, MICHAEL C
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
; FILE REFERENCE: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02147A
; FILING DATE: 19930309
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,629
; FILING DATE: 09-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH D., RICHARD L
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-7622
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cdna)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..58
PCT-US93-02147A-3

Query Match          15.5%; Score 29; DB 5; Length 636;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 414 TCCTGGGCTCAAGCAATCCTCTCGCTCA 386

RESULT 15
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; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
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; LOCATION: 64383
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; NAME/KEY: unsure
; LOCATION: 65471
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; NAME/KEY: unsure
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; LOCATION: 87130
; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
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; LOCATION: 89049
; OTHER INFORMATION: unknown
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US-09-791-211-10

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Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 21.3201 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June.16, 2003, 20:04:56 ; Search time 19.7691 Seconds  
(without alignments)  
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Perfect score: 187  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 5	35	18.7	548	9	US-10-198-846-11037
C 6	35	18.7	602	9	US-09-764-891-9533
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C 95	30	16.0	674	10	US-09-879-536-76	Sequence 415, Ap	C 168	29	15.5	170834	10	US-09-835-232-7	Sequence 7, Appli
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C 97	30	16.0	703	9	US-09-764-887-415	Sequence 415, Ap	C 170	28	15.0	401	10	US-09-795-668-1213	Sequence 1213, Ap
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559	28	15.0	1738	9	US-09-990-439-360	Sequence 360, App	632	28	15.0	1738	10	US-09-990-456-360	Sequence 360, App
560	28	15.0	1738	9	US-10-173-693-239	Sequence 239, App	633	28	15.0	1738	10	US-09-989-721-360	Sequence 239, App
561	28	15.0	1738	9	US-10-174-578-239	Sequence 239, App	634	28	15.0	1738	12	US-10-052-586-239	Sequence 239, App
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563	28	15.0	1738	9	US-10-175-750-239	Sequence 239, App	c 636	28	15.0	5139	10	US-09-764-869-1894	Sequence 1894, App
564	28	15.0	1738	9	US-10-176-986-239	Sequence 239, App	c 637	28	15.0	10093	9	US-10-091-504-1390	Sequence 1390, App
565	28	15.0	1738	9	US-10-184-641-239	Sequence 239, App	c 638	28	15.0	10093	10	US-09-764-869-1390	Sequence 1390, App
566	28	15.0	1738	9	US-10-187-888-239	Sequence 239, App	c 639	28	15.0	11186	10	US-09-957-997-1	Sequence 1, Appli
567	28	15.0	1738	9	US-10-194-360-239	Sequence 239, App	c 640	28	15.0	11216	9	US-09-728-552-7	Sequence 7, Appli
568	28	15.0	1738	9	US-10-194-365-239	Sequence 239, App	641	28	15.0	11811	9	US-10-091-572-473	Sequence 473, App
569	28	15.0	1738	9	US-10-195-895-239	Sequence 239, App	c 642	28	15.0	22756	9	US-09-764-891-6609	Sequence 6609, App
570	28	15.0	1738	9	US-10-195-898-239	Sequence 239, App	c 643	28	15.0	22756	9	US-10-091-504-2017	Sequence 2017, App
571	28	15.0	1738	9	US-10-196-759-239	Sequence 239, App	c 644	28	15.0	32195	10	US-09-764-869-2017	Sequence 2017, App
572	28	15.0	1738	9	US-10-199-302-239	Sequence 239, App	c 645	28	15.0	32195	10	US-09-764-869-2016	Sequence 2016, App
573	28	15.0	1738	9	US-10-201-323-239	Sequence 239, App	c 646	28	15.0	32219	10	US-09-764-869-2016	Sequence 2016, App
574	28	15.0	1738	9	US-10-205-510-239	Sequence 239, App	c 647	28	15.0	32219	10	US-10-091-504-2016	Sequence 2016, App
575	28	15.0	1738	9	US-10-205-891-239	Sequence 239, App	c 648	28	15.0	32249	9	US-10-091-504-2314	Sequence 2314, App
576	28	15.0	1738	9	US-10-205-904-239	Sequence 239, App	c 649	28	15.0	32249	10	US-09-764-869-2314	Sequence 2314, App
577	28	15.0	1738	9	US-10-206-917-239	Sequence 239, App	c 650	28	15.0	36651	10	US-09-964-463-3	Sequence 3, Appli
578	28	15.0	1738	9	US-10-207-923-239	Sequence 239, App	651	28	15.0	53542	10	US-09-801-574-61	Sequence 61, Appli
579	28	15.0	1738	9	US-10-207-924-239	Sequence 239, App	652	28	15.0	143306	10	US-09-729-920-3	Sequence 3, Appli
580	28	15.0	1738	9	US-10-208-028-239	Sequence 239, App	653	28	15.0	1503841	9	US-09-946-807-1	Sequence 1, Appli
581	28	15.0	1738	9	US-09-989-328-360	Sequence 360, App	c 654	28	15.0	1503841	10	US-09-946-807-1	Sequence 1, Appli
582	28	15.0	1738	9	US-09-993-583-360	Sequence 360, App	c 655	28	15.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
583	28	15.0	1738	9	US-10-121-062-239	Sequence 239, App	c 656	28	15.0	1503841	10	US-08-795-668-1	Sequence 1, Appli
584	28	15.0	1738	9	US-10-175-753-239	Sequence 239, App	c 657	28	15.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
585	28	15.0	1738	9	US-10-180-553-239	Sequence 239, App	c 658	28	15.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
586	28	15.0	1738	9	US-10-201-327-239	Sequence 239, App	c 659	27	14.4	230	9	US-10-198-846-12420	Sequence 12420, A
587	28	15.0	1738	9	US-09-941-992-360	Sequence 360, App	c 660	27	14.4	342	10	US-09-783-590-9790	Sequence 9790, App
588	28	15.0	1738	9	US-09-992-521-360	Sequence 360, App	c 661	27	14.4	357	10	US-09-764-864-1645	Sequence 1645, App
589	28	15.0	1738	9	US-10-173-696-239	Sequence 239, App	c 662	27	14.4	402	10	US-09-867-701-491	Sequence 491, App
590	28	15.0	1738	9	US-10-183-003-239	Sequence 239, App	c 663	27	14.4	412	9	US-10-198-846-4646	Sequence 4646, App
591	28	15.0	1738	9	US-10-183-016-239	Sequence 239, App	c 664	27	14.4	412	9	US-09-918-995-14025	Sequence 14025, A
592	28	15.0	1738	9	US-09-997-333-360	Sequence 360, App	c 665	27	14.4	464	9	US-09-918-995-9944	Sequence 9944, App
593	28	15.0	1738	9	US-09-997-384-360	Sequence 360, App	c 666	27	14.4	465	9	US-10-050-704-49	Sequence 49, Appli
594	28	15.0	1738	9	US-10-125-923A-239	Sequence 239, App	c 667	27	14.4	760	9	US-09-729-674-83	Sequence 83, Appli
595	28	15.0	1738	9	US-10-176-491-239	Sequence 239, App	c 668	27	14.4	808	10	US-09-822-849A-60	Sequence 60, Appli
596	28	15.0	1738	9	US-10-176-979-239	Sequence 239, App	c 669	27	14.4	2399	10	US-10-091-504-1693	Sequence 1693, App
597	28	15.0	1738	9	US-10-187-592-239	Sequence 239, App	670	27	14.4	6111	9	US-09-764-869-1693	Sequence 1693, App
598	28	15.0	1738	9	US-10-197-691-239	Sequence 239, App	c 671	27	14.4	6111	10	US-09-764-869-1693	Sequence 1693, App
599	28	15.0	1738	9	US-10-198-771-239	Sequence 239, App	c 672	27	14.4	6439	9	US-09-790-852-8	Sequence 8, Appli
600	28	15.0	1738	9	US-10-174-575A-239	Sequence 239, App	c 673	27	14.4	8294	12	US-10-084-037-2	Sequence 2, Appli
601	28	15.0	1738	9	US-10-179-520-239	Sequence 239, App	674	27	14.4	9591	9	US-09-764-891-6043	Sequence 6043, App
602	28	15.0	1738	9	US-10-201-325-239	Sequence 239, App	675	27	14.4	9591	9	US-10-091-438-268	Sequence 268, App
603	28	15.0	1738	9	US-10-202-941-239	Sequence 239, App	c 676	27	14.4	9968	9	US-10-102-627-100	Sequence 100, App

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678	27	14.4	12415	9	US-10-091-438-269	Sequence 269, App	C 751	25	13.4	229	9	US-09-918-995-31205	Sequence 31205, A
679	27	14.4	13205	9	US-10-274-371-3	Sequence 3, Appli	C 752	25	13.4	243	10	US-09-867-701-8641	Sequence 8641, Ap
680	27	14.4	15261	9	US-09-764-891-10186	Sequence 10186, A	C 753	25	13.4	252	10	US-09-867-701-9022	Sequence 9022, Ap
681	27	14.4	20565	9	US-09-764-891-6045	Sequence 6045, Ap	C 754	25	13.4	338	10	US-09-867-701-8221	Sequence 8221, Ap
682	27	14.4	20565	9	US-10-091-438-270	Sequence 270, App	C 755	25	13.4	340	9	US-09-764-891-8217	Sequence 8217, Ap
683	27	14.4	28818	10	US-09-764-877-2266	Sequence 2266, Ap	C 756	25	13.4	344	9	US-09-764-891-1609	Sequence 1609, Ap
684	27	14.4	31949	9	US-09-764-891-8098	Sequence 8098, Ap	C 757	25	13.4	373	9	US-09-918-995-29762	Sequence 29762, A
685	27	14.4	32152	9	US-09-764-872-518	Sequence 518, App	C 758	25	13.4	400	9	US-09-918-995-4202	Sequence 4202, Ap
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689	27	14.4	32187	9	US-10-102-627-109	Sequence 109, App	C 762	25	13.4	467	10	US-09-777-564-979	Sequence 979, App
690	27	14.4	32188	9	US-10-074-095-799	Sequence 799, App	C 763	25	13.4	475	10	US-09-918-995-11466	Sequence 11466, A
691	27	14.4	32188	10	US-09-764-860-799	Sequence 799, App	C 764	25	13.4	475	10	US-09-864-761-2490	Sequence 2490, Ap
692	27	14.4	32204	9	US-09-764-872-517	Sequence 517, App	C 765	25	13.4	477	10	US-09-764-853-45	Sequence 45, Appl
693	27	14.4	32204	9	US-10-072-349-327	Sequence 327, App	C 766	25	13.4	478	9	US-09-918-995-428	Sequence 428, App
694	27	14.4	32204	10	US-09-764-855-327	Sequence 327, App	C 767	25	13.4	480	9	US-09-918-995-27030	Sequence 27030, A
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696	27	14.4	174424	10	US-09-967-768A-314	Sequence 314, App	C 769	25	13.4	505	9	US-09-986-480-162	Sequence 162, App
697	27	14.4	174424	10	US-09-967-768A-314	Sequence 314, App	C 770	25	13.4	574	9	US-09-986-480-87	Sequence 648, App
698	27	14.4	180216	10	US-09-835-232-6	Sequence 6, Appli	C 771	25	13.4	728	9	US-09-986-480-87	Sequence 87, Appl
699	27	14.4	235033	9	US-10-301-844-1	Sequence 1, Appli	C 772	25	13.4	738	9	US-09-983-802-131	Sequence 131, App
700	26	13.9	182	10	US-09-867-701-10159	Sequence 10159, A	C 773	25	13.4	834	9	US-10-198-846-6311	Sequence 6311, Ap
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702	26	13.9	210	9	US-10-040-862-3447	Sequence 3447, Ap	C 775	25	13.4	1381	10	US-09-964-666-3	Sequence 3, Appli
703	26	13.9	258	9	US-10-040-739-1194	Sequence 1194, Ap	C 776	25	13.4	1381	10	US-09-964-412-3	Sequence 3, Appli
704	26	13.9	346	10	US-09-962-436-94	Sequence 94, Appli	C 777	25	13.4	1588	9	US-10-097-065-111	Sequence 111, App
705	26	13.9	356	10	US-09-879-536-339	Sequence 339, App	C 778	25	13.4	1603	9	US-10-198-846-14083	Sequence 14083, A
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707	26	13.9	401	9	US-09-946-807-908	Sequence 908, App	C 780	25	13.4	1984	10	US-09-864-761-2811	Sequence 2811, Ap
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712	26	13.9	423	10	US-09-867-701-1948	Sequence 1948, Ap	C 785	25	13.4	3585	9	US-09-764-868-1415	Sequence 1415, Ap
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714	26	13.9	436	10	US-09-867-701-4136	Sequence 4136, Ap	C 787	25	13.4	5216	9	US-10-125-540-607	Sequence 607, App
715	26	13.9	442	9	US-09-918-995-14404	Sequence 14404, A	C 788	25	13.4	5216	10	US-10-074-095-695	Sequence 695, App
716	26	13.9	500	9	US-09-918-995-12777	Sequence 12777, A	C 789	25	13.4	5216	10	US-09-764-870-607	Sequence 607, App
717	26	13.9	522	10	US-09-867-701-757	Sequence 757, App	C 790	25	13.4	5216	10	US-09-764-860-695	Sequence 695, App
718	26	13.9	2588	10	US-09-822-830A-47	Sequence 47, Appl	C 791	25	13.4	5216	10	US-09-764-891-5740	Sequence 5740, Ap
719	26	13.9	2752	9	US-10-050-882-50	Sequence 50, Appl	C 792	25	13.4	5966	9	US-09-764-891-6395	Sequence 6395, Ap
720	26	13.9	2810	9	US-10-087-993-35	Sequence 35, Appl	C 793	25	13.4	6071	9	US-09-764-868-1418	Sequence 1418, Ap
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723	26	13.9	4837	10	US-09-764-877-2839	Sequence 2839, Ap	C 796	25	13.4	6945	10	US-09-764-887-314	Sequence 314, App
724	26	13.9	5670	10	US-09-954-456-1146	Sequence 1146, Ap	C 797	25	13.4	6945	10	US-09-764-887-313	Sequence 313, App
725	26	13.9	5690	9	US-10-091-458-54	Sequence 54, Appl	C 798	25	13.4	6945	10	US-09-764-887-314	Sequence 314, App
726	26	13.9	6149	9	US-10-073-961-436	Sequence 436, App	C 799	25	13.4	7042	9	US-10-171-581-264	Sequence 264, App
727	26	13.9	6149	9	US-10-073-961-437	Sequence 437, App	C 800	25	13.4	7042	10	US-09-876-667-1	Sequence 1, Appli
728	26	13.9	6149	10	US-09-764-887-436	Sequence 436, App	C 801	25	13.4	7075	10	US-09-876-667-15	Sequence 15, Appl
729	26	13.9	6149	10	US-09-764-887-437	Sequence 437, App	C 802	25	13.4	7301	9	US-09-956-993-3	Sequence 3, Appli
730	26	13.9	7099	9	US-09-764-891-7570	Sequence 7570, Ap	C 803	25	13.4	8121	9	US-10-091-504-1689	Sequence 1689, Ap
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733	26	13.9	14796	9	US-10-138-618-35	Sequence 35, Appl	C 806	25	13.4	8253	9	US-09-764-891-6775	Sequence 6775, Ap
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735	26	13.9	14796	10	US-09-954-456-1636	Sequence 1636, Ap	C 808	25	13.4	9192	9	US-10-092-154-1246	Sequence 1246, Ap
736	26	13.9	14796	10	US-09-918-186A-3	Sequence 3, Appli	C 809	25	13.4	9192	10	US-09-764-877-1248	Sequence 1248, Ap
737	26	13.9	14796	10	US-09-918-186A-3	Sequence 3, Appli	C 810	25	13.4	9192	10	US-09-764-877-2218	Sequence 2218, Ap
738	26	13.9	15054	9	US-10-091-572-577	Sequence 577, App	C 811	25	13.4	11079	9	US-10-073-961-465	Sequence 465, App
739	26	13.9	15054	9	US-09-764-891-6721	Sequence 6721, Ap	C 812	25	13.4	11079	10	US-09-764-887-465	Sequence 465, App
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741	26	13.9	16939	9	US-09-764-891-7505	Sequence 7505, Ap	C 814	25	13.4	11298	9	US-10-092-154-1343	Sequence 1343, Ap
742	26	13.9	22689	9	US-09-764-891-7507	Sequence 7507, Ap	C 815	25	13.4	11298	10	US-09-764-847-1343	Sequence 1343, Ap
743	26	13.9	26928	9	US-10-020-141-7	Sequence 7, Appli	C 816	25	13.4	12259	9	US-10-091-504-1690	Sequence 1690, Ap
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745	26	13.9	26928	10	US-09-880-107-2278	Sequence 2278, Ap	C 818	25	13.4	13332	9	US-10-091-572-621	Sequence 621, App
746	26	13.9	26928	10	US-09-880-107-3949	Sequence 3949, Ap	C 819	25	13.4	13332	9	US-09-764-891-6774	Sequence 6774, Ap
747	26	13.9	126512	10	US-09-804-474A-3	Sequence 3, Appli	C 820	25	13.4	13630	9	US-09-764-868-1369	Sequence 1369, Ap
748	26	13.9	176373	9	US-10-095-407-17	Sequence 17, Appl	C 821	25	13.4	14299	9	US-10-073-961-466	Sequence 466, App
749	26	13.9	465237	10	US-09-933-267A-1	Sequence 1, Appli	C 822	25	13.4	14299	10	US-09-764-887-466	Sequence 466, App

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C 833	25	13.4	17216	10	US-09-764-877-3566	Sequence 3566, App	C 906	24	12.8	476	10	US-09-920-300A-626	Sequence 626, App
C 834	25	13.4	17450	9	US-09-764-891-8641	Sequence 8641, App	C 907	24	12.8	476	10	US-09-920-300A-1547	Sequence 1547, App
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C 842	25	13.4	22008	9	US-10-091-504-2110	Sequence 2110, App	C 915	24	12.8	484	10	US-09-998-598-708	Sequence 708, App
C 843	25	13.4	22008	10	US-09-764-869-2110	Sequence 2110, App	C 916	24	12.8	484	10	US-09-998-598-850	Sequence 850, App
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C 848	25	13.4	31766	9	US-10-288-478-5	Sequence 5, Appli	C 921	24	12.8	488	10	US-09-998-598-1046	Sequence 1046, App
C 849	25	13.4	31766	10	US-09-765-344-5	Sequence 5, Appli	C 922	24	12.8	488	10	US-09-998-598-1162	Sequence 1162, App
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C 872	24	12.8	261	10	US-09-867-701-9143	Sequence 9143, App	C 945	24	12.8	558	9	US-10-066-543-3295	Sequence 3295, App
C 873	24	12.8	269	10	US-09-783-590-4915	Sequence 4915, App	C 946	24	12.8	558	10	US-09-920-300A-687	Sequence 687, App
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C 887	24	12.8	402	10	US-09-867-701-4556	Sequence 4556, App	C 960	24	12.8	623	9	US-10-091-572-788	Sequence 788, App
C 888	24	12.8	424	10	US-09-783-590-10520	Sequence 10520, A	C 961	24	12.8	623	9	US-10-091-572-789	Sequence 789, App
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C 894	24	12.8	440	9	US-10-125-237-44	Sequence 44, Appl	C 967	24	12.8	658	9	US-09-764-872-707	Sequence 707, App
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969 24 12.8 688 9 US-10-198-846-3907 Sequence 3907, Ap  
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c 971 24 12.8 691 10 US-09-764-877-4009 Sequence 4009, Ap  
c 972 24 12.8 691 10 US-09-764-877-4010 Sequence 4010, Ap  
c 973 24 12.8 813 9 US-10-150-111-30 Sequence 30, Appl  
c 974 24 12.8 826 10 US-09-822-830A-561 Sequence 561, App  
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c 977 24 12.8 838 9 US-09-764-891-6901 Sequence 6901, Ap  
c 978 24 12.8 919 10 US-10-051-504-2159 Sequence 2159, Ap  
c 979 24 12.8 921 9 US-09-887-527-49 Sequence 49, Appl  
c 980 24 12.8 940 9 US-09-764-872-650 Sequence 650, App  
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c 983 24 12.8 940 9 US-09-764-891-9056 Sequence 9056, Ap  
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## ALIGNMENTS

RESULT 1  
US-09-764-877-2928  
; Sequence 2928, Application US/09764877  
; Patent No. US20020147140A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005  
; CURRENT APPLICATION NUMBER: US/09/764,877  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2928  
; LENGTH: 27483  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-2928  
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Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTT 62  
Db 25969 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTT 26004  
RESULT 2  
US-09-764-891-9663/c  
; Sequence 9663, Application US/09764891  
; Patent No. US20030077808A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC006

; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9663  
; LENGTH: 32250  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-891-9663  
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Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
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Db 1584 TACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCT 1549  
RESULT 3  
US-10-020-141-5  
; Sequence 5, Application US/10020141  
; Publication No. US20030092013A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Jeanette  
; APPLICANT: Adelson, Allen  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE  
; FILE REFERENCE: MM1-002  
; CURRENT APPLICATION NUMBER: US/10/020,141  
; CURRENT FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/313,097  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: US 60/327,485  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; ORGANISM: Homo sapiens  
US-10-020-141-5  
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Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 122191 CTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTC 122226  
RESULT 4  
US-09-867-701-7276/c  
; Sequence 7276, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
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; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-7276



Query Match 18.7%; Score 35; DB 10; Length 359;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
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Db 335 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 301  
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## RESULT 5

US-10-198-846-11037/c  
; Sequence 11037, Application US/10198846  
; Publication No. US2003009974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; LENGTH: 548  
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; ORGANISM: Homo sapiens  
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; OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-11037

Query Match 18.7%; Score 35; DB 9; Length 548;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-764-891-9533/c  
; Sequence 9533, Application US/09764891  
; Publication No. US20030077808A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC006  
; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9533  
; LENGTH: 602  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-891-9533

Query Match 18.7%; Score 35; DB 9; Length 602;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
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Db 230 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 196

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; Sequence 2835, Application US/10198846  
; Publication No. US2003009974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2835  
; LENGTH: 691  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
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; LOCATION: 2, 3, 5, 7, 8, 9, 13, 18, 19, 22, 125, 161, 260, 302, 306,  
; LOCATION: 313, 342, 349, 383, 389, 390, 417, 441, 478, 509, 588, 590,  
; LOCATION: 623, 636, 645, 648  
; OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-2835

Query Match 18.7%; Score 35; DB 9; Length 691;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 8

US-10-198-846-1806/c  
; Sequence 1806, Application US/10198846  
; Publication No. US2003009974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1806  
; LENGTH: 893  
; TYPE: DNA  
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; FEATURE:  
; NAME/KEY: misc feature  
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; LOCATION: 606, 612, 613, 614, 615, 623, 624, 625, 626, 627, 628, 629,  
; LOCATION: 630, 631, 632, 633, 638, 640, 641, 642, 643, 644, 645  
; OTHER INFORMATION: n = A,T,C or G

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; NAME/KEY: misc feature
; LOCATION: 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 660,
; LOCATION: 674, 682, 694, 709, 720, 721, 723, 727, 731, 732, 739,
; LOCATION: 748, 750, 754, 758, 767, 770, 777, 778, 784, 790, 794, 796,
; LOCATION: 798, 799, 804, 809, 814, 815, 816, 819, 829, 831, 838
; OTHER INFORMATION: n = A,T,C or G
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; NAME/KEY: misc feature
; LOCATION: 843, 845, 846, 849, 851, 852, 853, 854, 859, 864, 875, 876,
; LOCATION: 877, 892
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-1806

Query Match      18.7%; Score 35; DB 9; Length 893;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db      226 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 192

RESULT 9
US-09-822-830A-425/c
; Sequence 425, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 425
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-425

Query Match      18.7%; Score 35; DB 10; Length 1716;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 61
Db      1159 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 1125

RESULT 10
US-10-091-438-25
; Sequence 25, Application US/10091438
; Publication No. US20030077606A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT217C1
; CURRENT APPLICATION NUMBER: US/10/091,438
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,879
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
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; PRIOR APPLICATION NUMBER: 60/217,487
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; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
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; PRIOR APPLICATION NUMBER: 60/225,447
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; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
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; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
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; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR APPLICATION NUMBER: 60/251,868
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; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
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PRIOR APPLICATION NUMBER: 60/239,509	PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236,367	PRIOR FILING DATE: 2000-09-29
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PRIOR APPLICATION NUMBER: 60/236,370	PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802	PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037	PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040	PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935	PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937	PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474	PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532	PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216	PRIOR FILING DATE: 2008-11-17
PRIOR APPLICATION NUMBER: 60/249,210	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681	PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182	PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836	PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438	PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135	PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218	PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

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Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels

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Db 1827 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCT 1861

RESULT 11
US-09-764-853-242
; Sequence 242, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FJZ06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 242
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-242

Query Match 18.7%; Score 35; DB 10; Length 1948;

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Best Local Similarity	100.0%;	Pred. No. 6.1e-09;
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RESULT 12

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US-10-161-803-50/c
; Sequence 50, Application US/10161803
; Publication No. US20030092028A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Yuanhong
; APPLICANT: Lih, Chih-Jian
; APPLICANT: Chen, Fan
; APPLICANT: Fairman, Jeffery
; APPLICANT: Chen, Yii-Der I
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF INSULIN RESISTANCE AND RELATED CONDITIONS
; FILE REFERENCE: 421452000300
; CURRENT APPLICATION NUMBER: US/10/161.803
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/295,264
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 2308
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-803-50

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US-10-161-572-23
; Sequence 23, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGB AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 2642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-572-23

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RESULT 15

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US-10-198-846-9985/c
; Sequence 9985, Application US/10198846
; Publication No. US2003099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9985
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; LOCATION: 2800_
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9985
Query Match 18.7%; Score 35; DB 9; Length 2800;

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Qy 27 ACTCTGGGCTCAAGCAATCTCTCCTGCCTCAGCCT 61  
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Db 2507 ACTCTGGGCTCAAGCAATCTCTCCTGCCTCAGCCT 24

Search completed: June 17, 2003, 09:59:28  
Job time : 34.7691 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 212.5 Seconds  
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- 12: gb\_est3.\*
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- 19: em\_gss\_inv.\*
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- 24: em\_gss\_mus.\*
- 25: em\_gss\_othr.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	40	21.4	433	9 A1140075	A1140075 qab7c12.x
6	40	21.4	458	9 A1077461	A1077461 oz37d07.x

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AW846928	RC3-CT019
BF908113	RC1-UT008
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AQ177185	HS 3223.A
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AA722194	zh20d08.s
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BQ082506	K-EST0125
AI039436	ox35g04.s
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AQ270374	HS 2052.B
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AA677459	zj70a12.s
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BM693538	UI-E-CK1-
AI887627	wm16b10.x

C 80	35	18.7	525	17	AQ185916	HS 3062.B	C 153	34	18.2	506	10	AW996363	QV3-BN004
C 81	35	18.7	530	17	AQ429495	CITBI-EI-	154	34	18.2	511	13	BM314444	IQ54e11.x
C 82	35	18.7	531	10	AW604197	IL3-CT021	155	34	18.2	512	10	AW195612	xn84905.x
C 83	35	18.7	543	12	BF989856	QV4-GN011	C 156	34	18.2	514	9	AA525205	n152b03.s
C 84	35	18.7	548	17	AQ432974	HS 2208.A	157	34	18.2	514	17	AQ677500	HS 5529.A
C 85	35	18.7	559	9	AU158691	AU158691	C 158	34	18.2	543	14	BQ638831	hQ38806.Y
C 86	35	18.7	569	17	AQ534033	RPCI-11-3	C 159	34	18.2	549	17	AQ319730	RPCI11-10
C 87	35	18.7	572	14	BM671944	UT-E-EOO-	C 160	34	18.2	549	17	AQ552057	RPCI-11-4
C 88	35	18.7	582	17	AQ052781	RPCI11-49	161	34	18.2	549	17	AQ584340	RPCI-11-4
C 89	35	18.7	588	14	BQ348243	CM3-HT019	C 162	34	18.2	598	17	AQ552064	RPCI-11-4
C 90	35	18.7	594	9	A1114454	HA1036.Hu	163	34	18.2	604	17	AQ890397	HS 3131.A
C 91	35	18.7	600	17	AQ038706	CIT-HSP-2	C 164	34	18.2	610	17	AV727065	AV727065
C 92	35	18.7	604	10	AW938867	PMO-DT006	C 165	34	18.2	627	17	AQ552075	RPCI-11-4
C 93	35	18.7	613	12	BF935736	MR2-NT013	C 166	34	18.2	629	10	AV707276	AV707276
C 94	35	18.7	615	10	AW861568	RC4-CT032	167	34	18.2	648	17	AG042997	Pan trogl
C 95	35	18.7	622	14	BQ777823	1137d12.Y	168	34	18.2	663	17	AQ535539	RPCI-11-3
C 96	35	18.7	622	14	BM978805	UT-CF-DUI	169	34	18.2	679	17	AG115659	Pan trogl
C 97	35	18.7	626	17	AQ416377	RPCI-11-1	170	34	18.2	684	17	AG129727	Pan trogl
C 98	35	18.7	634	14	BM679621	UT-E-EOO-	C 171	34	18.2	691	17	AG115645	Pan trogl
C 99	35	18.7	640	9	AL704247	DKFZp686M	C 172	34	18.2	718	17	AG085965	Pan trogl
C 100	35	18.7	655	17	AG131162	Pan trogl	173	34	18.2	747	17	AG030820	Pan trogl
C 101	35	18.7	671	17	AG093536	Pan trogl	C 174	34	18.2	769	17	AG099959	Pan trogl
C 102	35	18.7	678	17	AG157581	Pan trogl	175	34	18.2	828	17	AQ891502	HS 3131.A
C 103	35	18.7	688	17	AQ037643	CIT-HSP-2	176	34	18.2	846	14	BQ689051	AGENCOURT
C 104	35	18.7	719	17	AG171172	Pan trogl	177	34	18.2	860	13	BI861930	603391476
C 105	35	18.7	723	17	AQ424250	CITBI-EI-	178	34	18.2	867	14	BQ687953	AGENCOURT
C 106	35	18.7	734	14	EQ05166	UT-1-BBp	179	34	18.2	869	14	BQ688301	AGENCOURT
C 107	35	18.7	737	14	BM971245	UT-CF-DUI	180	34	18.2	873	14	BQ898023	AGENCOURT
C 108	35	18.7	746	14	BM679680	UT-E-EOO-	181	34	18.2	880	14	BQ687265	AGENCOURT
C 109	35	18.7	755	9	AL572352	AL572352	182	34	18.2	887	12	BG387775	602412656
C 110	35	18.7	760	12	BG741015	602634742	183	34	18.2	889	12	BG506453	601861032
C 111	35	18.7	775	9	AL596490	DKFZp761D	184	34	18.2	914	13	BM006829	603615279
C 112	35	18.7	782	12	BE856643	601508847	185	34	18.2	920	14	BQ641632	AGENCOURT
C 113	35	18.7	831	9	AL538354	AL538354	186	34	18.2	927	14	BQ690195	AGENCOURT
C 114	35	18.7	832	17	AQ752359	HS 5565.B	187	34	18.2	928	14	BQ684796	AGENCOURT
C 115	35	18.7	834	14	BQ893749	AGENCOURT	188	34	18.2	938	14	BQ722797	AGENCOURT
C 116	35	18.7	835	12	BG681657	602627962	189	34	18.2	945	14	BQ711550	AGENCOURT
C 117	35	18.7	923	13	BI116411	602868828	190	34	18.2	949	14	BQ689618	AGENCOURT
C 118	35	18.7	934	12	BG255934	602367593	191	34	18.2	1018	13	BM550040	AGENCOURT
C 119	35	18.7	937	14	BQ646637	AGENCOURT	192	34	18.2	1022	14	BQ552061	AGENCOURT
C 120	35	18.7	955	14	BQ644740	AGENCOURT	193	34	18.2	1058	14	BQ892421	AGENCOURT
C 121	35	18.7	976	14	BQ723342	AGENCOURT	194	34	18.2	1078	13	BM476430	AGENCOURT
C 122	35	18.7	1038	13	BM557184	AGENCOURT	195	34	18.2	1119	14	BM918113	AGENCOURT
C 123	35	18.7	1040	17	AQ901036	HS 3203.B	196	33	17.6	220	14	H72054	YR99C03.s1
C 124	35	18.7	1860	11	EC021283	Homo sapi	197	33	17.6	257	9	AA093988	cl1521.se
C 125	35	18.7	2503	11	EC013892	Homo sapi	198	33	17.6	281	13	BI040057	MR4-NT014
C 126	35	18.7	2931	17	AQ899828	260L13-C4	199	33	17.6	285	9	AA004640	zh92b07.s
C 127	34	18.2	195	9	AA457186	aa88c04.r	C 200	33	17.6	286	12	BE765850	IL3-NT010
C 128	34	18.2	235	9	AA310229	EST18106	201	33	17.6	309	14	R16796	yf33d03.s1
C 129	34	18.2	258	9	AA328095	EST31528	202	33	17.6	318	9	AA334237	EST38445
C 130	34	18.2	279	10	BE045008	hm26a02.x	203	33	17.6	341	14	R05291	ye91e02.s1
C 131	34	18.2	280	14	R38238	yh94f09.r1	204	33	17.6	347	9	AA503446	ng1e101.s
C 132	34	18.2	286	14	R97371	yg52b10.s1	C 205	33	17.6	371	12	BF928726	IL5-NT022
C 133	34	18.2	287	9	AA744060	ny50d03.s	206	33	17.6	375	9	AA847847	od39a04.s
C 134	34	18.2	328	9	AA340852	EST46139	C 207	33	17.6	396	10	AA265752	xg76f10.x
C 135	34	18.2	330	9	AL702757	DKFZp6860	C 208	33	17.6	398	9	AA777266	zi96b02.s
C 136	34	18.2	342	13	BI023942	CM4-WT024	C 209	33	17.6	419	17	AQ392086	CITBI-EI-
C 137	34	18.2	369	17	AQ057630	CIT-HSP-2	210	33	17.6	427	14	BM703988	UT-E-CK1-
C 138	34	18.2	373	9	A1016321	ct78b10.s	211	33	17.6	429	9	AA583390	nn34d07.s
C 139	34	18.2	424	12	BF37203	PM4-KT004	C 212	33	17.6	437	9	AA004239	zh32b07.r
C 140	34	18.2	426	14	BQ357586	PM1-HT035	213	33	17.6	451	17	AQ202084	RPCI11-48
C 141	34	18.2	432	17	B98853	CIT-HSP-228	214	33	17.6	458	17	AQ151340	HS 2202.B
C 142	34	18.2	433	12	BF812241	QV1-CI017	C 215	33	17.6	458	17	AQ242344	HS 2061.A
C 143	34	18.2	435	14	N20833	yx49a06.s1	216	33	17.6	464	17	AQ770658	HS 5365.B
C 144	34	18.2	436	10	BE045159	hm28g10.x	217	33	17.6	473	9	AA847846	od39a03.s
C 145	34	18.2	441	17	AQ082771	RPCI11-54	218	33	17.6	474	17	B49067	RPCI11-4J13
C 146	34	18.2	445	9	AL601967	DKFZp313F	C 219	33	17.6	482	17	AQ665949	HS 5372.B
C 147	34	18.2	445	12	BF811950	QV1-CI017	220	33	17.6	483	10	AW270081	xv37g03.x
C 148	34	18.2	451	13	BM310143	in08d08.x	221	33	17.6	484	17	B89466	RPCI11-24H9
C 149	34	18.2	454	9	A1371165	ta09c02.x	222	33	17.6	491	17	AQ232072	HS 2021.A
C 150	34	18.2	457	13	BI321726	sat98c03	223	33	17.6	513	17	AQ148964	HS 3141.B
C 151	34	18.2	488	10	AW274699	xv32f11.x	224	33	17.6	514	14	BM823407	K-EST0094
C 152	34	18.2	496	17	AQ278609	CITBI-EI-	225	33	17.6	547	17	AQ547374	RPCI-11-4



C 226	33	17.6	566	9	AA428410	AA428410 zw57g904.s	C 299	31	16.6	395	12	BG193212	BG193212 RST12339
C 227	33	17.6	576	14	BM729138	BM729138 UT-E-EOL-	C 300	31	16.6	408	10	AW305124	AW305124 xv99h06.x
C 228	33	17.6	576	17	AQ419842	AQ419842 RPCI-11-1	C 301	31	16.6	411	10	AW084237	AW084237 xc53f08.x
C 229	33	17.6	586	12	BE931686	BE931686 QV4-HT053	C 302	31	16.6	412	14	R94177	R94177 y74f12.s1
C 230	33	17.6	590	14	W26920	W26920 17h6 Human	C 303	31	16.6	416	9	AI434126	AI434126 t136e01.x
C 231	33	17.6	605	17	AQ013403	AQ013403 RPCI11-24	C 304	31	16.6	416	12	BF738543	BF738543 PM3-KT003
C 232	33	17.6	647	17	AG152943	AG152943 Pan trogl	C 305	31	16.6	417	13	BG996748	BG996748 CM0-HT129
C 233	33	17.6	659	17	AG109493	AG109493 Pan trogl	C 306	31	16.6	419	17	B30683	B30683 HS-1003-A1-
C 234	33	17.6	668	10	AV723319	AV723319 AV723319	C 307	31	16.6	424	9	AI903485	AI903485 RC-BT029-
C 235	33	17.6	670	17	AG149798	AG149798 Pan trogl	C 308	31	16.6	433	17	AQ420463	AQ420463 RPCI-11-1
C 236	33	17.6	691	14	BM682065	BM682065 UT-E-EOL-	C 309	31	16.6	435	12	BF841250	BF841250 RC4-HT088
C 237	33	17.6	722	17	AG183270	AG183270 Pan trogl	C 310	31	16.6	436	9	AA694572	AA694572 ah23f10.s
C 238	33	17.6	736	12	BE960663	BE960663 601647975	C 311	31	16.6	436	9	AA604118	AA604118 ho72d12.s
C 239	33	17.6	745	13	BI038316	BI038316 IL3-NT028	C 312	31	16.6	438	14	N38889	N38889 yy81f11.s1
C 240	33	17.6	766	12	BG577057	BG577057 602599472	C 313	31	16.6	441	9	AI903483	AI903483 RC-BT029-
C 241	33	17.6	896	14	BQ212758	BQ212758 AGENCOURT	C 314	31	16.6	441	9	AI929235	AI929235 au58g06.x
C 242	33	17.6	938	10	BE622056	BE622056 601440917	C 315	31	16.6	443	9	AI903308	AI903308 RC-BT029-
C 243	33	17.6	1030	12	BG611194	BG611194 602612172	C 316	31	16.6	443	17	AQ042262	AQ042262 CIT-HSP-2
C 244	32	17.1	157	10	AW797448	AW797448 CM1-UM003	C 317	31	16.6	447	9	AI990175	AI990175 ws38b05.x
C 245	32	17.1	232	13	BM510001	BM510001 1996f09.x	C 318	31	16.6	453	9	AA494437	AA494437 ne28d05.s
C 246	32	17.1	266	17	AQ281914	AQ281914 RPCI11-85	C 319	31	16.6	456	9	AA736944	AA736944 nwl3e03.s
C 247	32	17.1	321	9	AA579352	AA579352 nf29b05.s	C 320	31	16.6	459	9	AA568459	AA568459 nm25c10.s
C 248	32	17.1	362	9	AA526829	AA526829 ni92c05.s	C 321	31	16.6	460	10	AW973943	AW973943 EST386166
C 249	32	17.1	391	9	AA593533	AA593533 nf29b06.s	C 322	31	16.6	462	9	AI651362	AI651362 wd05c12.x
C 250	32	17.1	398	9	AA457510	AA457510 aa99b05.s	C 323	31	16.6	463	9	AI929425	AI929425 au60c09.x
C 251	32	17.1	422	9	AI732225	AI732225 nf18e09.x	C 324	31	16.6	466	14	H09534	H09534 y196a01.s1
C 252	32	17.1	424	9	AI089568	AI089568 qb06h02.x	C 325	31	16.6	467	13	BI712105	BI712105 ie01f08.x
C 253	32	17.1	433	9	AA573644	AA573644 nf18e09.s	C 326	31	16.6	471	12	BF223032	BF223032 7c27g11.x
C 254	32	17.1	433	9	AA579542	AA579542 nf17a09.s	C 327	31	16.6	474	10	BE677579	BE677579 7d87r08.x
C 255	32	17.1	453	14	R38004	R38004 ynf7h09.r1	C 328	31	16.6	474	17	AQ186283	AQ186283 HS_3083_B
C 256	32	17.1	455	12	BF725051	BF725051 bx11f09.x	C 329	31	16.6	477	9	AI804109	AI804109 tc96d04.x
C 257	32	17.1	467	14	H00780	H00780 yj30c08.r1	C 330	31	16.6	481	9	AA548300	AA548300 nj99f06.s
C 258	32	17.1	467	17	BH140946	BH140946 UP_392-15	C 331	31	16.6	483	10	AW516009	AW516009 xv04a07.x
C 259	32	17.1	468	14	R76692	R76692 y61f02.s1	C 332	31	16.6	485	13	BM351888	BM351888 iq83g07.x
C 260	32	17.1	474	10	AW972965	AW972965 EST385062	C 333	31	16.6	488	17	AQ544321	AQ544321 CITBI-E1-
C 261	32	17.1	516	10	AW857473	AW857473 CM3-CIT031	C 334	31	16.6	493	17	AQ582765	AQ582765 RPCI-11-4
C 262	32	17.1	528	17	AQ262571	AQ262571 CITBI-E1-	C 335	31	16.6	497	17	AQ591529	AQ591529 HS_2126_B
C 263	32	17.1	537	17	AQ787097	AQ787097 HS_5480_A	C 336	31	16.6	499	10	AW085628	AW085628 xb41e03.x
C 264	32	17.1	591	12	BF628555	BF628555 IL0-HN008	C 337	31	16.6	505	17	AQ0505427	AQ0505427 RPCI-11-3
C 265	32	17.1	629	12	BF576984	BF576984 602134437	C 338	31	16.6	510	14	R59249	R59249 y97c05.r1
C 266	32	17.1	645	17	AG144818	AG144818 Pan trogl	C 339	31	16.6	515	17	AQ701400	AQ701400 HS_2133_A
C 267	32	17.1	655	12	BG435771	BG435771 602506877	C 340	31	16.6	524	9	AA179303	AA179303 zp5c03.s
C 268	32	17.1	655	17	AG061496	AG061496 Pan trogl	C 341	31	16.6	524	17	AQ366587	AQ366587 HS_5037_B
C 269	32	17.1	663	17	AG046860	AG046860 Pan trogl	C 342	31	16.6	528	9	AI581141	AI581141 t133h08.x
C 270	32	17.1	675	17	AG167399	AG167399 Pan trogl	C 343	31	16.6	535	13	BI713058	BI713058 ie01f08.y
C 271	32	17.1	678	10	AV763666	AV763666 AV763666	C 344	31	16.6	555	9	AU146499	AU146499 AUI146499
C 272	32	17.1	682	17	AG046384	AG046384 Pan trogl	C 345	31	16.6	553	9	AL038960	AL038960 DKF2p566P
C 273	32	17.1	719	17	AG232640	AG232640 Pan trogl	C 346	31	16.6	579	17	AQ629104	AQ629104 RPCI-11-4
C 274	32	17.1	875	14	BQ222361	BQ222361 AGENCOURT	C 347	31	16.6	639	17	B80027	B80027 CIT-HSP-204
C 275	32	17.1	911	12	BF672382	BF672382 602150620	C 348	31	16.6	640	10	AV723883	AV723883 AV723883
C 276	32	17.1	912	10	BE617249	BE617249 601441943	C 349	31	16.6	647	10	AV705708	AV705708 AV705708
C 277	32	17.1	1022	13	BM556059	BM556059 AGENCOURT	C 350	31	16.6	649	10	BE513817	BE513817 601315658
C 278	31	16.6	174	13	BG989744	BG989744 PM3-HT092	C 351	31	16.6	689	17	AG046676	AG046676 Pan trogl
C 279	31	16.6	250	10	AW837863	AW837863 CM1-LT004	C 352	31	16.6	689	17	AG097968	AG097968 Pan trogl
C 280	31	16.6	267	12	BF807023	BF807023 QV4-CIT015	C 353	31	16.6	701	17	AQ531646	AQ531646 RPCI-11-3
C 281	31	16.6	274	12	BF807024	BF807024 QV4-CIT015	C 354	31	16.6	719	17	AG153387	AG153387 Pan trogl
C 282	31	16.6	280	17	AQ094824	AQ094824 HS_3028_B	C 355	31	16.6	731	9	AQ627605	AQ627605 CITBI-E1-
C 283	31	16.6	285	9	AI868487	AI868487 tc51f06.x	C 356	31	16.6	752	9	AI816245	AI816245 au46b02.x
C 284	31	16.6	292	17	AQ582699	AQ582699 RPCI-11-4	C 357	31	16.6	785	10	BE396566	BE396566 601288992
C 285	31	16.6	293	14	R12832	R12832 yf57f09.r1	C 358	31	16.6	848	17	AQ752067	AQ752067 HS_55770_B
C 286	31	16.6	295	12	BF805606	BF805606 QV1-CIT017	C 359	31	16.6	859	17	AQ746029	AQ746029 HS_2277_A
C 287	31	16.6	305	12	BF834988	BF834988 PM3-HT092	C 360	31	16.6	911	12	BG432418	BG432418 602495449
C 288	31	16.6	324	9	AI240840	AI240840 qh54f07.x	C 361	31	16.6	958	13	BI829583	BI829583 60379319
C 289	31	16.6	325	12	BF833644	BF833644 PM3-HT092	C 362	31	16.6	1058	13	BM552320	BM552320 AGENCOURT
C 290	31	16.6	331	14	F07346	F07346 HSC22G051.n	C 363	30	16.0	103	10	AW818097	AW818097 CM4-ST027
C 291	31	16.6	336	17	AQ037232	AQ037232 CIT-HSP-2	C 364	30	16.0	113	10	BE155428	BE155428 PM1-HT035
C 292	31	16.6	337	9	AA470600	AA470600 nc69f12.r	C 365	30	16.0	123	14	T18553	T18553 hbc2055 Hum
C 293	31	16.6	348	9	AA836156	AA836156 odi6c07.s	C 366	30	16.0	129	17	AQ393826	AQ393826 CITBI-E1-
C 294	31	16.6	348	14	R07081	R07081 yf13e01.r1	C 367	30	16.0	166	12	BG236478	BG236478 naf28g07.
C 295	31	16.6	355	14	T90895	T90895 yd48b11.s1	C 368	30	16.0	174	10	AW848983	AW848983 IL3-CT021
C 296	31	16.6	371	9	AA470609	AA470609 nc59h09.s	C 369	30	16.0	191	12	BF844107	BF844107 MR2-HT104
C 297	31	16.6	375	12	BF174954	BF174954 MYE1124a	C 370	30	16.0	212	12	BF843242	BF843242 MR2-HT104
C 298	31	16.6	394	14	R43081	R43081 ygl7e07.s1	C 371	30	16.0	262	9	AA533836	AA533836 nj94d03.s

C 372	30	16.0	262	12	BF891514	BF891514 PM3-WT011	445	30	16.0	609	10	AW975001	AW975001 EST387106
C 373	30	16.0	274	9	AA281726	AA281726 zc07e04.s	446	30	16.0	623	17	AG157923	AG157923 Pan trogl
C 374	30	16.0	289	14	H63269	H63269 yrl5h05.s1	C 447	30	16.0	626	10	AW962581	AW962581 EST374654
C 375	30	16.0	295	9	AA834690	AA834690 od99b03.s	C 448	30	16.0	633	17	AQ279400	AQ279400 CITBI-EI-
C 376	30	16.0	305	9	AA635295	AA635295 wt71d04.s	C 449	30	16.0	642	17	AQ336538	AQ336538 RPCI-11-3
C 377	30	16.0	319	9	AI872352	AI872352 nm35c06.x	C 450	30	16.0	664	17	AQ309089	AQ309089 CITBI-EI-
C 378	30	16.0	319	10	BE145115	BE145115 CW4-HT019	C 451	30	16.0	671	17	AG057609	AG057609 Pan trogl
C 379	30	16.0	324	17	B82231	B82231 RPCI11-13M4	C 452	30	16.0	674	17	AG087269	AG087269 Pan trogl
C 380	30	16.0	333	9	AA846890	AA846890 oe08a01.s	C 453	30	16.0	679	9	AA715049	AA715049 nx94d12.s
C 381	30	16.0	337	9	AA584925	AA584925 nm33d04.s	C 454	30	16.0	685	17	AQ016886	AQ016886 CIT-HSP-2
C 382	30	16.0	337	14	N70409	N70409 za61a12.s1	C 455	30	16.0	689	17	AG125044	AG125044 Pan trogl
C 383	30	16.0	342	12	BF855008	BF855008 WR1-FN021	C 456	30	16.0	694	17	AG069532	AG069532 Pan trogl
C 384	30	16.0	343	14	H68086	H68086 yul5e04.s1	C 457	30	16.0	698	10	AV685392	AV685392 AV685392
C 385	30	16.0	357	9	AA094643	AA094643 cp0942.se	C 458	30	16.0	704	14	BM981128	BM981128 UI-CR-EN1
C 386	30	16.0	360	12	BF848352	BF848352 FW4-EN006	C 459	30	16.0	731	12	BM9259843	BM9259843 602371992
C 387	30	16.0	365	10	AW069667	AW069667 cr49h02.x	C 460	30	16.0	758	12	BG723353	BG723353 602694262
C 388	30	16.0	367	10	AW805877	AW805877 QV1-UM010	C 461	30	16.0	758	17	AG030513	AG030513 Pan trogl
C 389	30	16.0	372	9	AA283064	AA283064 zt14a11.r	C 462	30	16.0	761	17	AG186292	AG186292 Pan trogl
C 390	30	16.0	374	12	BF961453	BF961453 RC6-NN023	C 463	30	16.0	790	9	AL601348	AL601348 DKE2p313A
C 391	30	16.0	380	10	AW902186	AW902186 QV3-NN102	C 464	30	16.0	854	12	BG433829	BG433829 602497353
C 392	30	16.0	381	9	AA650145	AA650145 ns90g09.s	C 465	30	16.0	858	17	AQ741568	AQ741568 HS 5572.B
C 393	30	16.0	382	10	AW068977	AW068977 gr39f03.x	C 466	30	16.0	885	17	BF215212	BF215212 601846983
C 394	30	16.0	389	9	AA748026	AA748026 nx87d06.s	C 467	30	16.0	895	14	BQ213585	BQ213585 AGENCOURT
C 395	30	16.0	393	14	R43529	R43529 ygl9d05.s1	C 468	30	16.0	919	12	BE788574	BE788574 601476093
C 396	30	16.0	395	9	AI095204	AI095204 ov83c10.s	C 469	30	16.0	940	12	BE893063	BE893063 601436548
C 397	30	16.0	395	9	AI381434	AI381434 td01b01.x	C 470	30	16.0	957	12	BE895584	BE895584 601438382
C 398	30	16.0	397	14	T89762	T89762 yd99c02.r1	C 471	30	16.0	987	13	BM471500	BM471500 AGENCOURT
C 399	30	16.0	398	12	BF961435	BF961435 RC6-NN023	C 472	30	16.0	1112	13	BM548235	BM548235 AGENCOURT
C 400	30	16.0	400	10	AW663330	AW663330 hh7e02.y	C 473	29	15.5	126	9	AI312481	AI312481 ta91f02.x
C 401	30	16.0	413	9	AI285709	AI285709 qu81a02.x	C 474	29	15.5	162	9	AA347077	AA347077 EST53326
C 402	30	16.0	414	17	AQ323275	AQ323275 RPCI11-99	C 475	29	15.5	168	9	AA429130	AA429130 zw19b05.r
C 403	30	16.0	416	12	EG555296	EG555296 602582984	C 476	29	15.5	175	9	AQ263841	AQ263841 CITBI-EI-
C 404	30	16.0	417	17	AQ230188	AQ230188 HS-2041.B	C 477	29	15.5	218	17	AQ005651	AQ005651 CIT-HSP-2
C 405	30	16.0	419	14	BM721579	BM721579 UI-E-EOI-	C 478	29	15.5	238	17	AI625977	AI625977 ar91g02.x
C 406	30	16.0	423	17	AQ815322	AQ815322 HS 5014.A	C 479	29	15.5	259	9	BF929478	BF929478 IL2-NOT02
C 407	30	16.0	437	17	AQ110019	AQ110019 CIT-HSP-2	C 480	29	15.5	273	12	BF929478	BF929478 IL2-NOT02
C 408	30	16.0	439	17	AQ438712	AQ438712 HS 5141.A	C 481	29	15.5	275	9	AI933797	AI933797 wn92d08.x
C 409	30	16.0	441	9	AI821120	AI821120 ns90g09.y	C 482	29	15.5	285	9	AA601693	AA601693 no02d03.s
C 410	30	16.0	443	9	AA489868	AA489868 ab01b08.r	C 483	29	15.5	287	9	AI452770	AI452770 tc45c12.x
C 411	30	16.0	447	9	AA648731	AA648731 ns34d07.s	C 484	29	15.5	306	9	AA244239	AA244239 nj06a11.s
C 412	30	16.0	453	12	BG059520	BG059520 nah62h04.	C 485	29	15.5	309	9	AI039234	AI039234 ox32e09.s
C 413	30	16.0	453	13	BI712813	BI712813 le09e11.y	C 486	29	15.5	310	9	AA371011	AA371011 EST82835
C 414	30	16.0	454	9	AA813393	AA813393 aj33d02.s	C 487	29	15.5	312	14	BQ355605	BQ355605 MR4-HT126
C 415	30	16.0	458	17	AQ015673	AQ015673 CIT-HSP-2	C 488	29	15.5	314	9	AA663283	AA663283 ab81a08.s
C 416	30	16.0	472	9	AI972099	AI972099 wr52e02.x	C 489	29	15.5	316	10	AW613931	AW613931 hg71c08.x
C 417	30	16.0	472	9	AA491444	AA491444 ab01b08.s	C 490	29	15.5	317	13	BI045154	BI045154 RC6-FN020
C 418	30	16.0	485	9	AA028137	AA028137 zk07e03.s	C 491	29	15.5	322	10	AW351985	AW351985 CM0-HT009
C 419	30	16.0	488	9	AA658935	AA658935 nt85g04.s	C 492	29	15.5	325	10	AW196601	AW196601 xm35c06.x
C 420	30	16.0	501	14	BM672958	BM672958 UI-E-CQO-	C 493	29	15.5	333	14	BM672790	BM672790 UI-E-CQO-
C 421	30	16.0	505	14	BM686779	BM686779 UI-E-CQO-	C 494	29	15.5	338	14	M77904	M77904 EST01488.Fe
C 422	30	16.0	513	9	AI950421	AI950421 wq35c04.x	C 495	29	15.5	345	10	AV690340	AV690340 AV690340
C 423	30	16.0	523	13	EG993351	EG993351 MR3-HT099	C 496	29	15.5	348	10	AV685168	AV685168 AV685168
C 424	30	16.0	524	12	BF924273	BF924273 MR2-NOT13	C 497	29	15.5	351	9	AA687547	AA687547 nu27e03.s
C 425	30	16.0	525	9	AI821864	AI821864 ns90g09.x	C 498	29	15.5	351	17	B72993	B72993 RPCI11-10N1
C 426	30	16.0	538	12	BF854095	BF854095 MR2-EN009	C 499	29	15.5	355	10	AW613944	AW613944 hg71e08.x
C 427	30	16.0	538	12	BF956902	BF956902 RCI-NN023	C 500	29	15.5	358	10	AW105452	AW105452 xg52d07.x
C 428	30	16.0	541	10	AW979221	AW979221 EST391331	C 501	29	15.5	359	9	AI376993	AI376993 tc34g07.x
C 429	30	16.0	544	17	AQ344993	AQ344993 CITBI-EI-	C 502	29	15.5	361	9	AL710493	AL710493 DKE2p686H
C 430	30	16.0	545	17	AQ378718	AQ378718 RPCI-11-1	C 503	29	15.5	361	9	AL710493	AL710493 DKE2p686H
C 431	30	16.0	547	17	B48233	B48233 RPCI11-6G2.	C 504	29	15.5	368	14	N62686	N62686 za15f10.s1
C 432	30	16.0	548	10	BE145625	BE145625 IL0-HT020	C 505	29	15.5	370	14	BM706618	BM706618 UI-E-CQO-
C 433	30	16.0	550	17	AQ455175	AQ455175 HS 5079.B	C 506	29	15.5	372	12	BF766884	BF766884 CM3-CS000
C 434	30	16.0	555	17	AQ435224	AQ435224 CITBI-EI-	C 507	29	15.5	375	9	AI192587	AI192587 qe61f09.x
C 435	30	16.0	566	10	AW795447	AW795447 MR4-UM001	C 508	29	15.5	379	13	BI026468	BI026468 CM4-WT028
C 436	30	16.0	575	10	AW858657	AW858657 CM2-CT034	C 509	29	15.5	379	17	BI026468	BI026468 CM4-WT028
C 437	30	16.0	578	17	AQ469734	AQ469734 CITBI-EI-	C 510	29	15.5	382	10	AA287992	AA287992 z855d05.f
C 438	30	16.0	580	17	AQ311112	AQ311112 CITBI-EI-	C 511	29	15.5	382	10	BE181661	BE181661 QV1-HT063
C 439	30	16.0	587	17	AQ275024	AQ275024 RPCI-5-11	C 512	29	15.5	388	14	N48878	N48878 Y77b06.s1
C 440	30	16.0	587	17	AG016809	AG016809 Homo sapi	C 513	29	15.5	388	14	T96976	T96976 ye50h08.s1
C 441	30	16.0	595	17	AQ725304	AQ725304 HS-5404.A	C 514	29	15.5	390	14	BQ694126	BQ694126 1000269.H
C 442	30	16.0	595	17	AQ543268	AQ543268 RPCI-11-3	C 515	29	15.5	392	14	AA476418	AA476418 zx02a12.s
C 443	30	16.0	602	12	BG617170	BG617170 602615566	C 516	29	15.5	392	13	BI495581	BI495581 df119c03.
C 444	30	16.0	609	9	AA121504	AA121504 zk88b09.s	C 517	29	15.5				

c 518	29	15.5	393	13	BI495582	BI495582 df119c03..	c 591	29	15.5	529	12	BF668501
519	29	15.5	394	9	AA181902	AA181902 zp63d06.s	592	29	15.5	533	17	BI6189
520	29	15.5	395	9	AA640681	AA640681 nt70c10.s	593	29	15.5	535	14	T54095
521	29	15.5	403	9	AI453629	AI453629 tj45f08.x	594	29	15.5	536	9	AI732594
c 522	29	15.5	405	17	AQ112829	AQ112829 CIT-HSP-2	595	29	15.5	536	10	BE170274
523	29	15.5	410	10	AW265069	AW265069 xg60h07.x	c 596	29	15.5	537	10	AW846932
524	29	15.5	411	10	AW238203	AW238203 xp21e08.x	c 597	29	15.5	537	10	AW846932
525	29	15.5	413	10	AW471153	AW471153 xu08e02.x	598	29	15.5	541	9	AI809122
526	29	15.5	413	14	T50387	T50387 yb30a08.s1	c 599	29	15.5	541	17	AQ533134
c 527	29	15.5	414	13	BM021066	BM021066 ie75d02.x	600	29	15.5	544	17	B73164
528	29	15.5	414	17	AQ603768	AQ603768 HS.2126.A	c 601	29	15.5	546	14	BQ673038
529	29	15.5	417	9	AI839943	AI839943 wj88e04.x	602	29	15.5	551	17	AQ309709
530	29	15.5	418	9	AA635412	AA635412 nt68c07.s	c 603	29	15.5	552	17	AZ518780
531	29	15.5	420	9	AA054219	AA054219 wf52e02.s	604	29	15.5	555	17	AQ074924
532	29	15.5	422	9	AI984473	AI984473 zf83d10.x	c 605	29	15.5	555	17	AQ072759
533	29	15.5	425	9	AI050020	AI050020 an22d03.x	c 606	29	15.5	561	12	BF736316
534	29	15.5	428	17	AQ671819	AQ671819 HS.5458.B	c 607	29	15.5	561	12	BQ381485
535	29	15.5	430	9	AA639076	AA639076 nb03a06.F	608	29	15.5	561	17	AQ536306
536	29	15.5	430	17	AQ168926	AQ168926 HS.3174.A	609	29	15.5	570	17	AQ541858
537	29	15.5	430	17	AQ168946	AQ168946 HS.3174.A	610	29	15.5	571	17	AQ371948
538	29	15.5	434	9	AI809829	AI809829 wh77f12.x	c 611	29	15.5	571	17	AQ371948
c 539	29	15.5	434	9	AA430262	AA430262 zw65h04.F	612	29	15.5	581	9	AI341559
540	29	15.5	441	9	AA700314	AA700314 zj73h09.s	613	29	15.5	592	9	AA614340
c 541	29	15.5	443	9	AI734103	AI734103 zn19b05.Y	614	29	15.5	620	14	BQ776015
542	29	15.5	443	9	AA583227	AA583227 nm33f11.s	c 615	29	15.5	621	14	BM686415
543	29	15.5	444	10	AA265068	AA265068 xg60g07.x	c 616	29	15.5	626	17	BQ6951
544	29	15.5	445	9	AA132735	AA132735 zo18g06.s	c 617	29	15.5	629	10	AW937743
545	29	15.5	445	9	AA568308	AA568308 nf15b04.s	618	29	15.5	632	10	AW272208
546	29	15.5	445	17	AQ166168	AQ166168 HS.3070.B	c 619	29	15.5	633	10	AV711379
547	29	15.5	446	14	H66848	H66848 yr71c04.s1	c 620	29	15.5	633	17	AQ003147
548	29	15.5	448	9	AA021890	AA021890 ze67c12.F	c 621	29	15.5	639	17	AQ089588
549	29	15.5	451	9	AI025850	AI025850 ow12c06.s	622	29	15.5	641	17	AG147536
550	29	15.5	451	14	H61877	H61877 yr02c08.r1	623	29	15.5	643	13	BM044552
c 551	29	15.5	453	10	AW819579	AW819579 RC5-ST029	624	29	15.5	646	12	BF718626
552	29	15.5	454	12	BF854518	BF854518 MR2-EN009	c 625	29	15.5	647	10	AW962646
c 553	29	15.5	457	12	BF996660	BF996660 PM4-GN006	626	29	15.5	666	17	AG074231
554	29	15.5	458	12	BF116111	BF116111 7132b05.x	c 627	29	15.5	679	17	AG147935
555	29	15.5	459	17	AQ786548	AQ786548 HS.3086.B	c 628	29	15.5	683	17	AG165239
556	29	15.5	460	9	AI469824	AI469824 tj87e04.x	c 629	29	15.5	686	12	BG427545
c 557	29	15.5	461	9	AA179446	AA179446 zp45c03.F	c 630	29	15.5	689	17	AQ386353
558	29	15.5	468	9	AI034073	AI034073 ox12b07.x	c 631	29	15.5	691	17	AQ780061
559	29	15.5	468	9	AI478300	AI478300 tm39e01.x	632	29	15.5	696	17	B81466
560	29	15.5	468	10	AW264320	AW264320 qx98c06.x	633	29	15.5	707	17	AQ415514
c 561	29	15.5	468	12	BG007192	BG007192 PM2-GN001	634	29	15.5	713	17	AQ267177
c 562	29	15.5	473	10	AW819581	AW819581 RC5-ST029	c 635	29	15.5	717	17	AG177031
c 563	29	15.5	475	9	AI361719	AI361719 qz18h03.x	c 636	29	15.5	725	13	BI916155
564	29	15.5	486	12	BF853957	BF853957 MR2-EN009	c 637	29	15.5	725	10	AW850586
c 565	29	15.5	487	14	BM689148	BM689148 UI-E-CQ1-	c 638	29	15.5	727	14	W28851
566	29	15.5	487	14	H74185	H74185 yu02b03.s1	c 639	29	15.5	789	12	BG565408
c 567	29	15.5	488	17	AQ812921	AQ812921 HS.5300.B	640	29	15.5	822	13	BM012392
568	29	15.5	490	12	BF436024	BF436024 nab34a07.	641	29	15.5	825	12	BF665467
569	29	15.5	491	9	AI708321	AI708321 at04b03.x	642	29	15.5	843	12	BG499230
570	29	15.5	495	9	AI416596	AI416596 th02a05.x	643	29	15.5	871	14	BQ889198
571	29	15.5	496	17	AQ411061	AQ411061 HS.5064.B	c 644	29	15.5	886	12	BF967751
572	29	15.5	499	17	AQ245993	AQ245993 HS.2059.A	c 645	29	15.5	887	17	AG180245
573	29	15.5	503	13	BM662910	BM662910 UI-E-CK0-	646	29	15.5	897	14	BQ884289
c 574	29	15.5	505	9	AA234699	AA234699 z839g05.F	c 647	29	15.5	912	14	BQ876665
575	29	15.5	506	9	AI400709	AI400709 tg93g05.x	648	29	15.5	944	12	BG121050
576	29	15.5	506	17	AQ372034	AQ372034 RPC11-15	649	29	15.5	947	12	BG290621
c 577	29	15.5	509	17	AQ189357	AQ189357 HS.3199.B	650	29	15.5	957	12	BQ878431
578	29	15.5	511	9	AA978266	AA978266 op46b10.s	651	29	15.5	977	14	BQ950224
579	29	15.5	514	14	BQ183977	BQ183977 UI-H-EU0-	652	28	15.0	124	9	AA489088
580	29	15.5	515	17	AQ169206	AQ169206 HS.3175.B	c 653	28	15.0	156	12	BF929895
581	29	15.5	517	9	AA703833	AA703833 ag78g09.F	654	28	15.0	178	14	BM718789
c 582	29	15.5	517	17	AQ186702	AQ186702 HS.3115.A	655	28	15.0	223	9	AA558078
c 583	29	15.5	517	17	AQ534213	AQ534213 RPC1-11-3	c 656	28	15.0	224	12	BF854944
584	29	15.5	517	17	AQ244095	AQ244095 HS.2063.B	c 657	28	15.0	233	17	AA248704
c 585	29	15.5	520	10	BE069849	BE069849 CM4-BT039	c 658	28	15.0	236	17	B68583
c 586	29	15.5	521	17	AQ554188	AQ554188 RPC1-11-4	659	28	15.0	239	10	BE152023
c 587	29	15.5	521	17	AQ827518	AQ827518 HS.5304.A	660	28	15.0	240	10	BE067838
c 588	29	15.5	523	9	AA017574	AA017574 ze37e04.F	661	28	15.0	242	10	BE152096
c 589	29	15.5	528	10	BE166317	BE166317 QV4-HT049	662	28	15.0	247	10	AW083681
590	29	15.5	529	9	AA020904	AA020904 ze64h09.F	c 663	28	15.0	253	10	AW886174

c 664	28	15.0	297	14	R34029	R34029 yh83d06.r1	c 737	28	15.0	552	12	BGI89114	BI89114 RST8153 A
c 665	28	15.0	308	9	AA584677	AA584677 n09b07.s	738	28	15.0	558	17	AQ562775	AQ562775 HS 2079 B
c 666	28	15.0	311	14	R67777	R67777 y128h06.r1	c 739	28	15.0	561	17	AQ267549	AQ267549 RPCI11-73
c 667	28	15.0	309	14	R67756	R67756 y128e07.r1	740	28	15.0	563	9	AA482037	AA482037 z198h06.s
c 668	28	15.0	324	12	BF84904	BF84904 RPCI11-28M3	c 741	28	15.0	567	17	AQ421424	AQ421424 RPCI-11-1
c 669	28	15.0	328	12	BF817311	BF817311 PM3-CI011	c 742	28	15.0	576	17	AQ245110	AQ245110 HS 2059 A
c 670	28	15.0	338	10	AW009059	AW009059 w875g03.x	c 743	28	15.0	592	17	AQ120007	AQ120007 HS 3022 B
c 671	28	15.0	344	14	F35325	F35325 HSPD31385.H	c 744	28	15.0	622	17	AG161008	AG161008 Pan trogl
c 672	28	15.0	344	14	T83216	T83216 yd48b011.r1	c 745	28	15.0	640	10	AW971457	AW971457 EST383546
c 673	28	15.0	345	9	AA757872	AA757872 z940c11.s	746	28	15.0	643	17	AG154460	AG154460 Pan trogl
c 674	28	15.0	349	17	AQ839629	AQ839629 HS 4707 A	747	28	15.0	644	17	AG154268	AG154268 Pan trogl
c 675	28	15.0	361	17	B70512	B70512 CIT-HSP-205	c 748	28	15.0	654	17	AG053415	AG053415 Pan trogl
c 676	28	15.0	362	9	AA993968	AA993968 ou34c08.s	c 749	28	15.0	658	17	AZ520093	AZ520093 RPCI-11-2
c 677	28	15.0	362	9	AA508640	AA508640 nm66g12.s	c 750	28	15.0	659	17	AG086436	AG086436 Pan trogl
c 678	28	15.0	367	14	H23683	H23683 ym72c11.r1	c 751	28	15.0	661	17	AG160937	AG160937 Pan trogl
c 679	28	15.0	368	17	B88097	B88097 RPCI11-18G1	752	28	15.0	664	14	AW982678	AW982678 UI-CF-EN1
c 680	28	15.0	371	10	AW857889	AW857889 RC4-CT032	753	28	15.0	666	17	AQ395356	AQ395356 CITBI-EL-
c 681	28	15.0	371	14	R00488	R00488 ye74a05.s1	754	28	15.0	672	17	AG073268	AG073268 Pan trogl
c 682	28	15.0	375	9	AA634936	AA634936 ab28h07.r	c 755	28	15.0	673	17	AG137583	AG137583 Pan trogl
c 683	28	15.0	381	12	BG014646	BG014646 IL5-GN023	c 756	28	15.0	674	17	AG056575	AG056575 Pan trogl
c 684	28	15.0	383	17	AQ223300	AQ223300 HS 2016.A	757	28	15.0	674	17	AG070745	AG070745 Pan trogl
c 685	28	15.0	389	17	AQ036470	AQ036470 CIT-HSP-2	758	28	15.0	676	10	AW978209	AW978209 EST390318
c 686	28	15.0	395	9	AA954475	AA954475 on73d07.s	759	28	15.0	689	17	AG096816	AG096816 Pan trogl
c 687	28	15.0	395	12	BF805575	BF805575 QV1-CI017	c 760	28	15.0	694	12	BF344600	BF344600 602015221
c 688	28	15.0	395	14	H46876	H46876 y019e01.r1	c 761	28	15.0	703	17	AG002669	AG002669 Homo sapi
c 689	28	15.0	396	9	AA600325	AA600325 ag04d01.s	762	28	15.0	706	13	BI086004	BI086004 602870228
c 690	28	15.0	400	14	BQ354138	BQ354138 RC0-HI095	763	28	15.0	708	17	B02898	B02898 CSRL-162D12
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c 692	28	15.0	405	9	AA527830	AA527830 nm25d08.s	765	28	15.0	713	13	BI226587	BI226587 602951569
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c 697	28	15.0	426	9	AA504788	AA504788 ab02g07.r	770	28	15.0	779	14	W28662	W28662 49h10 Human
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c 702	28	15.0	445	14	H49368	H49368 yq18h10.s1	c 775	28	15.0	885	17	AQ738816	AQ738816 HS 5386 B
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c 709	28	15.0	460	17	AQ705348	AQ705348 HS 5526.B	c 782	28	15.0	1070	12	BF982751	BF982751 602304963
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c 732	28	15.0	533	9	AA805354	AA805354 oc15e06.s	c 805	27	14.4	246	17	AO017368	AO017368 CIT-HSP-2
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c 815	27	14.4	300	14	T05319	T05319 EST03208.Fe	c 888	27	14.4	442	12	BF111659	BF111659 7132g09.x
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c 991 27 14.4 666 17 AG133782
c 992 27 14.4 672 17 AG150099
c 993 27 14.4 672 17 AG151558
c 994 27 14.4 673 17 AG067879
c 995 27 14.4 674 17 AG067339
c 996 27 14.4 675 17 AG046145
c 997 27 14.4 675 12 BG218374
c 998 27 14.4 676 12 BG218374
c 999 27 14.4 676 17 AG148657
c1000 27 14.4 676 17 AG148657

```

## ALIGNMENTS

```

RESULT 1
AQ785529 459 bp DNA linear GSS 03-AUG-1999
LOCUS HS_3063_A2_H06_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3063 Col=12 Row=O, DNA sequence.
ACCESSION AQ785529
VERSION AQ785529.1 GI:5693153
KEYWORDS GSS.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 459)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington

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401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3063 row: O column: 12
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 459.
FEATURES
    source
        Location/Qualifiers
            1..459
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="Plate=3063 Col=12 Row=O"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /sex="male"
                /notes="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 118 a 114 c 89 g 138 t
ORIGIN
Query Match 22.5%; Score 42; DB 17; Length 459;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ATCATAGCTACGACGCTCATCTCTGGGCTCAAGCAAT 45
Db 229 ATCATAGCTACGACGCTCATCTCTGGGCTCAAGCAAT 270
RESULT 2
AA864787 166 bp mRNA linear EST 13-MAY-1998
LOCUS ch02f06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1456643 3'
DEFINITION similar to contains Alu repetitive element; contains element LTR7
repetitive element ;, mRNA sequence.
ACCESSION AA864787.1 GI:2959100
VERSION AA864787.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 644 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 129.
FEATURES
    source
        Location/Qualifiers
            1..166
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:1456643"
                /clone_lib="NCI_CGAP_Kid3"
                /lab_host="DH10B"
                /notes="Organ: kidney; Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors

```

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 47 a 38 c 38 g 43 t

ORIGIN  
Query Match 21.4%; Score 40; DB 9; Length 166;  
Best Local Similarity 100.0%; Pred. No. 6.8e-08;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 66  
|||||  
Db 39 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 78  
|||||

RESULT 3  
B49276/c  
DEFINITION  
RPCI11-5L13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-5L13, DNA sequence.

ACCESSION B49276  
VERSION B49276.1 GI:2601513

KEYWORDS GSS.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 252)  
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter J.C.

TITLE Use of BAC End Sequences for Sequence-Ready Map Building

JOURNAL

COMMENT

Unpublished (1997)

Other\_GSSs: RPCI11-5L13.TV

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@igr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..252

/organism="Homo sapiens"

/db\_xref="GDB:7501812"

/db\_xref="taxon:9606"

/clone="RPCI-11-5L13"

/clone\_lib="RPCI-11"

/sex="Male"

/cell\_type="Lymphocytes"

/note="vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"

71 a 53 c 68 g 60 t

BASE COUNT 71 a 53 c 68 g 60 t

ORIGIN  
Query Match 21.4%; Score 40; DB 17; Length 252;  
Best Local Similarity 100.0%; Pred. No. 6.2e-08;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 66  
|||||  
Db 94 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 55  
|||||

RESULT 4

AI139009

LOCUS

DEFINITION

q883g09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1736128

2' similar to contains Alu repetitive element; contains element LTR7

LTR7 repetitive element ; mRNA sequence.

AI139009

VERSION

AI139009.1 GI:3644981

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 388)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 665 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 363.

Location/Qualifiers

1..388

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1736128"

/clone\_lib="Soares\_testis\_NHT"

/sex="Male"

/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5']

TGTTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTT 3']

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo. "

109 a 73 c 110 g 96 t

BASE COUNT

ORIGIN

Query Match 21.4%; Score 40; DB 9; Length 388;

Best Local Similarity 100.0%; Pred. No. 5.7e-08;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 66  
|||||

Db 42 ACTCTGGGCTCAAGCAATCTCTGCTCAGCTTCCAA 81  
|||||

RESULT 5

AI140075

LOCUS

DEFINITION

q87c12.x1 Soares fetal heart NDHH19W Homo sapiens cDNA clone

IMAGE:1693750 3' similar to contains Alu repetitive element

; contains element LTR7 repetitive element ; mRNA sequence.

AI140075

VERSION

AI140075.1 GI:3647532

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AI140075 433 bp mRNA linear EST 11-APR-1999

q87c12.x1 Soares fetal heart NDHH19W Homo sapiens cDNA clone

IMAGE:1693750 3' similar to contains Alu repetitive element

; contains element LTR7 repetitive element ; mRNA sequence.

AI140075

VERSION

AI140075.1 GI:3647532

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 433)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1086 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 427.
FEATURES
source
1..433
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_hosts="DH10B (ampicillin resistant)"
/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatina Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHH19W."
BASE COUNT 121 a 81 c 122 g 109 t
ORIGIN
Query Match 21.4%; Score 40; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 66
|||||
Db 39 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 78
|||||
RESULT 6
LOCUS AI077461 458 bp mRNA linear EST 01-OCT-1998
DEFINITION o237d07.x1 Soares NhMPu.S1 Homo sapiens cDNA clone IMAGE:1677517
3' similar to contains Alu repetitive element; contains element LTR7
repetitive element ;, mRNA sequence.
ACCESSION AI077461
VERSION AI077461.1 GI:3411869
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 458)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 984 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES
source
1..458
/organism="Homo sapiens"

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```

/db_xref="taxon:9606"
/clone_lib="Soares_NhMPu.S1"
/tissue_type="pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/notes="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 128 a 86 c 130 g 114 t
ORIGIN
Query Match 21.4%; Score 40; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 66
|||||
Db 39 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCCAA 78
|||||
RESULT 7
LOCUS BQ182580 629 bp mRNA linear EST 30-APR-2002
DEFINITION UI-H-EU0-arj-n-01-0-UI.s1 NCI-CGAP_Carl Homo sapiens cDNA clone
IMAGE: 5849664 3', mRNA sequence.
ACCESSION BQ182580
VERSION BQ182580.1 GI:20358130
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 629)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 18-215, >LIM4_5 (matched complement) 224-394, >ALU
(matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
source
1..629
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP_Carl"
/tissue_type="Osteoarthritic Cartilage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI-CGAP Carl is a cDNA library containing the following
tissue(s): Osteoarthritic Cartilage The library was
constructed according to Bonaldo, Lennon and Soares,

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Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCAGCCT.

TAG LIB=UI-H-EUO  
TAG TISSUE=osteochondritic cartilage  
TAG\_SEQ=TGATCAGCCT"

BASE COUNT 128 a 114 c 118 g 269 t  
ORIGIN

Query Match 21.4%; Score 40; DB 14; Length 629;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08; Gaps 0;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66  
|||||  
Db 302 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 341  
|||||

RESULT 8  
AG172545 682 bp DNA linear GSS 09-JAN-2002  
LOCUS  
DEFINITION  
Pan troglodytes DNA, clone: RP43-042D19.T7, genomic survey sequence.

ACCESSION  
AG172545  
VERSION  
AG172545.1 GI:16702225  
KEYWORDS  
GSS; (genome survey sequence).  
SOURCE  
Pan troglodytes male lymphocytes DNA, clone lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-042D19.T7.

ORGANISM  
Pan troglodytes

REFERENCE  
1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library RPCI-43  
Unpublished  
2 (bases 1 to 682)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/; Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1. .682  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="RP43-042D19.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone lib="RPCI-43 Chimpanzee Male BAC Library"  
BASE COUNT 200 a 143 c 141 g 197 t  
ORIGIN

Query Match 21.4%; Score 40; DB 17; Length 682;  
Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCAGCCT.

TAG LIB=UI-H-EUO  
TAG TISSUE=osteochondritic cartilage  
TAG\_SEQ=TGATCAGCCT"

BASE COUNT 128 a 114 c 118 g 269 t  
ORIGIN

Query Match 21.4%; Score 40; DB 14; Length 629;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08; Gaps 0;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66  
|||||  
Db 302 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 341  
|||||

RESULT 8  
AG172545 682 bp DNA linear GSS 09-JAN-2002  
LOCUS  
DEFINITION  
Pan troglodytes DNA, clone: RP43-042D19.T7, genomic survey sequence.

ACCESSION  
AG172545  
VERSION  
AG172545.1 GI:16702225  
KEYWORDS  
GSS; (genome survey sequence).  
SOURCE  
Pan troglodytes male lymphocytes DNA, clone lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-042D19.T7.

ORGANISM  
Pan troglodytes

REFERENCE  
1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library RPCI-43  
Unpublished  
2 (bases 1 to 682)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/; Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1. .682  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="RP43-042D19.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone lib="RPCI-43 Chimpanzee Male BAC Library"  
BASE COUNT 200 a 143 c 141 g 197 t  
ORIGIN

Query Match 21.4%; Score 40; DB 17; Length 682;  
Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66  
|||||  
Db 587 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 626  
|||||

RESULT 9  
AQ599298 411 bp DNA linear GSS 08-JUN-1999  
LOCUS  
DEFINITION  
HS 5343\_B2\_B02\_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=919 Col=4 Row=D, DNA sequence.

ACCESSION  
AQ599298  
VERSION  
AQ599298.1 GI:5030391  
KEYWORDS  
GSS.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 411)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
99380589  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm) or from Research h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu  
Plate: 919 row: D column: 4  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 411.  
Location/Qualifiers  
1. .411  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="plate=919 Col=4 Row=D"  
/clone lib="RPCI-11 Human Male BAC Library"  
/sex="male"  
/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"  
BASE COUNT 103 a 87 c 94 g 122 t  
ORIGIN

Query Match 20.9%; Score 39; DB 17; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 66  
|||||  
Db 265 CTCTGGGCTCAAGCAATCTCTGCTCAGCCTTCCAA 303  
|||||

RESULT 10  
AQ685901 446 bp DNA linear GSS 28-JUN-1999  
LOCUS  
DEFINITION  
HS\_5550\_Al\_E10\_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1126 Col=19 Row=1, DNA sequence.

ACCESSION AQ685901  
 VERSION AQ685901.1 GI:5261972  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 446)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallaceu.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
 http://www.hsc.washington.edu  
 Plate: 1126 row: 1 column: 19  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 446.  
 Location/Qualifiers  
 1..446  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Plate:1126 Col=19 Row=1"  
 /clone\_lib="RPCI-11 Human Male BAC Library"  
 /sex="male"  
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACE3.6 vector at EcoRI sites"  
 BASE COUNT 126 a 82 c 97 g 139 t 2 others  
 ORIGIN  
 Query Match 20.9%; Score 39; DB 17; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GATCATAGCTCACTGCAGCCTCATCTCTGGGCTCAAG 41  
 |||||  
 DB 379 GATCATAGCTCACTGCAGCCTCATCTCTGGGCTCAAG 417  
 |||||  
 RESULT 11  
 AQ426550/c 463 bp DNA linear GSS 24-MAR-1999  
 LOCUS CITBI-EI-2574H6.TR CITBI-EI Homo sapiens genomic clone 2574H6, DNA  
 DEFINITION sequence.  
 ACCESSION AQ426550  
 VERSION AQ426550.1 GI:4499318  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 463)  
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and  
 Venter,J.C.  
 TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready  
 Map Building

JOURNAL Unpublished (1997)  
 COMMENT Other GSSs: CITBI-EI-2574H6.TF  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbeetigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC  
 end search page:  
 http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
 Seq primer: M13 Reverse  
 Class: BAC ends.  
 Location/Qualifiers  
 1..463  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="2574H6"  
 /clone\_lib="CITBI-EI"  
 /sex="male"  
 /cell\_type="sperm"  
 /note="Vector: pBelOBAC11; Site 1: EcoRI; Site 2: EcoRI;  
 Caltech Human BAC Library D"  
 BASE COUNT 115 a 126 c 103 g 119 t  
 ORIGIN  
 Query Match 20.3%; Score 38; DB 17; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-07;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 27 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCC 64  
 |||||  
 DB 155 ACTCTGGGCTCAAGCAATCTCTCTGCTCAGCCTTCC 118  
 |||||  
 RESULT 12  
 AI611434/c 239 bp mRNA linear EST 14-DEC-1999  
 LOCUS tt611434.X1 NCI-CGAP\_HSC4 Homo sapiens cDNA clone IMAGE:2245244 3'  
 DEFINITION similar to contains Alu repetitive element;; mRNA sequence.  
 ACCESSION AI611434  
 VERSION AI611434.1 GI:4620601  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 239)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-x@mail.nih.gov  
 Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,  
 M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Insert length: 293 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 POLYA-No.  
 Location/Qualifiers  
 1..239  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:2245244"  
 /clone\_lib="NCI CGAP HSC4"  
 /tissue\_type="CD34+, CD38- from normal bone marrow donor"

132 CTCCTGGGCTCAAGCAATCCTCTCGCTCAGCCTTCC 96

DB

RESULT 14  
AI280214  
LOCUS  
DEFINITION  
qm65g11.x1 Soares\_placenta\_8to5weeks\_2NbHP8co9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION  
AI280214  
VERSION  
AI280214.1 GI:3918447  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 415)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LML; contact the IMAGE Consortium ([info@image.lml.gov](mailto:info@image.lml.gov)) for further information.  
Insert Length: 658 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 367.

FEATURES  
source  
1..415  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1893668"  
/clone\_lib="Soares\_placenta\_8to5weeks\_2NbHP8co9W"  
/dev\_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCACTCTGAAGTCGGAGCGCGCGATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT  
ORIGIN  
93 a 122 c 87 g 113 t

Query Match 19.8%; Score 37; DB 9; Length 415;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CTCCTGGGCTCAAGCAATCCTCTCGCTCAGCCTTCC 64  
|||||  
DB 76 CTCCTGGGCTCAAGCAATCCTCTCGCTCAGCCTTCC 112  
|||||

RESULT 15  
AI874136  
LOCUS  
DEFINITION  
wm49f02.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2439291 3' similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION  
AI874136  
VERSION  
AI874136.1 GI:5548185  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 434)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LML; contact the IMAGE Consortium ([info@image.lml.gov](mailto:info@image.lml.gov)) for further information.  
Insert Length: 658 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 367.

JOURNAL COMMENT

Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 377;  
 Location/Qualifiers  
 1..434  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2439291"  
 /clone\_lib="NCI-CCAP\_Ut4"  
 /tissue\_types="serous Papillary carcinoma, high grade, 2 pooled tumors"  
 /lab\_host="DH10B"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"  
 108 a 108 c 95 g 122 t 1 others  
 BASE COUNT  
 ORIGIN

Query Match 19.8%; Score 37; DB 9; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTC 63  
 |||||  
 Db 81 ACTCTGGGCTCAAGCAATCTCTGCTCAGCCTTC 117

Search completed: June 17, 2003, 06:25:42  
 Job time : 256.75 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using gap model

Run on: June 16, 2003, 11:19:02 ; Search time 895.527 Seconds  
(without alignments)  
15794.017 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_7148\_7633

Perfect score: 486

Sequence: 1 agattgcagatgtgagccac.....cattgtcttagtcccaagc 486

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*\*

1: gb\_ba:\*\*

2: gb\_htg:\*\*

3: gb\_in:\*\*

4: gb\_on:\*\*

5: gb\_ov:\*\*

6: gb\_pat:\*\*

7: gb\_ph:\*\*

8: gb\_pl:\*\*

9: gb\_pr:\*\*

10: gb\_ro:\*\*

11: gb\_sts:\*\*

12: gb\_sy:\*\*

13: gb\_un:\*\*

14: gb\_vi:\*\*

15: em\_ba:\*\*

16: em\_fun:\*\*

17: em\_hum:\*\*

18: em\_in:\*\*

19: em\_mu:\*\*

20: em\_om:\*\*

21: em\_or:\*\*

22: em\_ov:\*\*

23: em\_pat:\*\*

24: em\_ph:\*\*

25: em\_pl:\*\*

26: em\_ro:\*\*

27: em\_sts:\*\*

28: em\_un:\*\*

29: em\_vi:\*\*

30: em\_htg\_hum:\*\*

31: em\_htg\_inv:\*\*

32: em\_htg\_other:\*\*

33: em\_htg\_mus:\*\*

34: em\_htg\_pln:\*\*

35: em\_htg\_rnd:\*\*

36: em\_htg\_man:\*\*

37: em\_htg\_vrt:\*\*

38: em\_ey:\*\*

39: em\_htgo\_hum:\*\*

40: em\_htgo\_mus:\*\*

41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	5492	9	AF123659 Homo sapi
2	486	100.0	9108	9	AF123653 Homo sapi
3	366	75.3	173264	2	AC025853 Homo sapi
C 4	38	7.8	97430	9	AL391334 Human DNA
C 5	31	6.4	137845	2	AC010367 Homo sapi
C 6	31	6.4	152786	9	AL135778 Human DNA
C 7	31	6.4	179959	9	AL160395 Human DNA
C 8	31	6.4	186415	9	AC008675 Homo sapi
9	31	6.4	186418	9	AC018757 Homo sapi
10	31	6.4	197456	2	AC005054 Homo sapi
11	30	6.2	161013	9	AC018709 Homo sapi
C 12	30	6.2	240000	2	AC012525 Homo sapi
C 13	29	6.0	150336	9	HSJ395C13 Human DNA
C 14	29	6.0	153234	2	AC026947 Homo sapi
C 15	29	6.0	182208	9	AC113193 Homo sapi
C 16	29	6.0	185102	9	AC113139 Homo sapi
17	29	6.0	186072	2	AC018960 Homo sapi
C 18	29	6.0	193281	2	AC079376 Homo sapi
C 19	29	6.0	200823	9	AC009652 Homo sapi
C 20	28	5.8	93974	9	AC084421 Homo sapi
21	28	5.8	97146	9	AL135929 Human DNA
C 22	28	5.8	124102	9	AC021148 Homo sapi
C 23	28	5.8	140966	9	AC023058 Homo sapi
C 24	28	5.8	157750	9	AL512599 Human DNA
C 25	28	5.8	158977	9	AP002469 Homo sapi
C 26	28	5.8	159887	2	AC067823 Homo sapi
27	28	5.8	175609	2	AC024663 Homo sapi
28	28	5.8	181598	9	AC026172 Homo sapi
29	28	5.8	181598	9	AC026194 Homo sapi
30	28	5.8	189994	9	AP002762 Homo sapi
31	28	5.8	191569	9	AC018506 Homo sapi
C 32	28	5.8	196852	9	AC084866 Homo sapi
C 33	28	5.8	213965	2	AL353721 Homo sapi
C 34	27	5.6	2702	9	HSICAMIAS X84737 H. sapiens I
C 35	27	5.6	43761	9	HS597B2 AL031346 Human DNA
C 36	27	5.6	65244	2	AC124302 Homo sapi
37	27	5.6	127431	9	AC027796 Homo sapi
38	27	5.6	129305	2	AL355983 Homo sapi
39	27	5.6	143423	9	AL161932 Human DNA
C 40	27	5.6	143517	9	AC083783 Homo sapi
41	27	5.6	146127	9	AL391838 Human DNA
42	27	5.6	147767	2	AC105030 Homo sapi
43	27	5.6	148278	9	AC006101 citb 338
C 44	27	5.6	149320	2	AC126357 Homo sapi
C 45	27	5.6	154214	9	AC079753 Homo sapi
C 46	27	5.6	154604	2	AC104974 Homo sapi
C 47	27	5.6	156503	9	AC011511 Homo sapi
C 48	27	5.6	159122	2	AC025556 Homo sapi
49	27	5.6	159397	2	AC027040 Homo sapi
50	27	5.6	160846	9	AC124306 Homo sapi
C 51	27	5.6	162886	2	AC025542 Homo sapi
C 52	27	5.6	165201	9	AC107081 Homo sapi
C 53	27	5.6	168613	9	AC091133 Homo sapi
C 54	27	5.6	169897	9	AL353674 Human DNA
C 55	27	5.6	170543	9	AC021012 Homo sapi
C 56	27	5.6	170544	9	CNS05TCC AL355093 Human chr
57	27	5.6	173987	9	AL450337 Human DNA
C 58	27	5.6	174311	2	AL365319 Homo sapi
C 59	27	5.6	178384	2	AL591026 Homo sapi
C 60	27	5.6	178825	2	AC074251 Homo sapi
61	27	5.6	179394	9	AC010619 Homo sapi
C 62	27	5.6	185854	2	AC027736 Homo sapi
C 63	27	5.6	197372	9	AC103592 Homo sapi
64	27	5.6	200418	9	AC074138 Homo sapi
65	27	5.6	200688	2	AC073266 Homo sapi

c	66	27	5.6	217657	9	HSMTW0	AL034384	Human chr	c	139	26	5.3	204485	2	AC114962	AC114962	Homo sapi
c	67	27	5.6	238697	2	AC084854	AC084854	Homo sapi	c	140	26	5.3	206710	2	AL844520	AL844520	Homo sapi
c	68	26	5.3	1523	9	AX054712	AX054712	Homo sapi	c	141	26	5.3	206909	9	AC016397	AC016397	Homo sapi
c	69	26	5.3	15862	9	AC114816	AC114816	Homo sapi	c	142	26	5.3	207256	9	AC010321	AC010321	Homo sapi
c	70	26	5.3	33931	9	AC022156	AC022156	Homo sapi	c	143	26	5.3	208813	2	AC092425	AC092425	Homo sapi
c	71	26	5.3	63684	9	AL357564	AL357564	Human DNA	c	144	26	5.3	210320	9	AC093873	AC093873	Homo sapi
c	72	26	5.3	67462	2	AC091595	AC091595	Homo sapi	c	145	26	5.3	211001	9	AC018695	AC018695	Homo sapi
c	73	26	5.3	67895	9	AL138807	AL138807	Human DNA	c	146	26	5.3	215441	9	AC005736	AC005736	Homo sapi
c	74	26	5.3	75761	9	AL359733	AL359733	Human DNA	c	147	26	5.3	240379	9	AC005077	AC005077	Homo sapi
c	75	26	5.3	76295	2	AC023542	AC023542	Homo sapi	c	148	26	5.3	242970	2	AC004803	AC004803	Homo sapi
c	76	26	5.3	87665	9	AL158840	AL158840	Human DNA	c	149	26	5.3	242970	2	AC004803	AC004803	Homo sapi
c	77	26	5.3	93418	9	AC008379	AC008379	Homo sapi	c	150	26	5.3	247924	2	AC080037	AC080037	Homo sapi
c	78	26	5.3	93714	2	AL161661	AL161661	Homo sapi	c	151	26	5.3	278524	2	AC074326	AC074326	Homo sapi
c	79	26	5.3	104660	9	AF000347	AF000347	Homo sapi	c	152	26	5.3	314989	2	AC009871	AC009871	Homo sapi
c	80	26	5.3	105362	9	AC012370	AC012370	Homo sapi	c	153	25	5.1	819	6	AX200941	AX200941	Sequence
c	81	26	5.3	106008	9	HS506	AL020993	Human DNA	c	154	25	5.1	819	6	AX267597	AX267597	Sequence
c	82	26	5.3	114084	2	AL445427	AL445427	Homo sapi	c	155	25	5.1	2455	6	AX201108	AX201108	Sequence
c	83	26	5.3	116131	9	AL139324	AL139324	Human DNA	c	156	25	5.1	2455	6	AX201109	AX201109	Sequence
c	84	26	5.3	120869	9	HSJ788L20	AL121722	Human DNA	c	157	25	5.1	2455	6	AX267907	AX267907	Sequence
c	85	26	5.3	121909	9	HSJ7492P14	AL121977	Human DNA	c	158	25	5.1	2455	6	AX267908	AX267908	Sequence
c	86	26	5.3	124278	2	AC104618	AC104618	Homo sapi	c	159	25	5.1	5908	9	AF043195	AF043195	Homo sapi
c	87	26	5.3	128398	9	AC004817	AC004817	Homo sapi	c	160	25	5.1	30826	9	AL807743	AL807743	Human DNA
c	88	26	5.3	132867	9	AC004601	AC004601	Human l1p	c	161	25	5.1	36648	2	AF209069	AF209069	Homo sapi
c	89	26	5.3	136312	9	HSJ657D16	AL050343	Human DNA	c	162	25	5.1	36651	6	AX357904	AX357904	Sequence
c	90	26	5.3	137718	9	AL137066	AL137066	Human DNA	c	163	25	5.1	36651	6	AX357904	AX357904	Sequence
c	91	26	5.3	138969	9	AC104600	AC104600	Homo sapi	c	164	25	5.1	39601	9	AC005581	AC005581	Homo sapi
c	92	26	5.3	147815	9	HS998H6	AL031687	Human DNA	c	165	25	5.1	39935	9	AC093231	AC093231	Homo sapi
c	93	26	5.3	149271	2	AC112489	AC112489	Homo sapi	c	166	25	5.1	43780	2	AC068017	AC068017	Homo sapi
c	94	26	5.3	149856	2	AC021411	AC021411	Homo sapi	c	167	25	5.1	43780	2	AC068017	AC068017	Homo sapi
c	95	26	5.3	154218	9	AC020663	AC020663	Homo sapi	c	168	25	5.1	54099	2	AC079963	AC079963	Homo sapi
c	96	26	5.3	155405	9	AC009812	AC009812	Homo sapi	c	169	25	5.1	60761	2	AC068568	AC068568	Homo sapi
c	97	26	5.3	158587	9	AC074325	AC074325	Homo sapi	c	170	25	5.1	61513	2	AL353610	AL353610	Human DNA
c	98	26	5.3	159593	2	AC026302	AC026302	Homo sapi	c	171	25	5.1	63930	2	AC106017	AC106017	Homo sapi
c	99	26	5.3	159766	9	AC104942	AC104942	Homo sapi	c	172	25	5.1	64455	2	AC084134	AC084134	Homo sapi
c	100	26	5.3	160463	2	AC110607	AC110607	Homo sapi	c	173	25	5.1	66256	2	AC087454	AC087454	Homo sapi
c	101	26	5.3	161421	2	AC068114	AC068114	Homo sapi	c	174	25	5.1	66792	9	AC008754	AC008754	Homo sapi
c	102	26	5.3	161593	9	HSBA49G10	AL121901	Human DNA	c	175	25	5.1	68035	2	AC103699	AC103699	Homo sapi
c	103	26	5.3	161973	9	HUAC002038	AC002038	Homo sapi	c	176	25	5.1	68109	9	AP000315	AP000315	Homo sapi
c	104	26	5.3	162243	9	AL513304	AL513304	Human DNA	c	177	25	5.1	70203	2	AC024012	AC024012	Homo sapi
c	105	26	5.3	165139	9	AC010182	AC010182	Homo sapi	c	178	25	5.1	72273	2	AC090859	AC090859	Homo sapi
c	106	26	5.3	165196	9	AC007151	AC007151	Homo sapi	c	179	25	5.1	73396	9	AC008848	AC008848	Homo sapi
c	107	26	5.3	167185	9	AC093132	AC093132	Papio cyn	c	180	25	5.1	75120	9	AC004666	AC004666	Homo sapi
c	108	26	5.3	167557	2	AC079866	AC079866	Homo sapi	c	181	25	5.1	75386	2	AC027760	AC027760	Homo sapi
c	109	26	5.3	168085	9	AC027687	AC027687	Homo sapi	c	182	25	5.1	75657	9	HSB11L7C8	HSB11L7C8	Homo sapi
c	110	26	5.3	169032	9	AC016931	AC016931	Homo sapi	c	183	25	5.1	77651	9	AC120118	AC120118	Homo sapi
c	111	26	5.3	169739	9	AC005082	AC005082	Homo sapi	c	184	25	5.1	79516	9	AC004834	AC004834	Homo sapi
c	112	26	5.3	169819	9	AC078991	AC078991	Homo sapi	c	185	25	5.1	81764	9	AL139080	AL139080	Human DNA
c	113	26	5.3	169844	2	AC025738	AL359372	Homo sapi	c	186	25	5.1	81831	9	AL365506	AL365506	Human DNA
c	114	26	5.3	170608	2	AL359372	AL359372	Homo sapi	c	187	25	5.1	85444	9	AP003900	AP003900	Homo sapi
c	115	26	5.3	170877	2	AC025610	AC025610	Homo sapi	c	188	25	5.1	86945	2	AC002490	AC002490	Homo sapi
c	116	26	5.3	171225	2	AC024431	AC024431	Homo sapi	c	189	25	5.1	87120	2	AC012225	AC012225	Homo sapi
c	117	26	5.3	171518	2	AL589697	AL589697	Homo sapi	c	190	25	5.1	90434	2	AC007952	AC007952	Homo sapi
c	118	26	5.3	175588	9	AL139326	AL139326	Human DNA	c	191	25	5.1	92118	9	AC074384	AC074384	Homo sapi
c	119	26	5.3	175620	2	AC127391	AC127391	Homo sapi	c	192	25	5.1	96120	9	AC093669	AC093669	Homo sapi
c	120	26	5.3	175789	2	AP000425	AP000425	Homo sapi	c	193	25	5.1	96874	9	AL138709	AL138709	Human DNA
c	121	26	5.3	177242	2	AC021923	AC021923	Homo sapi	c	194	25	5.1	97473	9	AC127165	AC127165	Homo sapi
c	122	26	5.3	179087	2	AC069489	AC069489	Homo sapi	c	195	25	5.1	97734	9	AC095066	AC095066	Homo sapi
c	123	26	5.3	179262	9	AL355343	AL355343	Human DNA	c	196	25	5.1	98274	9	HS714B7	HS714B7	Human DNA s
c	124	26	5.3	183695	9	AC012450	AC012450	Homo sapi	c	197	25	5.1	98908	9	AL139279	AL139279	Human DNA
c	125	26	5.3	183797	9	AC022400	AC022400	Homo sapi	c	198	25	5.1	100000	9	AP000080	AP000080	Homo sapi
c	126	26	5.3	184778	2	AC023567	AC023567	Homo sapi	c	199	25	5.1	100000	9	AP000165	AP000165	Homo sapi
c	127	26	5.3	187349	9	AP003352	AP003352	Homo sapi	c	200	25	5.1	100000	17	AP000118	AP000118	Homo sapi
c	128	26	5.3	187394	2	AC104573	AC104573	Homo sapi	c	201	25	5.1	100521	9	AC119397	AC119397	Homo sapi
c	129	26	5.3	187530	2	AC096875	AC096875	Pan trogl	c	202	25	5.1	104061	2	AC106019	AC106019	Homo sapi
c	130	26	5.3	192440	9	CNS01DXH	AL139316	Human chr	c	203	25	5.1	106465	2	AC090156	AC090156	Homo sapi
c	131	26	5.3	194771	2	AC109912	AC109912	Homo sapi	c	204	25	5.1	110885	9	HS191E19	HS191E19	Human DNA
c	132	26	5.3	195293	2	AC12169	AC12169	Homo sapi	c	205	25	5.1	112846	9	AC004991	AC004991	Homo sapi
c	133	26	5.3	196756	2	AC121858	AC121858	Mus musCu	c	206	25	5.1	116506	9	AL160163	AL160163	Human DNA
c	134	26	5.3	197431	9	AL360157	AL360157	Human DNA	c	207	25	5.1	116664	9	HS1191N16	HS1191N16	Human DNA
c	135	26	5.3	197870	2	AC091075	AC091075	Homo sapi	c	208	25	5.1	120873	9	AL445986	AL445986	Human DNA
c	136	26	5.3	198218	2	AC037447	AC037447	Homo sapi	c	209	25	5.1	122888	9	HS333H23	HS333H23	Human DNA
c	137	26	5.3	198952	2	AP002016	AP002016	Homo sapi	c	210	25	5.1	123866	9	AC008603	AC008603	Homo sapi
c	138	26	5.3	199208	2	AC019236	AC019236	Homo sapi	c	211	25	5.1	125041	2	AC068693	AC068693	Homo sapi

212	25	5.1	125780	9	CNS01DWK	AL137229 Human chr	c	285	25	5.1	162763	9	AL359262	Human DNA	
213	25	5.1	127148	2	AP002081	AP002081 Homo sapi	286	25	5.1	162810	9	AC083923	Homo sapi		
214	25	5.1	127413	9	AL137784	AL137784 Human DNA	287	25	5.1	163856	9	AC084797	Homo sapi		
c	215	25	5.1	127917	9	HS257A7	288	25	5.1	163996	2	AL139116	Homo sapi		
216	25	5.1	129719	9	AL358113	AL358113 Human DNA	c	289	25	5.1	163997	2	AL773524	Homo sapi	
217	25	5.1	130077	9	AL353643	AL353643 Human DNA	c	290	25	5.1	164113	2	AC086128	Homo sapi	
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219	25	5.1	130898	9	AL353770	AL353770 Human DNA	c	292	25	5.1	164598	2	AC093212	Homo sapi	
c	220	25	5.1	132937	2	AC115097	293	25	5.1	164801	9	AC13418	Homo sapi		
221	25	5.1	134210	9	AC005052	AC005052 Homo sapi	c	294	25	5.1	164857	9	AC110054	Homo sapi	
c	222	25	5.1	134896	9	AC006571	295	25	5.1	165007	9	AC019047	Homo sapi		
c	223	25	5.1	135300	9	AC008163	296	25	5.1	165183	2	AC010787	Homo sapi		
c	224	25	5.1	135331	9	AC008798	c	297	25	5.1	165570	2	AC015765	Homo sapi	
c	225	25	5.1	136931	9	HS1050C22	c	298	25	5.1	166308	9	CNS01DX2	Human chr	
c	226	25	5.1	137347	9	AL354674	299	25	5.1	166549	2	AC025990	Homo sapi		
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228	25	5.1	139388	9	AC007666	AC090820 Homo sapi	c	301	25	5.1	166664	9	AL441992	Human DNA	
c	229	25	5.1	140827	9	AL451123	c	302	25	5.1	167218	9	AC090461	Homo sapi	
c	230	25	5.1	141790	9	AL590636	AL590636 Human DNA	c	303	25	5.1	167357	2	AC026264	Homo sapi
c	231	25	5.1	142432	9	AC017074	AC017074 Homo sapi	c	304	25	5.1	167390	9	AC007263	Homo sapi
c	232	25	5.1	142560	2	AC021906	AC021906 Homo sapi	c	305	25	5.1	167439	2	AC130273	Papio cyn
c	233	25	5.1	142667	9	AC125387	AC125387 Homo sapi	c	306	25	5.1	167700	9	AC007036	Homo sapi
234	25	5.1	142669	2	AC018912	AC018912 Homo sapi	c	307	25	5.1	167722	9	AC073548	Homo sapi	
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c	236	25	5.1	142805	9	AL592525	AL592525 Homo sapi	c	309	25	5.1	168068	9	AL445668	Human DNA
c	237	25	5.1	143067	2	AC099796	AL592525 Homo sapi	c	310	25	5.1	168283	2	AL844892	Homo sapi
c	238	25	5.1	143638	9	AL157698	AL157698 Human DNA	c	311	25	5.1	168367	9	AC104440	Homo sapi
c	239	25	5.1	143785	2	AC092334	AL157698 Human DNA	c	312	25	5.1	168995	2	AP002359	Homo sapi
c	240	25	5.1	143804	2	AC012617	AC092334 Homo sapi	c	313	25	5.1	168995	9	AC126605	Homo sapi
c	241	25	5.1	143839	9	AC004701	AC012617 Homo sapi	c	314	25	5.1	169552	9	AC015976	Homo sapi
c	242	25	5.1	144079	2	AC024342	AC004701 Homo sapi	c	315	25	5.1	169585	2	AC113557	Homo sapi
c	243	25	5.1	146463	2	AC068306	AC024342 Homo sapi	c	316	25	5.1	169616	9	AL355336	Human DNA
c	244	25	5.1	146578	9	AC012468	AC068306 Homo sapi	c	317	25	5.1	170138	2	AC018794	Homo sapi
c	245	25	5.1	146641	2	AC011140	AC012468 Homo sapi	c	318	25	5.1	170216	9	AC008432	Homo sapi
c	246	25	5.1	146642	2	HSJ9617	AC011140 Homo sapi	c	319	25	5.1	170274	2	AC016462	Homo sapi
c	247	25	5.1	147122	9	AC090109	AJ009617 Homo sapi	c	320	25	5.1	170490	2	AC022042	Homo sapi
c	248	25	5.1	147519	2	AC079099	AC090109 Homo sapi	c	321	25	5.1	170507	9	AC087530	Homo sapi
c	249	25	5.1	147587	2	AC055800	AC079099 Homo sapi	c	322	25	5.1	170533	9	AP003356	Homo sapi
c	250	25	5.1	148835	9	AC011225	AC055800 Homo sapi	c	323	25	5.1	170586	2	HSBA536C5	Homo sapi
c	251	25	5.1	149089	9	AC090735	AC011225 Homo sapi	c	324	25	5.1	171056	2	AC026318	Homo sapi
c	252	25	5.1	149490	2	AL589985	AC090735 Homo sapi	c	325	25	5.1	171200	9	AP000864	Homo sapi
c	253	25	5.1	149901	2	AL356367	AL589985 Homo sapi	c	326	25	5.1	171386	2	AC130786	Papio cyn
c	254	25	5.1	150526	2	AC092339	AL356367 Homo sapi	c	327	25	5.1	171483	9	AL162580	Human DNA
c	255	25	5.1	150817	2	AC021762	AC092339 Homo sapi	c	328	25	5.1	171501	9	AL359704	Human DNA
c	256	25	5.1	150918	2	AC027364	AC021762 Homo sapi	c	329	25	5.1	171523	9	AC010206	Homo sapi
c	257	25	5.1	152185	2	AC012219	AC027364 Homo sapi	c	330	25	5.1	171621	2	AC011961	Homo sapi
c	258	25	5.1	152748	9	AC106730	AC012219 Homo sapi	c	331	25	5.1	171731	2	AC091659	Papio cyn
c	259	25	5.1	152798	9	AC004057	AC106730 Homo sapi	c	332	25	5.1	171742	30	AC069495	Homo sapi
c	260	25	5.1	153231	9	AL161452	AC004057 Homo sapi	c	333	25	5.1	172051	2	AC023493	Homo sapi
c	261	25	5.1	153382	2	AL359996	AL161452 Human DNA	c	334	25	5.1	172393	2	AC025740	Homo sapi
c	262	25	5.1	153586	2	AC016316	AL359996 Homo sapi	c	335	25	5.1	172579	9	AL596385	Human DNA
c	263	25	5.1	153617	9	AC012306	AC016316 Homo sapi	c	336	25	5.1	172883	2	AL391374	Human DNA
c	264	25	5.1	153619	2	AC130430	AC012306 Homo sapi	c	337	25	5.1	172915	2	AC010160	Homo sapi
c	265	25	5.1	154639	2	AC090175	AC130430 Homo sapi	c	338	25	5.1	173153	9	AC008119	Homo sapi
c	266	25	5.1	155146	2	AC025216	AC090175 Homo sapi	c	339	25	5.1	173354	9	HS149A16	Human DNA
c	267	25	5.1	155705	9	AC093823	AC025216 Homo sapi	c	340	25	5.1	173791	9	AC021035	Homo sapi
c	268	25	5.1	155952	9	AC004534	AC093823 Homo sapi	c	341	25	5.1	173886	2	AC097007	Pan trogl
c	269	25	5.1	156616	2	AC126566	AC004534 Homo sapi	c	342	25	5.1	174239	2	AC073830	Homo sapi
c	270	25	5.1	157762	9	AP001893	AC126566 Homo sapi	c	343	25	5.1	174366	9	AL590491	Human DNA
c	271	25	5.1	157918	2	AC024252	AP001893 Homo sapi	c	344	25	5.1	174700	2	AC025344	Homo sapi
c	272	25	5.1	157918	9	AL512422	AC024252 Homo sapi	c	345	25	5.1	175274	9	AP004286	Homo sapi
c	273	25	5.1	158060	2	AC024423	AL512422 Human DNA	c	346	25	5.1	176287	9	HSBA12M9	Human DNA
c	274	25	5.1	158116	2	AL357622	AC024423 Homo sapi	c	347	25	5.1	176470	9	AL353626	Human DNA
c	275	25	5.1	158574	2	AC024895	AL357622 Homo sapi	c	348	25	5.1	176473	2	AC090986	Homo sapi
c	276	25	5.1	158838	9	CNS05TDN	AC024895 Homo sapi	c	349	25	5.1	176562	2	AC130272	Papio cyn
c	277	25	5.1	159285	2	AL354816	AL358805 Human chr	c	350	25	5.1	177750	9	AC005874	Homo sapi
c	278	25	5.1	159582	2	AC015734	AL354816 Human DNA	c	351	25	5.1	177795	9	AC067743	Homo sapi
c	279	25	5.1	160069	2	AC023329	AC015734 Homo sapi	c	352	25	5.1	177993	9	AC067743	Homo sapi
c	280	25	5.1	161422	2	AC021544	AC023329 Homo sapi	c	353	25	5.1	177947	9	AF134471	Homo sapi
c	281	25	5.1	161549	9	AC044913	AC021544 Homo sapi	c	354	25	5.1	177993	9	AC093133	Papio cyn
c	282	25	5.1	161610	2	AC011728	AC044913 Homo sapi	c	355	25	5.1	177993	9	AC093133	Papio cyn
c	283	25	5.1	161699	9	AC107300	AC011728 Homo sapi	c	356	25	5.1	178338	2	AC125603	Homo sapi
c	284	25	5.1	162478	9	AC125634	AC107300 Homo sapi	c	357	25	5.1	178344	2	AC067846	Homo sapi

c 358	25	5.1	178611	2	AC024631	Homo sapi
c 359	25	5.1	178796	2	AC020667	Homo sapi
c 360	25	5.1	179919	2	AC007456	Homo sapi
c 361	25	5.1	180269	9	AC016025	Homo sapi
c 362	25	5.1	180368	2	AC024276	Homo sapi
c 363	25	5.1	180818	9	AP000821	Homo sapi
c 364	25	5.1	181054	2	AC025019	Homo sapi
c 365	25	5.1	181182	2	AC084832	Homo sapi
c 366	25	5.1	181191	9	AC117379	Homo sapi
c 367	25	5.1	181254	2	AP000825	Homo sapi
c 368	25	5.1	181589	9	AP000868	Homo sapi
c 369	25	5.1	182105	9	AC009136	Homo sapi
c 370	25	5.1	182496	2	AC011190	Homo sapi
c 371	25	5.1	184313	9	AL445584	Human DNA
c 372	25	5.1	184477	2	AC028277	Homo sapi
c 373	25	5.1	185143	2	AC025861	Homo sapi
c 374	25	5.1	186147	2	AC020739	Homo sapi
c 375	25	5.1	186183	9	AC026827	Homo sapi
c 376	25	5.1	186635	2	AC051645	Homo sapi
c 377	25	5.1	186635	2	AC051645	Homo sapi
c 378	25	5.1	186812	9	AC110291	Homo sapi
c 379	25	5.1	187691	2	AL359982	Homo sapi
c 380	25	5.1	187857	2	AC044850	Homo sapi
c 381	25	5.1	188410	2	AC124073	Homo sapi
c 382	25	5.1	188639	9	AC011236	Homo sapi
c 383	25	5.1	188743	2	AC069195	Homo sapi
c 384	25	5.1	188755	9	AC013562	Homo sapi
c 385	25	5.1	188928	9	AC020612	Homo sapi
c 386	25	5.1	189022	2	AC016270	Homo sapi
c 387	25	5.1	189396	2	AL161418	Homo sapi
c 388	25	5.1	190277	9	AF254983	Homo sapi
c 389	25	5.1	190363	9	AC000052	Homo sapi
c 390	25	5.1	190482	9	AC004106	Homo sapi
c 391	25	5.1	191152	9	AC005722	Homo sapi
c 392	25	5.1	191871	2	AC084133	Homo sapi
c 393	25	5.1	191942	9	AC079951	Homo sapi
c 394	25	5.1	192068	2	AC036208	Homo sapi
c 395	25	5.1	192618	9	AC092811	Homo sapi
c 396	25	5.1	192651	2	AC092406	Papio cyn
c 397	25	5.1	193234	2	AC024293	Homo sapi
c 398	25	5.1	193605	2	AC130472	Homo sapi
c 399	25	5.1	193772	9	AC007073	Homo sapi
c 400	25	5.1	194079	9	AC020559	Homo sapi
c 401	25	5.1	194615	2	AC024190	Homo sapi
c 402	25	5.1	194863	2	AC105344	Homo sapi
c 403	25	5.1	195529	2	AC025612	Homo sapi
c 404	25	5.1	195668	9	AL353729	Human DNA
c 405	25	5.1	197550	9	CNS01RHP	
c 406	25	5.1	199036	9	AC025449	Homo sapi
c 407	25	5.1	200379	9	AC098614	Homo sapi
c 408	25	5.1	200542	2	CNS01RG3	
c 409	25	5.1	200673	9	AC021396	Homo sapi
c 410	25	5.1	202544	9	AC104447	Homo sapi
c 411	25	5.1	203279	9	AL354826	Human DNA
c 412	25	5.1	203912	9	AC008755	Homo sapi
c 413	25	5.1	204720	2	AC008052	Homo sapi
c 414	25	5.1	205473	2	AC092554	Papio cyn
c 415	25	5.1	206312	2	AC092725	Homo sapi
c 416	25	5.1	207362	2	AL355484	Homo sapi
c 417	25	5.1	207850	2	AC096510	Homo sapi
c 418	25	5.1	209112	2	AC084146	Homo sapi
c 419	25	5.1	209794	9	AL390878	Human DNA
c 420	25	5.1	210133	2	AC013564	Homo sapi
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c 422	25	5.1	211550	9	AC073912	Homo sapi
c 423	25	5.1	214530	9	AC020916	Homo sapi
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c 426	25	5.1	215077	9	AC112504	Homo sapi
c 427	25	5.1	216812	2	AC084037	Homo sapi
c 428	25	5.1	219139	2	AC084418	Homo sapi
c 429	25	5.1	223797	2	AC021978	Homo sapi
c 430	25	5.1	224360	2	AC090670	Homo sapi
c 431	25	5.1	224573	9	AC008758	Homo sapi

c 431	25	5.1	227632	9	AC087382	Homo sapi
c 432	25	5.1	231566	2	AL158811	Homo sapi
c 433	25	5.1	231566	2	AL158811	Homo sapi
c 434	25	5.1	233461	2	AC092978	Homo sapi
c 435	25	5.1	233738	9	AC007956	Homo sapi
c 436	25	5.1	260409	9	AC004019	Homo sapi
c 437	25	5.1	270105	2	AC099650	Homo sapi
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c 439	25	5.1	271144	9	HSXDPB	
c 440	25	5.1	281116	9	HS21C001	Homo sapi
c 441	25	5.1	304623	2	AC021052	Homo sapi
c 442	25	5.1	340000	9	AP001719	Homo sapi
c 443	24	4.9	644	9	HS342650	Homo sapi
c 444	24	4.9	699	9	HS343753	Homo sapi
c 445	24	4.9	725	9	HS343586	Homo sapi
c 446	24	4.9	726	9	HS343588	Homo sapi
c 447	24	4.9	730	9	HSU50463	Homo sapi
c 448	24	4.9	1516	9	AK024577	Human inter
c 449	24	4.9	4993	9	HSY11341	Homo sapi
c 450	24	4.9	25094	9	AC003045	Human BAC
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c 453	24	4.9	33458	9	HSJ202D23	Human DNA
c 454	24	4.9	35476	9	HS398F6	Human DNA
c 455	24	4.9	38653	6	AX244215	Sequence
c 456	24	4.9	38897	9	AC021092	Homo sapi
c 457	24	4.9	39608	9	AC009004	Homo sapi
c 458	24	4.9	40883	9	AC005776	Homo sapi
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c 460	24	4.9	42497	9	AC004798	Homo sapi
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c 462	24	4.9	47542	9	HS162H14	Human DNA
c 463	24	4.9	48723	9	AL645992	Human DNA
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c 466	24	4.9	66374	2	AC13501	Homo sapi
c 467	24	4.9	69096	2	AC124072	Homo sapi
c 468	24	4.9	70834	9	AC011402	Homo sapi
c 469	24	4.9	76428	9	AP005401	Homo sapi
c 470	24	4.9	77538	9	AC004500	Homo sapi
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c 474	24	4.9	80398	9	AL513485	Human DNA
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c 477	24	4.9	81188	2	AP001128	Homo sapi
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c 479	24	4.9	83557	9	AL138735	Human DNA
c 480	24	4.9	84684	2	AC023321	Homo sapi
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c 483	24	4.9	89507	9	AL357132	Human DNA
c 484	24	4.9	91692	9	AC084253	Homo sapi
c 485	24	4.9	92203	2	AP001920	Homo sapi
c 486	24	4.9	92998	9	AC092019	Homo sapi
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c 488	24	4.9	96075	9	AL590639	Human DNA
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c 493	24	4.9	100000	9	AP000104	Homo sapi
c 494	24	4.9	100000	9	AP000180	Homo sapi
c 495	24	4.9	100000	2	AP000502	Homo sapi
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c 497	24	4.9	106317	9	AL136958	Human DNA
c 498	24	4.9	108408	2	AC022210	Homo sapi
c 499	24	4.9	111763	9	AC092783	Homo sapi
c 500	24	4.9	112417	9	AC006015	Homo sapi
c 501	24	4.9	113546	2	HSAC000382	
c 502	24	4.9	113996	2	AC026438	Homo sapi
c 503	24	4.9	117145	9	AC011370	Homo sapi

AC087382	Homo sapi
AL158811	Homo sapi
AL158811	Homo sapi
AC029978	Homo sapi
AC007956	Homo sapi
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AC099650	Homo sapi
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AL590763	Homo sapi
AL163201	Homo sapi
AC021052	Homo sapi
AP001719	Homo sapi
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AJ343753	Homo sapi
AJ343586	Homo sapi
AJ343588	Homo sapi
U50463	Human inter
AK024577	Homo sapi
Y11341	Homo sapi
AC003045	Human BAC
AF217491	Homo sapi
AP000274	Homo sapi
AL109656	Human DNA
AL023882	Human DNA
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AC021092	Homo sapi
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AL139408	Human DNA
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AC004257	Homo sapi
Z98047	Human DNA
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AC013501	Homo sapi
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AC004500	Homo sapi
AP000483	Homo sapi
AC114937	Homo sapi
AC036211	Homo sapi
AL513485	Human DNA
AC107040	Pan trogl
AP001128	Homo sapi
AP004715	Homo sapi
AL138735	Human DNA
AC023321	Homo sapi
AC021216	Homo sapi
AL357132	Human DNA
AC084253	Homo sapi
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AC092019	Homo sapi
AC015854	Homo sapi
AL590639	Human DNA
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AC084728	Homo sapi
AX410782	Sequence
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AP000502	Homo sapi
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AC006015	Homo sapi
HSAC000382	
AC026438	Homo sapi
AC011370	Homo sapi



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505	24	4.9 120116	8	AC092390	AC092390 Oryza sat	c 578	24	4.9 163218	9	AC005837	Homo sapi
506	24	4.9 120612	9	AC108518	AC108518 Homo sapi	579	24	4.9 163375	2	AC027777	Homo sapi
507	24	4.9 120857	9	AC116334	AC116334 Homo sapi	c 580	24	4.9 163819	2	AC022758	Homo sapi
508	24	4.9 122568	9	AF196972	AF196972 Homo sapi	c 581	24	4.9 163836	9	AC073917	Homo sapi
509	24	4.9 122764	9	HSJ831D17	AL109984 Human DNA	c 582	24	4.9 163970	2	AC115247	Rattus no
510	24	4.9 123817	9	AL713980	AL713980 Human DNA	583	24	4.9 164350	9	AC068919	Homo sapi
511	24	4.9 125698	9	HS692C8	AL034561 Human DNA	584	24	4.9 164482	9	AC092474	Homo sapi
512	24	4.9 126910	9	AC026794	AC026794 Homo sapi	585	24	4.9 164731	9	AC007485	Homo sapi
513	24	4.9 128152	9	AL136313	AL136313 Human DNA	c 586	24	4.9 164928	9	AC087752	Homo sapi
514	24	4.9 129083	2	AC096853	AC096853 Sus scrof	c 587	24	4.9 164974	2	AC019082	Homo sapi
515	24	4.9 130754	2	AC008508	AC008508 Homo sapi	c 588	24	4.9 165062	9	AC087834	Pan trogl
516	24	4.9 131098	9	AC010607	AC010607 Homo sapi	c 589	24	4.9 165385	2	AC093003	Homo sapi
517	24	4.9 131359	9	AC019068	AC019068 Homo sapi	c 590	24	4.9 165720	9	AC025524	Homo sapi
518	24	4.9 131378	9	AC112653	AC112653 Homo sapi	591	24	4.9 166049	2	AC037470	Homo sapi
519	24	4.9 132764	9	AC073842	AC073842 Homo sapi	c 592	24	4.9 166093	2	AC015462	Homo sapi
520	24	4.9 132424	9	AL607128	AL607128 Human DNA	c 593	24	4.9 166173	2	AC023060	Homo sapi
521	24	4.9 134474	9	HS33F8	AL022160 Human DNA	594	24	4.9 166174	2	AC009633	Homo sapi
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523	24	4.9 135664	2	AC016559	AC016559 Homo sapi	c 596	24	4.9 168108	9	AL445687	Human DNA
524	24	4.9 136693	9	HS164F3	AL033422 Human DNA	597	24	4.9 169594	9	AC025480	Homo sapi
525	24	4.9 138264	9	AC008722	AC008722 Homo sapi	598	24	4.9 169753	9	AC087506	Homo sapi
526	24	4.9 138350	2	AC010801	AC010801 Homo sapi	599	24	4.9 169980	2	AC023981	Homo sapi
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533	24	4.9 143009	9	AC022447	AC022447 Homo sapi	606	24	4.9 172335	2	AC104451	Homo sapi
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537	24	4.9 144430	9	AC091155	AC091155 Homo sapi	c 610	24	4.9 173438	9	AP003967	Homo sapi
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539	24	4.9 145100	2	AC024641	AC024641 Homo sapi	612	24	4.9 174327	2	AL672191	Homo sapi
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544	24	4.9 148293	9	AC087730	AC087730 Pan trogl	617	24	4.9 176512	9	AC012323	Homo sapi
545	24	4.9 149110	9	AP003692	AP003692 Homo sapi	618	24	4.9 176932	9	AC016772	Homo sapi
546	24	4.9 149394	2	AP000828	AP000828 Homo sapi	619	24	4.9 177273	9	AC074194	Homo sapi
547	24	4.9 150813	9	AC118758	AC118758 Homo sapi	620	24	4.9 177289	2	AC090176	Homo sapi
548	24	4.9 151041	8	AP003258	AP003258 Oryza sat	621	24	4.9 177319	2	AC098698	Papio cyn
549	24	4.9 151371	2	AC091889	AC091889 Homo sapi	622	24	4.9 177505	9	AC022276	Homo sapi
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552	24	4.9 153185	2	AC073228	AC073228 Homo sapi	625	24	4.9 178460	2	AL139040	Homo sapi
553	24	4.9 153629	9	AC092325	AC092325 Homo sapi	626	24	4.9 178518	2	AC025332	Homo sapi
554	24	4.9 153788	2	AC023971	AC023971 Homo sapi	c 627	24	4.9 178653	2	AC090088	Homo sapi
555	24	4.9 154101	2	AL357565	AL357565 Homo sapi	628	24	4.9 178980	9	AP001591	Homo sapi
556	24	4.9 154147	2	AL356487	AL356487 Homo sapi	c 629	24	4.9 179090	2	AC011014	Homo sapi
557	24	4.9 154325	2	AC008452	AC008452 Homo sapi	630	24	4.9 179272	2	AC022659	Homo sapi
558	24	4.9 154616	2	AC067772	AC067772 Homo sapi	c 631	24	4.9 179310	9	AC006160	Homo sapi
559	24	4.9 154904	9	AL162272	AL162272 Human DNA	632	24	4.9 179562	2	AP001323	Homo sapi
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561	24	4.9 155385	2	AL357552	AL357552 Homo sapi	c 634	24	4.9 180283	9	AF134726	Homo sapi
562	24	4.9 155770	2	AC092381	AC092381 Homo sapi	c 635	24	4.9 180365	9	AC046143	Homo sapi
563	24	4.9 156442	9	AL354915	AL354915 Human DNA	636	24	4.9 180419	2	AC108691	Homo sapi
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566	24	4.9 157268	2	AC025063	AC025063 Homo sapi	c 639	24	4.9 181210	9	AC011742	Homo sapi
567	24	4.9 157289	2	AC021447	AC021447 Homo sapi	640	24	4.9 181755	2	AC013283	Homo sapi
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570	24	4.9 159971	2	AC091951	AC091951 Homo sapi	643	24	4.9 182547	9	AP001201	Homo sapi
571	24	4.9 160232	9	AC079313	AC079313 Homo sapi	644	24	4.9 183182	2	AC019207	Homo sapi
572	24	4.9 160999	2	AP003369	AP003369 Oryza sat	645	24	4.9 183279	9	AC073263	Homo sapi
573	24	4.9 161685	2	AC013629	AC013629 Homo sapi	c 646	24	4.9 183768	9	AC020900	Homo sapi
574	24	4.9 162511	9	AC009470	AC009470 Homo sapi	647	24	4.9 183976	9	AL356056	Human DNA
575	24	4.9 162813	2	AC021833	AC021833 Homo sapi	648	24	4.9 184036	2	AC026638	Homo sapi
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652	24	4.9	186236	2	AC123982	Pan trogl	AC123982	Pan trogl	C 725	23	4.7	5864	6	AR140568	Sequence
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654	24	4.9	187628	9	AC011311	Homo sapi	AC011311	Homo sapi	C 727	23	4.7	10918	9	HS010395	Homo sapi
655	24	4.9	188095	4	AC091505	Sus scrof	AC091505	Sus scrof	C 728	23	4.7	11174	9	AC104104	Homo sapi
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662	24	4.9	190815	9	AC007066	Homo sapi	AC007066	Homo sapi	C 735	23	4.7	24888	9	HS78H10	Human DNA
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665	24	4.9	190931	2	AC057921	Homo sapi	AC057921	Homo sapi	C 738	23	4.7	31705	9	HS4400626	Homo sapi
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667	24	4.9	191768	9	AC092357	Homo sapi	AC092357	Homo sapi	C 740	23	4.7	33466	2	AC087046	Homo sapi
668	24	4.9	192046	2	AC113688	Rattus no	AC113688	Rattus no	C 741	23	4.7	35528	9	AC004495	Homo sapi
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671	24	4.9	196247	2	HSJ651N20	Homo sapi	AL117346	Homo sapi	C 744	23	4.7	36955	9	AP000543	Homo sapi
672	24	4.9	196662	9	AP001107	Homo sapi	AP001107	Homo sapi	C 745	23	4.7	38580	9	HSNOD1G1	Homo sapi
673	24	4.9	196917	2	AC087828	Homo sapi	AC087828	Homo sapi	C 746	23	4.7	39188	9	AC004754	Homo sapi
674	24	4.9	197905	2	AL645536	Homo sapi	AL645536	Homo sapi	C 747	23	4.7	39443	9	AC010505	Homo sapi
675	24	4.9	198105	2	AC028160	Homo sapi	AC028160	Homo sapi	C 748	23	4.7	39915	9	AC010512	Homo sapi
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677	24	4.9	199503	9	AC018901	Homo sapi	AC018901	Homo sapi	C 750	23	4.7	41569	9	HS141418	Human DNA
678	24	4.9	200498	2	AC092378	Homo sapi	AC092378	Homo sapi	C 751	23	4.7	42642	9	AC006277	Homo sapi
679	24	4.9	200948	2	AP000944	Homo sapi	AP000944	Homo sapi	C 752	23	4.7	43346	9	AC005787	Homo sapi
680	24	4.9	201572	9	AC007298	Homo sapi	AC007298	Homo sapi	C 753	23	4.7	43411	9	AC004643	Homo sapi
681	24	4.9	202517	2	AC055872	Homo sapi	AC055872	Homo sapi	C 754	23	4.7	43712	9	HS984G1	Human DNA
682	24	4.9	202933	9	AC009854	Homo sapi	AC009854	Homo sapi	C 755	23	4.7	44957	9	AC005372	Homo sapi
683	24	4.9	207293	9	AC012564	Homo sapi	AC012564	Homo sapi	C 756	23	4.7	47722	2	AC113140	Homo sapi
684	24	4.9	207997	9	AC009093	Homo sapi	AC009093	Homo sapi	C 757	23	4.7	48068	9	AL589983	Human DNA
685	24	4.9	209907	2	AL731733	Homo sapi	AL731733	Homo sapi	C 758	23	4.7	55176	9	AC080153	Homo sapi
686	24	4.9	211345	2	AL731733	Homo sapi	AL731733	Homo sapi	C 759	23	4.7	56306	9	HSJ698015	Human DNA
687	24	4.9	212237	9	AC079235	Homo sapi	AC079235	Homo sapi	C 760	23	4.7	56408	9	AF527418	Homo sapi
688	24	4.9	212752	9	AC063977	Homo sapi	AC063977	Homo sapi	C 761	23	4.7	57296	2	AC111159	Homo sapi
689	24	4.9	212819	2	AC028550	Homo sapi	AC028550	Homo sapi	C 762	23	4.7	57722	2	HSC833B10	Homo sapi
690	24	4.9	215936	9	CNS05TCA	Human chr	AC035076	Human chr	C 763	23	4.7	60555	2	AC100824	Homo sapi
691	24	4.9	216523	9	AC073587	Homo sapi	AC073587	Homo sapi	C 764	23	4.7	61095	9	AL3390780	Human DNA
692	24	4.9	216978	9	AC018554	Homo sapi	AC018554	Homo sapi	C 765	23	4.7	61431	2	AL596186	Human DNA
693	24	4.9	217956	2	AL355388	Homo sapi	AL355388	Homo sapi	C 766	23	4.7	61663	2	AC080042	Homo sapi
694	24	4.9	218230	2	AC090390	Homo sapi	AC090390	Homo sapi	C 767	23	4.7	61896	2	AC090992	Homo sapi
695	24	4.9	220491	2	AL445206	Homo sapi	AL445206	Homo sapi	C 768	23	4.7	62493	9	HS193G15	Human DNA
696	24	4.9	226239	2	AC126174	Homo sapi	AC126174	Homo sapi	C 769	23	4.7	62493	9	HSU193G15	Human DNA
697	24	4.9	232613	9	AC008679	Homo sapi	AC008679	Homo sapi	C 770	23	4.7	63954	2	AC087789	Homo sapi
698	24	4.9	233089	9	AC000353	Homo sapi	AC000353	Homo sapi	C 771	23	4.7	63954	2	AC087789	Homo sapi
699	24	4.9	243230	2	AC008741	Homo sapi	AC008741	Homo sapi	C 772	23	4.7	64738	2	AC110600	Human DNA
700	24	4.9	243558	9	AC010310	Homo sapi	AC010310	Homo sapi	C 773	23	4.7	65138	9	AL590812	Human DNA
701	24	4.9	250762	2	AL662840	Homo sapi	AL662840	Homo sapi	C 774	23	4.7	66539	9	HSJ583K24	Human DNA
702	24	4.9	278911	9	AE006465	Homo sapi	AE006465	Homo sapi	C 775	23	4.7	67392	9	AC107220	Homo sapi
703	24	4.9	302859	2	AC044785	Homo sapi	AC044785	Homo sapi	C 776	23	4.7	68037	9	AY046055	Homo sapi
704	24	4.9	340000	9	AP001671	Homo sapi	AP001671	Homo sapi	C 777	23	4.7	68581	9	AP000563	Homo sapi
705	24	4.9	340000	9	AP001714	Homo sapi	AP001714	Homo sapi	C 778	23	4.7	69793	9	AC104646	Homo sapi
706	24	4.9	340000	9	AP001752	Homo sapi	AP001752	Homo sapi	C 779	23	4.7	70339	9	AL513123	Human DNA
707	24	4.9	340000	9	HS21C049	Homo sapi	AL163249	Homo sapi	C 780	23	4.7	70824	2	AC118661	Homo sapi
708	24	4.9	348189	2	AC119567	Homo sapi	AC119567	Homo sapi	C 781	23	4.7	73079	8	AC006202	Arabidops
709	23	4.7	343	6	AX390203	Sequence	AX390203	Sequence	C 782	23	4.7	74037	2	AC024314	Homo sapi
710	23	4.7	851	9	HSJDK008	Macaca fa	AF067016	Macaca fa	C 783	23	4.7	74507	9	AC004031	Homo sapi
711	23	4.7	1297	9	AB062949	Drosophila	AB061174	Drosophila	C 784	23	4.7	75120	9	AC004666	Homo sapi
712	23	4.7	1423	3	AK061174	Homo sapi	AK001322	Homo sapi	C 785	23	4.7	76211	6	HSJ3336M4	Human DNA
713	23	4.7	1754	9	AK001322	Homo sapi	AK023338	Homo sapi	C 786	23	4.7	81001	6	AX063464	Sequence
714	23	4.7	2414	9	AK023338	Homo sapi	AK000725	Homo sapi	C 787	23	4.7	81437	2	AX063464	Sequence
715	23	4.7	2658	9	AK000725	Homo sapi	AK022939	Homo sapi	C 788	23	4.7	81437	2	AX063464	Sequence
716	23	4.7	2852	9	AK022939	Homo sapi	AX189753	Sequence	C 789	23	4.7	82101	9	AC005694	Homo sapi
717	23	4.7	3201	6	AX189753	Sequence	AB072970	Homo sapi	C 790	23	4.7	83127	9	AC011990	Homo sapi
718	23	4.7	3550	9	AB072970	Homo sapi	AK139969	Sequence	C 791	23	4.7	84113	2	AC073063	Homo sapi
719	23	4.7	3807	6	AK139969	Sequence	AK140288	Sequence	C 792	23	4.7	84157	2	AC016260	Homo sapi
720	23	4.7	3807	6	AK140288	Sequence	AL140566	Sequence	C 793	23	4.7	84613	9	AL136140	Human DNA
721	23	4.7	3807	6	AL140566	Sequence	AL832641	Homo sapi	C 794	23	4.7	86684	9	AC010605	Homo sapi
722	23	4.7	5250	9	HSN803951	Homo sapi	AL832641	Homo sapi	C 795	23	4.7	88027	2	AL162401	Homo sapi

796	23	4.7	88428	9	AL133388	AL133388 Human DNA	c 869	23	4.7	124882	9	AC108729	AC108729 Homo sapi
797	23	4.7	89944	9	AC093127	AC093127 Papio cyn	870	23	4.7	125674	2	AP002018	AP002018 Homo sapi
798	23	4.7	90256	9	AP001582	AP001582 Homo sapi	c 871	23	4.7	126138	9	HSAX180000	Y18000 Homo sapien
799	23	4.7	90422	9	AC023880	AC023880 Homo sapi	872	23	4.7	126150	9	AC005152	AC005152 Homo sapi
800	23	4.7	90923	2	AL159157	AL159157 Homo sapi	873	23	4.7	126651	9	AC092815	AC092815 Homo sapi
c 801	23	4.7	91261	8	AC005851	AC005851 Arabidops	874	23	4.7	127079	9	HS214K23	Z74739 Human DNA s
c 802	23	4.7	91767	9	AC097748	AC097748 Homo sapi	c 875	23	4.7	127079	9	HS214K23	Z74739 Human DNA s
803	23	4.7	91874	9	AC093284	AC093284 Homo sapi	c 876	23	4.7	127148	9	AC098583	AC098583 Homo sapi
804	23	4.7	92216	2	AC098662	AC098662 Rattus n	877	23	4.7	128216	9	HS214K23	AL079341 Human DNA
805	23	4.7	92510	9	HS390B3	Z91096 Human DNA s	c 878	23	4.7	128484	9	AC035270	AC035270 Homo sapi
806	23	4.7	93187	2	AC092769	AC092769 Homo sapi	c 879	23	4.7	129293	9	AC092289	AC092289 Homo sapi
807	23	4.7	93395	2	AC087882	AC087882 Homo sapi	c 880	23	4.7	131133	2	AC097946	AC097946 Homo sapi
c 808	23	4.7	93667	9	AL591708	AL591708 Human DNA	c 881	23	4.7	131271	9	AC111151	AC111151 Homo sapi
809	23	4.7	93744	9	AC097724	AC097724 Homo sapi	c 882	23	4.7	132724	9	AC068713	AC068713 Homo sapi
810	23	4.7	94359	9	AP000974	AP000974 Homo sapi	c 883	23	4.7	133053	9	AC053479	AC053479 Homo sapi
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c 812	23	4.7	97037	9	AC004973	AC004973 Homo sapi	c 885	23	4.7	133925	9	AC011444	AC011444 Homo sapi
813	23	4.7	97495	9	AC093014	AC093014 Homo sapi	c 886	23	4.7	134060	9	AL358354	AL358354 Human DNA
c 814	23	4.7	97621	9	AL607089	AL607089 Human DNA	c 887	23	4.7	135274	2	AC097580	AC097580 Rattus no
c 815	23	4.7	97995	9	AC011602	AC011602 Homo sapi	c 888	23	4.7	135692	9	AC023315	AC023315 Homo sapi
c 816	23	4.7	98876	9	AC009488	AC009488 Homo sapi	c 889	23	4.7	135711	9	AL590075	AL590075 Human DNA
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c 818	23	4.7	99589	2	AC093299	AC093299 Homo sapi	c 891	23	4.7	137230	9	AC027793	AC027793 Homo sapi
c 819	23	4.7	100000	9	AP000211	AP000211 Homo sapi	c 892	23	4.7	137271	9	AC004552	AC004552 Homo sapi
c 820	23	4.7	100000	17	AP0000133	AP0000133 Homo sapi	c 893	23	4.7	137272	9	AL137062	AL137062 Human DNA
821	23	4.7	101800	9	AC003103	AC003103 Homo sapi	c 894	23	4.7	137499	9	AC015931	AC015931 Homo sapi
c 822	23	4.7	102313	9	AL603749	AL603749 Human DNA	c 895	23	4.7	138985	9	AL139156	AL139156 Human DNA
823	23	4.7	103009	9	AC087225	AC087225 Homo sapi	c 896	23	4.7	139904	9	HS97D16	AL009179 Human DNA
c 824	23	4.7	103616	9	AL138689	AL138689 Human DNA	c 897	23	4.7	140094	9	HS20113	AL035423 Human DNA
c 825	23	4.7	103718	9	AL139175	AL139175 Human DNA	c 898	23	4.7	140132	2	AC128089	AL035423 Human DNA
c 826	23	4.7	103727	9	AL136360	AL136360 Human DNA	c 899	23	4.7	140330	9	AC026777	AC026777 Homo sapi
c 827	23	4.7	104844	9	HSJ1057J7	AL109936 Human DNA	c 900	23	4.7	140531	2	AC105341	AC105341 Homo sapi
c 828	23	4.7	105047	2	AP000669	AP000669 Homo sapi	c 901	23	4.7	140717	9	AL133545	AL133545 Human DNA
c 829	23	4.7	105087	2	AC093884	AC093884 Homo sapi	c 902	23	4.7	141822	2	AC115994	AC115994 Homo sapi
c 830	23	4.7	105008	9	HS506	AL020993 Human DNA	c 903	23	4.7	142233	9	AC090458	AC090458 Homo sapi
831	23	4.7	107298	9	AC000059	AC000059 Homo sapi	c 904	23	4.7	142323	9	AC044839	AC044839 Homo sapi
c 832	23	4.7	108090	9	AC009533	AC009533 Homo sapi	c 905	23	4.7	142362	2	AC036162	AC036162 Homo sapi
c 833	23	4.7	108726	2	AL355866	AL355866 Homo sapi	c 906	23	4.7	142689	9	HSB348B13	AL121872 Human DNA
834	23	4.7	110000	2	AC092789	Continuation (2 of	c 907	23	4.7	142756	9	AC005844	AC005844 Homo sapi
c 835	23	4.7	110000	2	AC092931	Continuation (3 of	c 908	23	4.7	143517	9	AL356752	AL356752 Human DNA
c 836	23	4.7	110000	2	AC098775	Continuation (3 of	c 909	23	4.7	143701	9	HS29C18	Z97192 Human DNA s
c 837	23	4.7	110000	2	AC098773	Continuation (4 of	c 910	23	4.7	143799	9	AC011059	AC011059 Homo sapi
c 838	23	4.7	110000	2	AC011600	AC011600 Homo sapi	c 911	23	4.7	143834	9	AC004960	AC004960 Homo sapi
c 839	23	4.7	110000	2	AC011600	Continuation (3 of	c 912	23	4.7	144165	9	AC002127	AC002127 Human BAC
c 840	23	4.7	110000	2	AL683889	Continuation (4 of	c 913	23	4.7	144833	2	AL139128	AL139128 Human DNA
c 841	23	4.7	110000	2	HS171M	Continuation (3 of	c 914	23	4.7	145133	2	AC013822	AC013822 Homo sapi
c 842	23	4.7	110227	9	AC121160	AC121160 Homo sapi	c 915	23	4.7	145250	9	HSB24775	AL035534 Homo sapi
c 843	23	4.7	110227	9	AC125287	AC125287 Homo sapi	c 916	23	4.7	145366	2	AC024945	AC024945 Homo sapi
844	23	4.7	110293	9	HS29C18	AL049766 Human DNA	c 917	23	4.7	145459	9	AC010748	AC010748 Homo sapi
845	23	4.7	110602	2	AL358592	AL358592 Homo sapi	c 918	23	4.7	145528	9	AC097491	AC097491 Homo sapi
846	23	4.7	110716	9	AL135918	AL135918 Human DNA	c 919	23	4.7	146463	2	AC068306	AC068306 Homo sapi
c 847	23	4.7	112303	9	AC093836	AC093836 Homo sapi	c 920	23	4.7	146954	9	AL590640	AL590640 Human DNA
c 848	23	4.7	113250	9	AC004900	AC004900 Homo sapi	c 921	23	4.7	147913	9	HS29C18	AL123990 Human DNA
c 849	23	4.7	113980	2	AP001540	AP001540 Homo sapi	c 922	23	4.7	148203	2	AC022187	AC022187 Homo sapi
c 850	23	4.7	114191	9	AL451007	AL451007 Human DNA	c 923	23	4.7	148280	9	AC004474	AC004474 Homo sapi
851	23	4.7	114957	9	CNS05TEH	AL359219 Human chr	c 924	23	4.7	148308	9	AC113192	AC113192 Homo sapi
852	23	4.7	115725	30	AC025481	AC025481 Homo sapi	c 925	23	4.7	148316	2	AL356483	AL356483 Homo sapi
c 853	23	4.7	115770	9	AC107450	AC107450 Homo sapi	c 926	23	4.7	148420	2	AC069266	AC069266 Homo sapi
c 854	23	4.7	116481	9	AC092287	AC092287 Homo sapi	c 927	23	4.7	148463	2	AC012140	AC012140 Homo sapi
c 855	23	4.7	117264	2	AC127024	AC127024 Homo sapi	c 928	23	4.7	149000	9	AC091814	AC091814 Homo sapi
c 856	23	4.7	118724	9	AC105074	AC105074 Homo sapi	c 929	23	4.7	149006	9	AC025812	AC025812 Homo sapi
857	23	4.7	119022	2	AC055721	AC055721 Homo sapi	c 930	23	4.7	149188	9	AC114781	AC114781 Homo sapi
c 858	23	4.7	119918	2	AP000713	AP000713 Homo sapi	c 931	23	4.7	149488	2	AC026026	AC026026 Homo sapi
c 859	23	4.7	119951	2	AC025267	AC025267 Homo sapi	c 932	23	4.7	149620	2	AC069397	AC069397 Homo sapi
c 860	23	4.7	120099	9	AC011449	AC011449 Homo sapi	c 933	23	4.7	149751	2	AC048339	AC048339 Homo sapi
c 861	23	4.7	120335	9	HSU441A12	AL121574 Human DNA	c 934	23	4.7	149901	2	AC022243	AC022243 Homo sapi
c 862	23	4.7	120426	9	HS1116H23	AL121890 Human DNA	c 935	23	4.7	150129	2	AC036909	AC036909 Homo sapi
c 863	23	4.7	120551	9	AL391215	AL391215 Human DNA	c 936	23	4.7	150377	2	AC102797	AC102797 Homo sapi
864	23	4.7	120703	9	AC002364	AC002364 Homo sapi	c 937	23	4.7	150505	2	AC009274	AC009274 Homo sapi
c 865	23	4.7	122303	9	AC008681	AC008681 Homo sapi	c 938	23	4.7	150614	2	AC126757	AC126757 Homo sapi
c 866	23	4.7	123947	9	AC005045	AC005045 Homo sapi	c 939	23	4.7	151162	9	AC009364	AC009364 Human chr
c 867	23	4.7	124041	9	CNS01DSJ	AL121808 Human chr	c 940	23	4.7	151432	2	AC083966	AC083966 Homo sapi
c 868	23	4.7	124740	9	AC011308	AC011308 Homo sapi	c 941	23	4.7	151553	9	AL139342	AL139342 Human DNA

942	23	4.7	151630	9	AC005154	Homo sapi
943	23	4.7	151677	9	AC090957	Homo sapi
944	23	4.7	151990	9	AL354989	Human DNA
945	23	4.7	152244	9	AF000352	Homo sapi
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947	23	4.7	152863	9	AL162417	Human DNA
948	23	4.7	152891	2	AC011772	Homo sapi
949	23	4.7	153019	2	AC079323	Homo sapi
950	23	4.7	153206	9	AC006356	Homo sapi
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955	23	4.7	153786	2	AL845446	Homo sapi
956	23	4.7	153865	2	AC016301	Homo sapi
957	23	4.7	154054	2	AC034114	Homo sapi
958	23	4.7	154365	2	AC118985	Papio cyn
959	23	4.7	154412	9	AC091753	Rattus no
960	23	4.7	154607	2	AC084749	Homo sapi
961	23	4.7	155067	9	AC010301	Homo sapi
962	23	4.7	155236	2	AC009701	Homo sapi
963	23	4.7	155359	9	AL358777	Human DNA
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967	23	4.7	156813	9	HSJ631M13	Human DNA
968	23	4.7	156843	2	AC011145	Homo sapi
969	23	4.7	156949	9	AL161652	Human DNA
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972	23	4.7	157306	9	AL161417	Human DNA
973	23	4.7	157400	2	AC016104	Homo sapi
974	23	4.7	157548	2	AC021972	Homo sapi
975	23	4.7	157572	9	AL513210	Human DNA
976	23	4.7	157827	2	AC027260	Homo sapi
977	23	4.7	157866	9	AL139132	Human DNA
978	23	4.7	157975	9	HSB346K17	Human DNA
979	23	4.7	157979	9	CNS05TD4	Human chr
980	23	4.7	158171	2	AC022258	Homo sapi
981	23	4.7	158863	2	AC118586	Pan trogl
982	23	4.7	159769	2	AC007337	Homo sapi
983	23	4.7	159802	2	AC019262	Homo sapi
984	23	4.7	160015	9	AL158038	Human DNA
985	23	4.7	160262	9	AC005242	Homo sapi
986	23	4.7	160342	2	AC025492	Homo sapi
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993	23	4.7	161008	9	AC087591	Homo sapi
994	23	4.7	161179	2	AC083954	Homo sapi
995	23	4.7	161306	2	AC091056	Homo sapi
996	23	4.7	161504	9	AC006517	Homo sapi
997	23	4.7	161551	2	AC027509	Homo sapi
998	23	4.7	161580	9	HUAC002307	Homo sapi
999	23	4.7	161608	2	AC015955	Homo sapi
1000	23	4.7	161826	2	AC026157	Homo sapi

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source

gene

CDS

100.0%; Score 486; DB 9; Length 5492;

Best Local Similarity 100.0%; Pred. No. 1.4e-261;

Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTGACATGTGAGCAGCACCGTCGCTGGCCAGAGTTTCTTTTATTTCTTTCTTTT 60

Db 3557 AGATTGACATGTGAGCAGCACCGTCGCTGGCCAGAGTTTCTTTTATTTCTTTT 3616

Qy 61 CTTTCT 120

Db 3617 CTTTCT 3676

Qy 121 ATTTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Db 3677 ATTTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 3736

Qy 181 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

Db 3737 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3796

Qy 241 CCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

Db 3797 CCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3856

Qy 301 CTTCT 360

Db 3857 CTTCT 3916

Qy 361 CAGATGACCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

## ALIGNMENTS

RESULT 1  
AF123659  
LOCUS Homo sapiens FEZ1 (FEZ1) mRNA, complete cds. linear PRI 07-APR-1999  
DEFINITION Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.  
ACCESSION AF123659  
VERSION AF123659.1 GI:4572475  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

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Db 3917 CAGAGTCACTTTCTGTGGCTGGCTCTACCTTCCCTGCTCCCTGAGGTAAACGGTGCCA 3976
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Qy 421 TCCTGCCATCTCAACGACAGAGAGCTTTCTTGGAAATTTCAACCACTTCTTAGTC 480
|||||
Db 3977 TCCTGCCATCTCAACGACAGAGAGCTTTCTTGGAAATTTCAACCACTTCTTAGTC 4036
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Qy 481 CCAAGC 486
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Db 4037 CCAAGC 4042

RESULT 2
AF123653 9108 bp DNA linear PRI 07-APR-1999
DEFINITION Homo sapiens FEZ1 (FEZ1) gene, complete cds.
ACCESSION AF123653
VERSION AF123653.1 GI:4572463
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9108)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 9p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
PUBMED 10097140
REFERENCE 2 (bases 1 to 9108)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
FEATURES
source
1. 9108
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p22"
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join(112. 456,1707. 2510,4912. 5553)
/gene="FEZ1"
/codon_start=1
/product="FEZ1"
/protein_id="AAD23834.1"
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GFSODGHGKSSKMGSEDPFYFKVQKARGSHHPDYATLSSDGLGQAGVDPDPT
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ELKPLCSGLSDSGRSMSLPHSTSSSVQLDPLVTPVPTSRFGSHNITQGLV
LQDSNMMLKALSFSDGSKLGHNSKADGFCVRSPTSDGSIQLEOKLLREGA
LQKQRFSEKELASSLAYBERPRRCDELEGPFGKGNKKQASQKRAQVLLHQ
VLQKQKRLQRLSELMKEQDLLETKLRSYERKTSFGPALEETQWECVQKSGEIS
LLKQKLESQTEVNAKASEILGLKAQLTRGKLEGLRLTQDLEGALRTKGLELYC
ENELQKNEALLREKVNLEQLQELRAQALARDMGPTTPEDVPALQRELERLR
ALREERQGHQMSGFQHERLVWKEKEKVIQYQKQLQSQSYVMYQNRLEKALQO
LARGDSAGEPLEVDLEADIPYEDIATETI"
BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others
ORIGIN
Query Match 100.0%; Score 486; DB 9; Length 9108;
Best Local Similarity 100.0%; Pred. No. 1.4e-261;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGATTGCAGATGTGAGCCACCGCTGCGGCGAGATTTTCTTTTATTCTTCTTTCTTTT
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Db 7208 AGATTGCAGATGTGAGCCACCGCTGCGGCGAGATTTTCTTTTATTCTTCTTTT 7267
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Qy 61 CTTTGTGCTTTCTGTGCTTTTTCAGAGCAAGCAGACCTAGCAGGCTGTTCATGTTCT 120
|||||
Db 7268 CTTTGTGCTTTCTGTGCTTTTTCAGAGCAAGCAGACCTAGCAGGCTGTTCATGTTCT 7327
|||||
Qy 121 ATTTTGACTGTAGCCACAGCTGCTGTGTTCTCAGGACAGCATCCCTCCACATGCCTGCG 180
|||||
Db 7328 ATTTTGACTGTAGCCACAGCTGCTGTGTTCTCAGGACAGCATCCCTCCACATGCCTGCG 7387
|||||
Qy 181 CTTGCTGCTGCTGAGATGAGGAGGGAGGCTCTGGAACTTTCGCGAGTCAAGGCCAGTC 240
|||||
Db 7388 CTTGCTGCTGCTGAGATGAGGAGGGAGGCTCTGGAACTTTCGCGAGTCAAGGCCAGTC 7447
|||||
Qy 241 CCATTTCTGCTCGCTCACCGCTGCGCTTAGAGACCCCGAGGTAGGGTGGGAGATG 300
|||||
Db 7448 CCATTTCTGCTCGCTCACCGCTGCGCTTAGAGACCCCGAGGTAGGGTGGGAGATG 7507
|||||
Qy 301 CTTCTCTCTTGGCCCCCGCCCTCATGGGTCCTAGCCCTTCCCTGAGTGGGGCTGAGGC 360
|||||
Db 7508 CTTCTCTCTTGGCCCCCGCCCTCATGGGTCCTAGCCCTTCCCTGAGTGGGGCTGAGGC 7567
|||||
Qy 361 CAGAGTCACCTTTTCTGTGCTGCTCTACCTTCTGCTGCTGAGGTTAAACGGTGCCCA 420
|||||
Db 7568 CAGAGTCACCTTTTCTGTGCTGCTCTACCTTCTGCTGCTGAGGTTAAACGGTGCCCA 7627
|||||
Qy 421 TCTGCGCATCTCTAAAGCAGAGGAGCTTTCTTGGAAATTTCAACCACTTCTCTTAGTC 480
|||||
Db 7628 TCTGCGCATCTCTAAAGCAGAGGAGCTTTCTTGGAAATTTCAACCACTTCTCTTAGTC 7687
|||||
Qy 481 CCAAGC 486
|||||
Db 7688 CCAAGC 7693

RESULT 3
AC025853 173264 bp DNA linear HTG 17-JUN-2002
LOCUS Homo sapiens chromosome 8 clone RP11-353K12 map 8, *** SEQUENCING
DEFINITION IN PROGRESS ***, 3 unordered pieces.
ACCESSION AC025853
VERSION AC025853.13 GI:21431202
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173264)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-353K12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173264)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
Boguslavsky,L., Bouckhealter,B., Brown,A., Burkett,G.,
Campiano,A., Casle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teshaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
```



chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>  
 RP11-142F1 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-142F1 it may be shorter because we sequence overlapping sections only once, except for a short overlap.  
 The true left end of clone RP11-142F1 is at 1 in this sequence. The true left end of clone RP11-390B4 is at 95431 in this sequence. The true right end of clone RP11-161K20 is at 28876 in this sequence.

## FEATURES

source

1. 97430  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-142F1"  
 /clone\_lib="RPCI-11.1"

BASE COUNT 29078 a 20172 c 20123 g 28057 t

## ORIGIN

Query Match 7.8%; Score 38; DB 9; Length 97430;  
 Best Local Similarity 100.0%; Pred. NO. 8.8e-10;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CAGATGTGAGCCACCGTGGCCAGATTTTCTTTT 44  
 |||||  
 Db 26327 CAGATGTGAGCCACCGTGGCCAGATTTTCTTTT 26290

## RESULT 5

AC010367

LOCUS

DEFINITION Homo sapiens chromosome 5 clone CTD-2044L23, WORKING DRAFT  
 SEQUENCE, 17 unordered pieces.

AC010367

VERSION

AC010367.4 GI:13699509

KEYWORDS

HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 137845)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished

2 (bases 1 to 137845)

DOE Joint Genome Institute.

Direct Submission

Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Apr 20, 2001 this sequence version replaced gi:7710742.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

-----

Project Information

Center Project Name: 644732

Center clone name: CITB-H1\_2044L23

-----

Summary Statistics

Consensus quality: 122756 bases at least Q40

Consensus quality: 127174 bases at least Q30

Consensus quality: 123642 bases at least Q20

Estimated insert size: 121000; pulse field gel estimation

Estimated insert size: 136245; sum-of-contigs estimation

Quality coverage: 6.63 in Q20 bases; pulse-field gel estimation

Quality coverage: 5.89 in Q20 bases; sum-of-contigs estimation.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 17 contigs. The true order of the pieces

\* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1041: contig of 1041 bp in length  
 \* 1042  
 \* 1141: gap of unknown length  
 \* 1142  
 \* 2183: contig of 1042 bp in length  
 \* 2184  
 \* 2283: gap of unknown length  
 \* 2284  
 \* 3529: contig of 1246 bp in length  
 \* 3530  
 \* 3629: gap of unknown length  
 \* 3630  
 \* 4897: contig of 1268 bp in length  
 \* 4898  
 \* 4997: gap of unknown length  
 \* 4998  
 \* 6540: contig of 1543 bp in length  
 \* 6541  
 \* 6640: gap of unknown length  
 \* 6641  
 \* 7735: contig of 1095 bp in length  
 \* 7736  
 \* 7835: gap of unknown length  
 \* 7836  
 \* 8852: contig of 1017 bp in length  
 \* 8853  
 \* 10065: gap of unknown length  
 \* 10066  
 \* 10165: gap of unknown length  
 \* 10166  
 \* 11335: contig of 1170 bp in length  
 \* 11336  
 \* 11435: gap of unknown length  
 \* 11436  
 \* 12444: contig of 1009 bp in length  
 \* 12445  
 \* 12544: gap of unknown length  
 \* 12545  
 \* 13853: contig of 1308 bp in length  
 \* 13854  
 \* 13952: gap of unknown length  
 \* 13953  
 \* 15056: contig of 1104 bp in length  
 \* 15057  
 \* 15156: gap of unknown length  
 \* 15157  
 \* 23003: contig of 7847 bp in length  
 \* 23004  
 \* 23103: gap of unknown length  
 \* 23104  
 \* 41386: contig of 18283 bp in length  
 \* 41387  
 \* 68942: contig of 27456 bp in length  
 \* 68943  
 \* 89042: gap of unknown length  
 \* 89043  
 \* 98301: contig of 29259 bp in length  
 \* 98302  
 \* 98401: gap of unknown length  
 \* 98402  
 \* 137845: contig of 39444 bp in length.

## FEATURES

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1. 137845  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
 /clone="CTD-2044L23"  
 /clone\_lib="CalTech human BAC library D"

BASE COUNT 38706 a 29368 c 29046 g 39089 t 1636 others

## ORIGIN

Query Match 6.4%; Score 31; DB 2; Length 137845;  
 Best Local Similarity 100.0%; Pred. NO. 7.5e-06;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GATTGAGATGTGAGCCACCGTGGCCGCA 32  
 |||||  
 Db 36892 GATTGAGATGTGAGCCACCGTGGCCGCA 36922

## RESULT 6

AL135778/c

LOCUS

DEFINITION

Human DNA sequence from clone RP1-119C5 on chromosome 6, complete

sequence.

AL135778

ACCESSION

AL135778.9

VERSION

HTG.

KEYWORDS

human.

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152786)

Kimberley, A.

Direct Submission

AL135778 152786 bp DNA linear PRI 27-JAN-2001  
 Human DNA sequence from clone RP1-119C5 on chromosome 6, complete

sequence.

AL135778.9 GI:12330708

ACCESSION

AL135778

VERSION

HTG.

KEYWORDS

human.

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152786)

Kimberley, A.

Direct Submission



## JOURNAL

Submitted (27-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Jan 22, 2001 this sequence version replaced gi:10715708.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>  
Rpl-119C5 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: PCYPAC2

This sequence is the entire insert of clone RPl-119C5 The true left end of clone RPl-327D12 is at 77349 in this sequence. The true left end of clone RPl-126E20 is at 128858 in this sequence. The true right end of clone RPl-146G22 is at 135074 in this sequence.

## FEATURES

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/db\_xref="taxon:9606"  
/chromosome="6"  
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/clone\_lib="RPCI-1"

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repeat\_region 1193. .1503  
/note="L1MC/D repeat: matches 5352. .7010 of consensus"  
repeat\_region 1968. .2190  
/note="MLT1B repeat: matches 82. .310 of consensus"  
repeat\_region 2223. .2345  
/note="MST-INTERNAL repeat: matches 1518. .1649 of consensus"  
repeat\_region 2779. .3260  
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repeat\_region 3261. .3557  
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repeat\_region 3558. .3656  
/note="L1MC5 repeat: matches 7771. .7871 of consensus"  
repeat\_region 3696. .3842  
/note="FRAM repeat: matches 0. .146 of consensus"  
repeat\_region 4228. .4538  
/note="AluSp repeat: matches 2. .313 of consensus"  
repeat\_region 4550. .4752  
/note="HAL1 repeat: matches 1521. .1714 of consensus"  
repeat\_region 4753. .5068  
/note="AluX repeat: matches 1. .310 of consensus"  
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/note="HAL1 repeat: matches 902. .1521 of consensus"  
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repeat\_region 7569. .8002

/note="MSTC repeat: matches 2. .405 of consensus"  
8003. .8018  
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8019. .8319  
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8320. .8409  
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8679. .9302  
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9349. .10135  
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10168. .10768  
/note="L1MB8 repeat: matches 5562. .6168 of consensus"  
10769. .11916  
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11917. .12211  
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12212. .12628  
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12678. .13054  
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13055. .13357  
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13358. .13545  
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13555. .14247  
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14370. .14443  
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14533. .14730  
/note="AluSg/x repeat: matches 89. .294 of consensus"  
14745. .14878  
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15035. .15110  
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17361. .17606  
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18005. .18139  
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18179. .18368  
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18438. .18654  
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19158. .19564  
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21068. .21178  
/note="L2 repeat: matches 2589. .2692 of consensus"  
21476. .21560  
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22115. .22280  
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22504. .22781  
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23353. .23650  
/note="AluSg repeat: matches 1. .298 of consensus"  
24073. .24154  
/note="MLT11 repeat: matches 317. .402 of consensus"  
24204. .24259  
/note="MLT1J repeat: matches 312. .367 of consensus"  
24762. .25075  
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25707. .26058  
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26070. .26125  
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26126. .26189  
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26196. .26228  
/note="MLT2FB repeat: matches 367. .399 of consensus"



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/notes="WIR repeat: matches 77..146 of consensus"
repeat_region 28323..28460
/notes="L2 repeat: matches 2571..2703 of consensus"
repeat_region 28992..29605
/notes="MER41B repeat: matches 1..635 of consensus"
repeat_region 29842..29883
/notes="21 copies 2 mer tt 85% conserved"
repeat_region 31794..32080
/notes="AluSq repeat: matches 1..291 of consensus"
repeat_region 32366..32526
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repeat_region 33419..33632
/notes="AluJo repeat: matches 86..299 of consensus"
repeat_region 34415..34620
/notes="MER3 repeat: matches 1..209 of consensus"
repeat_region 35454..35574
/notes="FLAM C repeat: matches 1..122 of consensus"
repeat_region 36427..37101
/notes="L1MB1 repeat: matches 5444..6151 of consensus"
repeat_region 37230..37336
/notes="L1MB3 repeat: matches 6061..6155 of consensus"
repeat_region 37337..37647
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repeat_region 37648..37766
/notes="L1MB3 repeat: matches 5904..6061 of consensus"
repeat_region 40066..40381
/notes="AluSq repeat: matches 1..313 of consensus"
repeat_region 41450..41503
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repeat_region 41452..41508
/notes="19 copies 3 mer at 87% conserved"
repeat_region 42164..42270
/notes="WIR repeat: matches 46..150 of consensus"
repeat_region 42376..42635
/notes="AluJo repeat: matches 52..297 of consensus"
repeat_region 42654..42758
/notes="L2 repeat: matches 2597..2706 of consensus"
repeat_region 42904..43196

Query Match 6.4%; Score 31; DB 9; Length 152786;
Best Local Similarity 100.0%; Pred.No. 7.5e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CAGATGTGAGCCACCGCTGCGCCAGATTT 37
Db 31818 CAGATGTGAGCCACCGCTGCGCCAGATTT 31788

RESULT 7
AL160395 179959 bp DNA linear PRI 17-MAR-2001
LOCUS Human DNA sequence from clone RP11-474D23 on chromosome 13q33.1-34,
DEFINITION complete sequence.
ACCESSION AL160395
VERSION AL160395.24 GI:13396423
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 179959)
AUTHORS Smith,M.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 20, 2001 this sequence version replaced gi:12655257.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

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variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; SW,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-474D23 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-474D23. The true
left end of clone RP11-190K22 is at 105916 in this sequence. The
true right end of clone RP11-494P5 is at 37339 in this sequence.

FEATURES             Location/Qualifiers
     source            1..179959
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="13"
                        /map="q33.1-34"
                        /clone="RP11-474D23"
                        /clone_lib="RPCI-11.2"
     misc_feature       6..454
                        /notes="match: GSS: Em:AQ831485"
     misc_feature      13..304
                        /notes="match: GSS: Em:AQ525749"
     misc_feature      25..463
                        /notes="match: GSS: Em:AQ634626"
     repeat_region     217..567
                        /note="THE1C repeat: matches 1..371 of consensus"
     repeat_region     1248..1535
                        /notes="MLT1C repeat: matches 8..283 of consensus"
     repeat_region     2198..2293
                        /note="L1MB8 repeat: matches 5521..5618 of consensus"
     repeat_region     2294..2640
                        /note="MLT1A1 repeat: matches 13..365 of consensus"
     repeat_region     2654..2921
                        /note="L1MB8 repeat: matches 5615..5894 of consensus"
     repeat_region     3106..3248
                        /note="AluJb repeat: matches 142..284 of consensus"
     repeat_region     3333..3498
                        /notes="L2 repeat: matches 2079..2266 of consensus"
     repeat_region     4415..4466
                        /notes="26 copies 2 mer gg 71% conserved"
     repeat_region     5113..5418
                        /note="AluX repeat: matches 5..312 of consensus"
     misc_feature      5502..5910
                        /note="match: STS: Em:HSPH25D3"
     repeat_region     7094..7277
                        /notes="2 copies 92 mer 96% conserved"
     misc_feature      8059..8455
                        /note="match: GSS: Em:AQ205997"
     repeat_region     8130..8211
                        /notes="2 copies 41 mer 89% conserved"
     repeat_region     9508..9577
                        /note="MIR repeat: matches 23..95 of consensus"
     repeat_region     9649..9720
                        /note="2 copies 36 mer 90% conserved"
     misc_feature      9704..10214
                        /note="Cpg island"
                        /evidence="not_experimental"

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repeat_region 9850. .9953
/note="2 copies 52 mer 90% conserved"
9888. .10004
/note="3 copies 39 mer 85% conserved"
repeat_region 10022. .10138
/note="3 copies 39 mer 83% conserved"
repeat_region 10119. .10222
/note="2 copies 52 mer 91% conserved"
misc_feature complement(12824. .13054)
/note="match: GSS: Em:AQ008472"
repeat_region 13051. .13542
/note="LTR38 repeat: matches 35. .603 of consensus"
misc_feature 13804. .14058
/note="Sequence from overlapping clone BA494P5 (AL139086).
Assembly confirmed by restriction digest."
repeat_region 14054. .16280
/note="L1MB6 repeat: matches 3900. .6148 of consensus"
repeat_region 16270. .17065
/note="L1M4 repeat: matches 1299. .2069 of consensus"
repeat_region 17066. .17420
/note="THS1C repeat: matches 1. .371 of consensus"
repeat_region 17421. .18640
/note="L1M4 repeat: matches -12. .1299 of consensus"
misc_feature 18456. .18874
/note="match: GSS: Em:B43739"
misc_feature complement(19474. .20004)
/note="match: GSS: Em:AQ725415"
repeat_region 20661. .20819
/note="MLT1F repeat: matches 300. .501 of consensus"
repeat_region 20799. .21111
/note="MLT1F repeat: matches 6. .332 of consensus"
repeat_region 21598. .22003
/note="MLT1B repeat: matches 6. .390 of consensus"
repeat_region 22842. .22923
/note="2 copies 41 mer 92% conserved"
repeat_region 22878. .23067
/note="5 copies 38 mer 83% conserved"
repeat_region 25852. .26039
/note="Aluub repeat: matches 116. .302 of consensus"
repeat_region 28738. .29038
/note="Aluux repeat: matches 1. .310 of consensus"
repeat_region 30142. .30536
/note="HERVL repeat: matches 4031. .4458 of consensus"
repeat_region 30579. .31009
/note="MSTB repeat: matches 1. .426 of consensus"
repeat_region 31902. .32285
/note="MSTA repeat: matches 1. .426 of consensus"
repeat_region 32370. .32924
/note="L1MB1 repeat: matches 5613. .6163 of consensus"
repeat_region 32925. .33227
/note="AluSC repeat: matches 1. .303 of consensus"
repeat_region 33228. .33465
/note="L1MB1 repeat: matches 5378. .5613 of consensus"
repeat_region 33466. .33768
/note="AluV repeat: matches 1. .303 of consensus"
repeat_region 33769. .35161
/note="L1MB1 repeat: matches 3934. .5378 of consensus"
repeat_region 35189. .37037
/note="L1M1 repeat: matches 1648. .3555 of consensus"
repeat_region 37038. .37332
/note="AluDb repeat: matches 1. .294 of consensus"
repeat_region 37333. .37630
/note="L1M1 repeat: matches 3555. .3841 of consensus"
repeat_region 37633. .37762
/note="FLAM C repeat: matches 3. .132 of consensus"
repeat_region 37871. .38362
/note="L1MB1 repeat: matches 5556. .6059 of consensus"
repeat_region 38531. .38570
/note="20 copies 2 mer aa 77% conserved"
misc_feature complement(40607. .41026)
/note="match: GSS: Em:AQ110612"
misc_feature 40640. .41524
/note="Single clone region. Sequence from reads from a
```

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short insert library derived from a clone PCR. Restriction
digest data confirm the assembly."
41021. .41050
/note="5 copies 6 mer cctct 96% conserved"
repeat_region 41053. .41136
/note="FLAM repeat: matches 53. .131 of consensus"
repeat_region 41161. .41303
/note="MER69A repeat: matches 23. .177 of consensus"
misc_feature 41285. .41455
/note="match: GSS: Em:AQ091575"
repeat_region 41462. .41696
/note="5 copies 47 mer 67% conserved"
repeat_region 41478. .41705
/note="6 copies 38 mer 66% conserved"
repeat_region 41523. .41669
/note="3 copies 49 mer 74% conserved"
repeat_region 41539. .41814
/note="3 copies 92 mer 71% conserved"
repeat_region 41572. .41787
/note="4 copies 54 mer 68% conserved"
repeat_region 41619. .41698
/note="5 copies 16 mer 72% conserved"
misc_feature 41692. .41696
/note="Single clone region. Sequence from reads from a
short insert library derived from a clone PCR. Restriction
digest data confirm the assembly."
42031. .42369
/note="L1PA3 repeat: matches 5809. .6146 of consensus"
repeat_region 42779. .43376
/note="MER77 repeat: matches 54. .620 of consensus"
repeat_region 45002. .45401
/note="MLT1D repeat: matches 88. .501 of consensus"
repeat_region 45602. .45983
/note="L2 repeat: matches 251. .704 of consensus"

Query Match 6.4%; Score 31; DB 9; Length 179959;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GATTGAGATGTGAGCCACCGTCGTCGCCA 32
|||||
Db 165585 GATTGAGATGTGAGCCACCGTCGTCGCCA 165615

RESULT 8
AC008675/c 186415 bp DNA linear PRI 20-DEC-2000
LOCUS Homo sapiens chromosome 5 clone CTB-4518, complete sequence.
DEFINITION AC008675
ACCESSION AC008675
VERSION AC008675.5 GI:11908270
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 186415)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186415)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 186415)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 20, 2000 this sequence version replaced gi:7709256.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
```

www-shgc.stanford.edu  
 Quality: Phrap Quality >=40 99.4% of Sequence;  
 Estimated Total Number of Errors is 1.3.

## FEATURES

source  
 1. .186415  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
 /clone="CTB-45J8"  
 BASE COUNT 53455 a 41083 c 40655 g 51222 t  
 ORIGIN

Query Match 6.4%; Score 31; DB 9; Length 186418;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 32  
 |||||  
 DB 112668 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 112638

## RESULT 9

AC018757 186418 bp DNA linear PRI 03-OCT-2001  
 LOCUS  
 DEFINITION Homo sapiens chromosome 5 clone CTB-45J8, complete sequence.  
 AC018757  
 VERSION  
 KEYWORDS HTG.

SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 DIRECT SUBMISSION  
 UNPUBLISHED  
 2 (bases 1 to 186418)  
 DIRECT SUBMISSION  
 TITLE  
 JOURNAL

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 DIRECT SUBMISSION  
 UNPUBLISHED  
 2 (bases 1 to 186418)  
 DIRECT SUBMISSION  
 TITLE  
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REFERENCE  
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 2 (bases 1 to 186418)  
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REFERENCE  
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 DIRECT SUBMISSION  
 UNPUBLISHED  
 2 (bases 1 to 186418)  
 DIRECT SUBMISSION  
 TITLE  
 JOURNAL

Db 73750 GATTGCAGATGTGAGCCACCGTGCCTGGCCA 73780

## RESULT 10

AC005054 197456 bp DNA linear HTG 17-AUG-2000  
 LOCUS  
 DEFINITION Homo sapiens chromosome UNK clone CTB-45H5, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, 18 unordered pieces.  
 AC005054  
 VERSION  
 KEYWORDS HTG; HTGS PHASE1.  
 SOURCE  
 ORGANISM

AC005054.2 GI:9838352

HTG; HTGS PHASE1.

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

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Homo sapiens

\* 129372 164242: contig of 34871 bp in length  
 \* 164243 164342: gap of unknown length  
 \* 164343 164840: contig of 498 bp in length  
 \* 164841 164940: gap of unknown length  
 \* 164941 167875: contig of 2935 bp in length  
 \* 167876 167975: gap of unknown length  
 \* 167976 172505: contig of 4530 bp in length  
 \* 172506 172605: gap of unknown length  
 \* 172606 176804: contig of 4199 bp in length  
 \* 176805 176904: gap of unknown length  
 \* 176905 180960: contig of 4056 bp in length  
 \* 180961 181060: gap of unknown length  
 \* 181061 185808: contig of 4748 bp in length  
 \* 185809 185908: gap of unknown length  
 \* 185909 190832: contig of 4924 bp in length  
 \* 190833 190932: gap of unknown length  
 \* 190933 197456: contig of 6524 bp in length.

## FEATURES

source  
 1. 197456  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="UNK"  
 /clones="CTB-45H5"  
 1. 5084  
 /note="assembly\_name:Contig100"  
 5185. 14399  
 /note="assembly\_name:Contig101"  
 14500. 22836  
 /note="assembly\_name:Contig103"  
 22937. 33373  
 /note="assembly\_name:Contig104"  
 33474. 47419  
 /note="assembly\_name:Contig105"  
 47520. 66575  
 /note="assembly\_name:Contig106"  
 66676. 81990  
 /note="assembly\_name:Contig107"  
 82091. 105847  
 /note="assembly\_name:Contig108"  
 105948. 129271  
 /note="assembly\_name:Contig109"  
 129372. 164242  
 /note="assembly\_name:Contig110"  
 164343. 164840  
 /note="assembly\_name:Contig18"  
 164941. 167875  
 /note="assembly\_name:Contig191"  
 167976. 172505  
 /note="assembly\_name:Contig194"  
 172606. 176804  
 /note="assembly\_name:Contig195"  
 176905. 180960  
 /note="assembly\_name:Contig196"  
 181061. 185808  
 /note="assembly\_name:Contig197"  
 185909. 190832  
 /note="assembly\_name:Contig198"  
 190933. 197456  
 /note="assembly\_name:Contig199"  
 51971 a 47509 c 46808 g 49428 t 1740 others

## BASE COUNT

Query Match 6.4%; Score 31; DB 2; Length 197456;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATTGCAGATGTGAGCCACCGTGGCCCA 32

Db 151689 GATTGCAGATGTGAGCCACCGTGGCCCA 151719

RESULT 11  
 AC018709

LOCUS AC018709 161013 bp DNA linear PRI 09-JAN-2002  
 DEFINITION Homo sapiens BAC clone RP11-215A19 from 4, complete sequence.  
 AC018709  
 AC018709.9 GI:15431210  
 VERSION HTG.  
 KEYWORDS Homo sapiens.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 161013)  
 Sulston, J.E. and Waterston, R.  
 Toward a complete human genome sequence  
 Genome Res. 8 (11), 1097-1108 (1998)  
 99063792  
 9847074  
 2 (bases 1 to 161013)  
 Harkins, C. and Kozlowski, A.  
 The sequence of Homo sapiens BAC clone RP11-215A19  
 Unpublished (2001)  
 3 (bases 1 to 161013)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (16-DEC-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 4 (bases 1 to 161013)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (05-SEP-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 5 (bases 1 to 161013)  
 Waterston, R.  
 Direct Submission  
 Submitted (09-JAN-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Sep 5, 2001 this sequence version replaced gi:15383864.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc  
 Contact: sapiens@wustl.wustl.edu  
 ----- Summary Statistics  
 -----  
 Center project name: H\_NH0215A19  
 -----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenio, M., Catanes, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute

(http://bacpac.med.buffalo.edu)  
 VECTOR: pBACe3.6  
 NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the right is AC015601. Actual start of this  
 clone is at base position 1 of RP11-215A19; actual end is at base  
 position 161013 of RP11-215A19.

Unresolved tandem repeats from base position 92006 to 96846 and  
 from 136330 to 138682.

## FEATURES

## Source

## Location/Qualifiers

1. 161013  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="4"  
 /map="4"

/clone="RP11-215A19"

/clone.lib="RCI-11"

972..7069

/rpt\_family="MER121"

1089..1119

/rpt\_family="AT\_rich"

1646..1986

/rpt\_family="MaLR"

2635..2935

/rpt\_family="Alu"

3270..3308

/rpt\_family="L1"

3346..3383

/rpt\_family="T-rich"

3358..3664

/rpt\_family="Alu"

4164..4192

/rpt\_family="(TTTTTG)n"

4659..4686

/rpt\_family="AT\_rich"

6039..6349

/rpt\_family="Alu"

6428..6525

/rpt\_family="MaLR"

7200..7281

/rpt\_family="L2"

7760..7941

/rpt\_family="MIR"

8830..9056

/rpt\_family="Alu"

9801..10106

/rpt\_family="Alu"

10081..10106

/rpt\_family="(CAAAA)n"

10132..10354

/rpt\_family="MER1\_type"

10696..10727

/rpt\_family="Alu"

10728..10928

/rpt\_family="Alu"

11144..11369

/rpt\_family="Alu"

12940..12960

/rpt\_family="AT\_rich"

13120..13240

/rpt\_family="AchHobo"

13388..13686

/rpt\_family="Alu"

15179..15594

/rpt\_family="MaLR"

15667..16695

/rpt\_family="L1"

16718..16848

/rpt\_family="Alu"

16848..16874

/rpt\_family="(TA)n"

17005..17196

/rpt\_family="L1"

repeat\_region 17298..17427  
 /rpt\_family="L1"  
 repeat\_region 17429..17848  
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 repeat\_region 17875..18060  
 /rpt\_family="L1"  
 repeat\_region 18068..18689  
 /rpt\_family="L1"  
 repeat\_region 18694..18839  
 /rpt\_family="Alu"  
 repeat\_region 18840..19457  
 /rpt\_family="ERV1"  
 repeat\_region 19458..19773  
 /rpt\_family="ERV1"  
 repeat\_region 20819..21214  
 /rpt\_family="MaLR"  
 repeat\_region 22075..22454  
 /rpt\_family="MaLR"  
 repeat\_region 22730..23725  
 /rpt\_family="ERVK"  
 repeat\_region 23921..24249  
 /rpt\_family="ERVK"  
 repeat\_region 24265..25207  
 /rpt\_family="L2"  
 repeat\_region 25227..25258  
 /rpt\_family="AT\_rich"  
 repeat\_region 26245..26641  
 /rpt\_family="ERV1"  
 repeat\_region 27656..27877  
 /rpt\_family="MIR"  
 repeat\_region 28374..28465  
 /rpt\_family="L1"  
 repeat\_region 28481..28523  
 /rpt\_family="AT\_rich"  
 repeat\_region 29331..29614  
 /rpt\_family="Alu"  
 repeat\_region 29613..29669  
 /rpt\_family="(TAA)n"  
 repeat\_region 29820..30548  
 /rpt\_family="L1"  
 repeat\_region 30534..30562  
 /rpt\_family="AT\_rich"  
 repeat\_region 30645..31005  
 /rpt\_family="L1"  
 repeat\_region 31007..31112  
 /rpt\_family="MaLR"  
 misc\_feature 31097..32264  
 /note="CpG island (GCG=56.9, o/e=0.90, #CpGs=83)"  
 repeat\_region 32251..32430  
 /rpt\_family="MaLR"  
 repeat\_region 32433..32560  
 /rpt\_family="L2"  
 repeat\_region 33839..34129  
 /rpt\_family="Alu"

Query Match 6.2%; Score 30; DB 9; Length 161013;  
 Best Local Similarity 100.0%; Pred.No. 2.7e-05;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATTGAGATGTGAGCCACCGTGGCTGGCC 31  
 |||||  
 Db 10900 GATTGAGATGTGAGCCACCGTGGCTGGCC 10929

## RESULT 12

AC012525/c

LOCUS

DEFINITION Homo sapiens chromosome 4, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 12  
 unrounded pieces.

AC012525

VERSION AC012525.6 GI:6573826

KEYWORDS HTG; HTGS PHASE1.

SOURCE Homo sapiens.

AC012525 240000 bp DNA linear HTG 14-DEC-1999

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 240000)
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 240000)
AUTHORS Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1999) Department of Genetics, Stanford Human
Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT On Dec 14, 1999 this sequence version replaced gi:6503313.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1219: contig of 1219 bp in length
* 1220 4866: gap of unknown length
* 4867 9403: contig of 4536 bp in length
* 9403 13049: gap of unknown length
* 13050 18200: contig of 5151 bp in length
* 18201 21846: gap of unknown length
* 21847 28549: contig of 6703 bp in length
* 28550 32196: gap of unknown length
* 32196 54074: gap of unknown length
* 54074 68978: contig of 14904 bp in length
* 68978 72624: gap of unknown length
* 72624 93784: contig of 21160 bp in length
* 93785 97430: gap of unknown length
* 97431 116930: contig of 19500 bp in length
* 116931 120576: gap of unknown length
* 120577 134768: contig of 14192 bp in length
* 134769 138414: gap of unknown length
* 138415 164480: contig of 26066 bp in length
* 164481 168126: gap of unknown length
* 168127 192568: contig of 24442 bp in length
* 192569 196214: gap of unknown length
* 196215 240000: contig of 43786 bp in length.
FEATURES             Location/Qualifiers
     source           1..240000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
BASE COUNT  59361 a 41510 c 41283 g 57734 t 40112 others
ORIGIN
Query Match      6.2%; Score 30; DB 2; Length 240000;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2  GATTGCAGATGTCGACCCACCGTCCTGCC 31
      |||||
Db   178588 GATTGCAGATGTCGACCCACCGTCCTGCC 178559

RESULT 13
HSJ395C13/c LOCUS      150336 bp      DNA      linear      PRI 02-MAR-2000
DEFINITION Human DNA sequence from clone RP3-395C13 on chromosome 6q25.2-26.
              Contains STSs, GSSs and a putative CpG island, complete sequence.
ACCESSION   AL117344
VERSION     AL117344.12 GI:6634463
KEYWORDS    HTG; CpG island.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 150336)
AUTHORS Laird,G.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
COMMENT On Dec 23, 1999 this sequence version replaced gi:6523733.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known,
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-395C13 is
from the library RPCI-3 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RP3-395C13. This
sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6.
FEATURES             Location/Qualifiers
     repeat_region    1..237
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     repeat_region    250..504
                     /note="L1M4 repeat: matches 3829..4093 of consensus"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="q25.2-26"
                     /clone="RP3-395C13"
                     /clone_lib="RPCI-3"
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                     /note="AluX repeat: matches 1..237 of consensus"
     repeat_region    250..504
                     /note="L1M4 repeat: matches 3829..4093 of consensus"
                     /db_xref="taxon:9606"
     repeat_region    506..1074
                     /notes="MER73 repeat: matches 54..634 of consensus"
                     /notes="MER66B repeat: matches 9..80 of consensus"
     repeat_region    1071..1142
                     /note="AluX repeat: matches 1..295 of consensus"
     repeat_region    1143..1438
                     /note="MER66B repeat: matches 79..486 of consensus"
     repeat_region    1439..1843
                     /note="match: GSS: Em:AQ712830"
     misc_feature      1786..2449
                     /note="match: GSS: Em:AQ743356"
     repeat_region    1844..1901
                     /note="MER73 repeat: matches 1..62 of consensus"
     repeat_region    2270..2416
                     /note="L1M4 repeat: matches 6717..6864 of consensus"
     repeat_region    2417..2728
                     /note="AluX repeat: matches 1..312 of consensus"
     repeat_region    2729..3089
                     /notes="L1M4 repeat: matches 6864..7217 of consensus"
     repeat_region    3090..3381
                     /note="AluJb repeat: matches 1..286 of consensus"
     repeat_region    3382..3577
                     /note="L1M4 repeat: matches 7217..7414 of consensus"
     repeat_region    4253..4501
                     /note="AluJo repeat: matches 42..287 of consensus"
     repeat_region    5315..5559
                     /note="L1M4 repeat: matches 7410..7674 of consensus"

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repeat\_region 5857. .6153  
/note="AluY repeat: matches 12. .308 of consensus"  
repeat\_region 6289. .6602  
/note="AluYb8 repeat: matches 1. .313 of consensus"  
repeat\_region 6610. .6837  
/note="AluSp repeat: matches 1. .300 of consensus"  
repeat\_region 7519. .7637  
/note="L1R16C repeat: matches 86. .208 of consensus"  
repeat\_region 7638. .8168  
/note="MER1A repeat: matches 1. .527 of consensus"  
repeat\_region 8169. .8325  
/note="L1R16C repeat: matches 208. .351 of consensus"  
repeat\_region 8576. .8773  
/note="MIR repeat: matches 33. .230 of consensus"  
repeat\_region 8955. .9352  
/note="MER57B repeat: matches 1. .403 of consensus"  
repeat\_region 9671. .9767  
/note="L2 repeat: matches 2294. .2389 of consensus"  
repeat\_region 9818. .10015  
/note="L2 repeat: matches 2543. .2750 of consensus"  
repeat\_region 10049. .10292  
/note="MER8 repeat: matches 2. .239 of consensus"  
repeat\_region 10668. .11164  
/note="MLR1B repeat: matches 54. .564 of consensus"  
misc\_feature complement(11061. .11548)  
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repeat\_region 11272. .11383  
/note="L1MC5 repeat: matches 7676. .7783 of consensus"  
repeat\_region 11912. .12069  
/note="MIR repeat: matches 48. .240 of consensus"  
misc\_feature 12124. .14438  
/note="CpG island"  
/evidences=not\_experimental  
repeat\_region 13176. .13202  
/note="9 copies 3 mer gag 96% conserved"  
repeat\_region 17042. .17173  
/note="AluJo repeat: matches 2. .134 of consensus"  
repeat\_region 17191. .17475  
/note="AluJo repeat: matches 1. .291 of consensus"  
repeat\_region 17758. .17867  
/note="MIR repeat: matches 20. .153 of consensus"  
repeat\_region 17896. .18173  
/note="MIR repeat: matches 3. .262 of consensus"  
repeat\_region 18128. .18182  
/note="L2 repeat: matches 2699. .2746 of consensus"  
repeat\_region 18318. .18459  
/note="FLAM C repeat: matches 1. .133 of consensus"  
repeat\_region 19810. .19928  
/note="L2 repeat: matches 2633. .2750 of consensus"  
misc\_feature 20131. .20372  
/note="match: STS: Em:H66317"  
repeat\_region 21259. .21591  
/note="L1MC4 repeat: matches 7634. .7976 of consensus"  
repeat\_region 21585. .22046  
/note="L1MEC repeat: matches 1027. .2134 of consensus"  
misc\_feature complement(22773. .23157)  
/note="match: GSS: Em:AQ054658"  
repeat\_region 23974. .24075  
/note="L1ME repeat: matches 5751. .5864 of consensus"  
repeat\_region 24739. .24766  
/note="L4 copies 2 mer tg 100% conserved"  
repeat\_region 24947. .25271  
/note="AluSp repeat: matches 1. .313 of consensus"  
repeat\_region 26360. .26599  
/note="MLR1G repeat: matches 23. .250 of consensus"  
repeat\_region 26777. .26880  
/note="MLR1B repeat: matches 430. .542 of consensus"  
repeat\_region 27249. .27558  
/note="AluJo repeat: matches 1. .305 of consensus"  
repeat\_region 27608. .27902  
/note="AluSC repeat: matches 2. .296 of consensus"  
repeat\_region 29348. .29826  
/note="MLR1D repeat: matches 1. .501 of consensus"

repeat\_region 30094. .30193  
/note="50 copies 2 mer cc 65% conserved"  
repeat\_region 32671. .33086  
/note="L2 repeat: matches 2267. .2695 of consensus"  
repeat\_region 33513. .33558  
/note="MIR repeat: matches 99. .145 of consensus"  
repeat\_region 34826. .35127  
/note="AluX repeat: matches 1. .293 of consensus"  
repeat\_region 36069. .36166  
/note="MIR repeat: matches 119. .227 of consensus"  
repeat\_region 36227. .36527  
/note="AluY repeat: matches 1. .304 of consensus"  
repeat\_region 37336. .37624  
/note="AluSq repeat: matches 1. .291 of consensus"  
repeat\_region 38649. .38748  
/note="MER91B repeat: matches 79. .179 of consensus"  
repeat\_region 38763. .38893  
/note="MER91B repeat: matches 1. .123 of consensus"  
repeat\_region 39165. .39317  
/note="MIR repeat: matches 31. .214 of consensus"  
repeat\_region 40216. .40397  
/note="MLT1J repeat: matches 342. .515 of consensus"  
repeat\_region 40398. .41010  
/note="L1PA10 repeat: matches 5543. .6158 of consensus"  
repeat\_region 41011. .41318  
/note="MLT1J repeat: matches 5. .342 of consensus"  
repeat\_region 41622. .41734  
/note="L2 repeat: matches 2620. .2744 of consensus"  
repeat\_region 41904. .42172  
/note="AluX repeat: matches 52. .311 of consensus"  
misc\_feature 42753. .43222  
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repeat\_region 42787. .43087  
/note="AluSC repeat: matches 1. .301 of consensus"  
repeat\_region 43143. .43243  
/note="MER5B repeat: matches 1. .104 of consensus"  
repeat\_region 43308. .43493  
/note="L1MD2 repeat: matches 5873. .6071 of consensus"  
repeat\_region 43740. .43810  
/note="L1MD3 repeat: matches 7666. .7740 of consensus"  
repeat\_region 43865. .43912  
/note="MER5B repeat: matches 129. .176 of consensus"  
repeat\_region 43981. .44030  
/note="25 copies 2 mer ta 72% conserved"

Query Match 6.0%; Score 29; DB 9: Length 150336;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGTGAGCCACCGTGGCCGAGATTTT 39  
|||||  
Db 73670 TGTGAGCCACCGTGGCCGAGATTTT 73642

RESULT 14  
AC026947/c  
LOCUS 153234 bp DNA linear HTG 24-AUG-2002  
DEFINITION Homo sapiens chromosome 11 clone RP11-305L22 map 11, WORKING DRAFT  
SEQUENCE, 13 unordered pieces.  
AC026947  
VERSION AC026947.2 GI:7622423  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 153234)  
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 11, clone RP11-305L22  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 153234)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Sever, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tsefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 153234)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F., Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Sever, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tsefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 20, 2000 this sequence version replaced gi:7328812.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L7852  
Center clone name: 305\_L\_22  
----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 145261 bases at least Q40  
Consensus quality: 149899 bases at least Q30  
Consensus quality: 151298 bases at least Q20  
Insert size: 139000; agarose-fp  
Insert size: 152034; sum-of-contigs  
Quality coverage: 4.6 in Q20 bases; agarose-fp  
Quality coverage: 4.2 in Q20 bases; sum-of-contigs  
-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces

\* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 1285: contig of 1285 bp in length  
\* 1286 1395: gap of 100 bp  
\* 1396 4149: contig of 2764 bp in length  
\* 4150 4249: gap of 100 bp  
\* 4250 9346: contig of 5097 bp in length  
\* 9347 9446: gap of 100 bp  
\* 9447 15111: contig of 5665 bp in length  
\* 15112 15211: gap of 100 bp  
\* 15212 22415: contig of 7204 bp in length  
\* 22416 22515: gap of 100 bp  
\* 22516 33763: contig of 11248 bp in length  
\* 33764 33863: gap of 100 bp  
\* 33864 44898: contig of 11035 bp in length  
\* 44899 44998: gap of 100 bp  
\* 44999 55715: contig of 10717 bp in length  
\* 55716 55815: gap of 100 bp  
\* 55816 68530: contig of 12715 bp in length  
\* 68531 68630: gap of 100 bp  
\* 68631 83353: contig of 14723 bp in length  
\* 83354 83453: gap of 100 bp  
\* 83454 98362: contig of 14909 bp in length  
\* 98363 98462: gap of 100 bp  
\* 98463 123453: contig of 24991 bp in length  
\* 123454 123553: gap of 100 bp  
\* 123554 153234: contig of 29681 bp in length.

FEATURES  
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/organism="Homo sapiens"  
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1. .1285  
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1386. .4149  
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4250. .9346  
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9447. .15111  
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15212. .22415  
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22516. .33763  
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vector\_side:right  
33864. .44898  
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44999. .55715  
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83454. .98362  
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43264 a 32774 c 32544 g 43451 t 1201 others

Query Match 6.0%; Score 29; DB 2; Length 153234;



Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGTGAGCACCGTGCCTGGCCAGATTTTTT 39

Db 134823 TGTGAGCACCGTGCCTGGCCAGATTTTTT 134795

# RESULT 15

AC113193 AC113193 182208 bp DNA linear PRI 17-AUG-2002  
 LOCUS Homo sapiens chromosome 11, clone RP11-1026G19, complete sequence.  
 DEFINITION AC113193  
 ACCESSION AC113193  
 VERSION AC113193.6 GI:22296723  
 KEYWORDS HTG.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 182208)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 11, clone RP11-1026G19

## JOURNAL

REFERENCE Unpublished

## AUTHORS

2 (bases 1 to 182208)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
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 Gande,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
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 Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,  
 Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,  
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 Mieng,A., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,  
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,  
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,  
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,  
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,  
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

## JOURNAL

Submitted (26-FEB-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## REFERENCE

## AUTHORS

3 (bases 1 to 182208)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
 Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,  
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,  
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,  
 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mieng,A.,  
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,  
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,  
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,  
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
 Zembek,L., Zimmer,A. and Zody,M.

## TITLE

## JOURNAL

Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## REFERENCE

## AUTHORS

4 (bases 1 to 182208)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

## TITLE

## JOURNAL

## COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L23157

Center clone name: 1026\_G\_19

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Only the first 182.2 kilobases of this clone are being submitted.

The remainder overlaps accession number AC023950 [WICGR project

L6298].

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Search completed: June 17, 2003, 03:59:32  
Job time : 944.527 secs

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repeat_region complement(11838..12410)
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repeat_region /rpt family="AluY"
repeat_region 13554..13732
repeat_region /rpt family="L1PA11"
repeat_region 13775..13801
repeat_region /rpt family="(TC)n"
repeat_region complement(13833..14167)
repeat_region /rpt family="L1ME4A"
repeat_region complement(14213..14500)
repeat_region /rpt family="AluJb"
repeat_region complement(14587..14837)
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repeat_region complement(15582..15825)
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repeat_region /rpt family="L2"
repeat_region 16341..16551
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repeat_region /rpt family="MIR"
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repeat_region 22284..22326
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGTGAGCCACCGTCGTCGCCAGATTTT 39  
Db 20361 TGTGAGCCACCGTCGTCGCCAGATTTT 20389

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 85.7978 Seconds

(without alignments)  
12756.396 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_7148\_7633

Perfect score: 486

Sequence: 1 agattgcagatgtgagccac.....cattgctcttagtccccaagc 486

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq 101002.\*

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22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	5492	21	AAAG4508
2	486	100.0	9048	21	AAAG4507
3	396	81.5	1855	22	AA181887
4	33	6.8	2688	18	AAT72165
5	28	5.8	547	24	ABQ60451
6	28	5.8	1660	22	AAH98314
7	28	5.8	1660	22	AAH98825
8	27	5.6	28866	20	AAH22304
9	26	5.3	251	24	ABL85166

10	26	5.3	371	24	ABL84945	Human ovarian canc
11	26	5.3	434	21	AACT75926	Human ORFX ORF1481
12	26	5.3	29449	22	AAAD16646	Human novel protei
13	26	5.3	29449	22	AAO88186	DNA encoding rena
14	26	5.3	169739	24	ABO88186	Human osteoblast d
15	25	5.1	603	23	ABV51351	Human prostate exp
16	25	5.1	819	22	AAH93326	Human prostate-cdn
17	25	5.1	819	22	AAH93833	Human prostate-spe
18	25	5.1	819	22	AAH95297	Human P776P splice
19	25	5.1	2455	22	AAH95297	Human cDNA P776P s
20	25	5.1	2455	22	AAH93326	Human cDNA P776P s
21	25	5.1	2455	22	AAH93326	P776P full length
22	25	5.1	2455	22	AAH93326	P776P full length
23	25	5.1	2455	24	ABL95533	Human P776P splice
24	25	5.1	2455	24	ABL95533	Human P776P splice
25	25	5.1	6226	23	ABK43074	Genomic sequence #
26	25	5.1	32191	22	AAH93326	Human genomic DNA
27	25	5.1	36651	24	AAH93326	Human kinase genom
28	25	5.1	37736	22	AAH93326	Human immune/haema
29	25	5.1	122888	24	AAH93326	Human cDNA differe
30	24	4.9	340	23	ABV57872	Human prostate exp
31	24	4.9	436	23	ABV16371	Human prostate exp
32	24	4.9	500	23	ABV46169	Human prostate exp
33	24	4.9	1003	22	AAH91403	Human digestive sy
34	24	4.9	1003	22	AAH91403	Human digestive sy
35	24	4.9	1003	22	AAH91403	Human colorectal c
36	24	4.9	1003	22	AAH91403	Human colorectal c
37	24	4.9	9454	22	AAH91403	Human immune/haema
38	24	4.9	16920	22	AAH91403	Human immune/haema
39	24	4.9	26040	22	AAH91403	Nucleotide sequenc
40	24	4.9	34897	22	AAH91403	Human immune/haema
41	24	4.9	36485	22	AAH91403	Human immune/haema
42	24	4.9	36485	22	AAH91403	Human immune/haema
43	24	4.9	36485	22	AAH91403	Human immune/haema
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45	23	4.7	99014	24	ABN96931	Gene #3429 used to
46	23	4.7	170	22	AAH96931	Human immune/haema
47	23	4.7	170	22	AAH96931	Human immune/haema
48	23	4.7	170	22	AAH96931	Human immune/haema
49	23	4.7	257	21	AAH96931	Human colon cancer
50	23	4.7	298	24	ABL81883	Human ovarian canc
51	23	4.7	330	24	ABL81883	Human ovarian canc
52	23	4.7	338	22	AAH81949	Human polynucleoti
53	23	4.7	343	24	ABN65164	Human cancer relat
54	23	4.7	381	24	ABL83966	Human ovarian canc
55	23	4.7	404	23	ABV14185	Human prostate exp
56	23	4.7	408	21	AAH97437	Human secreted pro
57	23	4.7	438	23	ABV35279	Human prostate exp
58	23	4.7	438	23	ABV44116	Human prostate exp
59	23	4.7	461	22	AAH91116	Human polynucleoti
60	23	4.7	465	24	ABL79720	Human ovarian canc
61	23	4.7	518	23	ABK42912	Genomic sequence #
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63	23	4.7	571	23	ABV51791	Human prostate exp
64	23	4.7	576	22	AAH12126	Human cDNA clone (
65	23	4.7	796	21	AAH13767	Human stem cell fa
66	23	4.7	798	16	AAH04886	Human SCF genomic
67	23	4.7	1035	22	AAH04886	DNA encoding novel
68	23	4.7	1035	22	AAH04886	Human reproductive
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70	23	4.7	1039	22	AAH04886	Human reproductive
71	23	4.7	1090	22	AAH94448	Human foetal cDNA,
72	23	4.7	1754	22	AAH14168	Human cDNA sequenc
73	23	4.7	2056	22	ABH14751	Human nervous syst
74	23	4.7	2414	22	AAH17968	Human cDNA sequenc
75	23	4.7	2852	22	AAH17968	Human cDNA sequenc
76	23	4.7	3178	22	AAH80499	Human immune/haema
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78	23	4.7	3470	23	ABV25066	Human prostate exp
79	23	4.7	3807	22	AAH10456	Human stem cell fa
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81	23	4.7	3807	22	AAH10456	Human genomic SCF
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C 84	23	4.7	3807	22	AAF99100	Human stem cell fa	C 157	22	4.5	755	24	ABO89771	Human prostate exp
C 85	23	4.7	3807	22	AAD35473	Human stem cell fa	C 158	22	4.5	768	20	AAZ15376	Human gene express
C 86	23	4.7	4063	12	AAQ11540	Human Stem Cell Fa	C 159	22	4.5	851	22	ABAI2862	Human nervous syst
C 87	23	4.7	4573	22	ABAI18241	Human nervous syst	C 160	22	4.5	883	21	AAH51580	Human MGSII relat
C 88	23	4.7	5414	22	AAK78291	Human immune/haema	C 161	22	4.5	1000	21	AAH51580	Human Ras GTP enzy
C 89	23	4.7	5864	22	AAH10458	Human stem cell fa	C 162	22	4.5	1059	24	ABL49889	Human immune/haema
C 90	23	4.7	5864	22	AAH11342	Human stem cell fa	C 163	22	4.5	1090	22	AAK74902	Human immune/haema
C 91	23	4.7	5864	22	AAH11342	Human stem cell fa	C 164	22	4.5	1126	22	AAK76186	Human immune/haema
C 92	23	4.7	5864	22	AAH11342	Human stem cell fa	C 165	22	4.5	1126	22	AAK76187	Human immune/haema
C 93	23	4.7	5864	22	AAH23900	Human SCF (stem ce	C 166	22	4.5	1126	22	AAK76188	Human immune/haema
C 94	23	4.7	5864	22	AAH23900	Human SCF (stem ce	C 167	22	4.5	1126	22	AAK76189	Human immune/haema
C 95	23	4.7	5864	22	AAH23900	Human stem cell fa	C 168	22	4.5	1126	22	AAK78007	Human immune/haema
C 96	23	4.7	5864	22	AAH23900	Human immune/haema	C 169	22	4.5	1126	22	AAK78007	Human nervous syst
C 97	23	4.7	8960	22	AAH23900	Human immune/haema	C 170	22	4.5	1200	22	AAK76190	Human immune/haema
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C 99	23	4.7	10721	23	ABLI71118	Drosophila melanog	C 172	22	4.5	1989	22	AAH17365	Human cDNA sequenc
C 100	23	4.7	12024	22	AAH23900	Human genomic DNA	C 173	22	4.5	2443	22	AAH17546	Human cDNA sequenc
C 101	23	4.7	12024	22	AAH23900	Human novel protei	C 174	22	4.5	2605	22	ABAI18632	Human nervous syst
C 102	23	4.7	12025	22	AAH23900	Human genomic DNA	C 175	22	4.5	3089	21	AAH264958	Membrane-bound pro
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C 104	23	4.7	13982	22	AAH23900	Human immune/haema	C 177	22	4.5	3089	22	AAH264958	Human Prol151 (UNQ
C 105	23	4.7	13982	22	AAH23900	Human immune/haema	C 178	22	4.5	3227	22	AAH264958	Human immune/haema
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C 111	23	4.7	81001	22	AAH23900	Human osteoblast d	C 184	22	4.5	5587	22	AAH264958	Human benign prost
C 112	23	4.7	139904	22	AAH23900	Human apolipoprote	C 185	22	4.5	6004	24	ABK64820	Colon adenocarcino
C 113	23	4.7	147309	24	ABK49450	Human cDNA differe	C 186	22	4.5	6209	22	AAH264958	Human immune/haema
C 114	23	4.7	154465	24	AAH264958	Human transporter	C 187	22	4.5	7042	20	AAH264958	Apoptosis inducer
C 115	23	4.7	158245	24	AAH264958	Human AKAP allelic	C 188	22	4.5	7042	21	AAH264958	Human full-length
C 116	23	4.7	161425	22	AAH264958	Human AKAP allelic	C 189	22	4.5	7042	21	AAH264958	Human type Apal-1 c
C 117	23	4.7	162025	22	AAH264958	Human AKAP10 gene	C 190	22	4.5	7042	24	AAH264958	Human apoptotic pr
C 118	23	4.7	162025	24	AAH264958	Human AKAP allelic	C 191	22	4.5	7075	20	AAH264958	Apoptosis inducer
C 119	23	4.7	162025	24	AAH264958	Human AKAP allelic	C 192	22	4.5	7970	22	AAH264958	DNA encoding novel
C 120	23	4.7	201143	24	AAH264958	Human DNA differen	C 193	22	4.5	8213	22	AAH264958	Human differential
C 121	23	4.7	227968	24	AAH264958	Human cDNA differe	C 194	22	4.5	8213	22	AAH264958	Pancreas cancer re
C 122	23	4.7	227968	24	AAH264958	Human Ras GTP enzy	C 195	22	4.5	8213	22	AAH264958	Human nervous syst
C 123	23	4.7	227968	24	AAH264958	Human Ras GTP enzy	C 196	22	4.5	8213	22	AAH264958	Human immune/haema
C 124	23	4.7	227968	24	AAH264958	Human silent SNP c	C 197	22	4.5	10296	22	AAH264958	Human nervous syst
C 125	23	4.7	227968	24	AAH264958	Human silent SNP c	C 198	22	4.5	10899	22	AAH264958	Human DNA for a no
C 126	23	4.7	227968	24	AAH264958	Human secreted pro	C 199	22	4.5	11076	22	AAH264958	Human reproductive
C 127	23	4.7	227968	24	AAH264958	Human secreted pro	C 200	22	4.5	11076	22	AAH264958	Human immune/haema
C 128	23	4.7	227968	24	AAH264958	Human gene express	C 201	22	4.5	11076	22	AAH264958	Human breast or ov
C 129	23	4.7	227968	24	AAH264958	Human secreted pro	C 202	22	4.5	11301	22	AAH264958	Human immune/haema
C 130	23	4.7	227968	24	AAH264958	Human cancer relat	C 203	22	4.5	12278	22	AAH264958	Human nervous syst
C 131	23	4.7	227968	24	AAH264958	Human polynucleoti	C 204	22	4.5	12278	22	AAH264958	Human nervous syst
C 132	23	4.7	227968	24	AAH264958	Human polynucleoti	C 205	22	4.5	12758	22	AAH264958	Human nervous syst
C 133	23	4.7	227968	24	AAH264958	Human immune/haema	C 206	22	4.5	12842	22	AAH264958	Human nervous syst
C 134	23	4.7	227968	24	AAH264958	Human immune/haema	C 207	22	4.5	12970	22	AAH264958	Human reproductive
C 135	23	4.7	227968	24	AAH264958	Human polynucleoti	C 208	22	4.5	12970	23	AAH264958	Human testicular a
C 136	23	4.7	227968	24	AAH264958	Novel human diagno	C 209	22	4.5	13204	20	AAH264958	Human platelet gly
C 137	23	4.7	227968	24	AAH264958	Human polynucleoti	C 210	22	4.5	13401	22	AAH264958	Human digestive sy
C 138	23	4.7	227968	24	AAH264958	Human polynucleoti	C 211	22	4.5	13403	22	AAH264958	Human digestive sy
C 139	23	4.7	227968	24	AAH264958	Human brain expres	C 212	22	4.5	13493	22	AAH264958	Human immune/haema
C 140	23	4.7	227968	24	AAH264958	Human colon cancer	C 213	22	4.5	13493	22	AAH264958	Human immune/haema
C 141	23	4.7	227968	24	AAH264958	Human polynucleoti	C 214	22	4.5	14040	22	AAH264958	Human ovarian and
C 142	23	4.7	227968	24	AAH264958	Human immune/haema	C 215	22	4.5	14040	22	AAH264958	Human reproductive
C 143	23	4.7	227968	24	AAH264958	Human immune/haema	C 216	22	4.5	14040	22	AAH264958	Human reproductive
C 144	23	4.7	227968	24	AAH264958	Human polynucleoti	C 217	22	4.5	18389	22	AAH264958	Human immune/haema
C 145	23	4.7	227968	24	AAH264958	Human cardiovascular	C 218	22	4.5	18389	22	AAH264958	Human immune/haema
C 146	23	4.7	227968	24	AAH264958	Human polynucleoti	C 219	22	4.5	20365	22	AAH264958	Human immune/haema
C 147	23	4.7	227968	24	AAH264958	Human breast cance	C 220	22	4.5	20365	22	AAH264958	Human immune/haema
C 148	23	4.7	227968	24	AAH264958	Human prostate exp	C 221	22	4.5	20365	22	AAH264958	Human immune/haema
C 149	23	4.7	227968	24	AAH264958	Human nervous syst	C 222	22	4.5	20365	22	AAH264958	Human immune/haema
C 150	23	4.7	227968	24	AAH264958	Human prostate exp	C 223	22	4.5	20444	22	AAH264958	Human DNA for a no
C 151	23	4.7	227968	24	AAH264958	Human prostate exp	C 224	22	4.5	20444	22	AAH264958	Human reproductive
C 152	23	4.7	227968	24	AAH264958	Human immune/haema	C 225	22	4.5	20444	22	AAH264958	Human immune/haema
C 153	23	4.7	227968	24	AAH264958	Human immune/haema	C 226	22	4.5	21446	22	AAH264958	Human breast or ov
C 154	23	4.7	227968	24	AAH264958	Human cardiovascular	C 227	22	4.5	21446	22	AAH264958	Human immune/haema
C 155	23	4.7	227968	24	AAH264958	Human secreted pro	C 228	22	4.5	21446	22	AAH264958	Human immune/haema

229	22	4.5	21446	22	AAK82629	Human immune/haema	c 302	21	4.3	358	22	AAI89752	Human polynucleoti
230	22	4.5	21446	22	AAK82629	Human immune/haema	c 303	21	4.3	359	22	AAI85150	Human polynucleoti
231	22	4.5	21621	22	AAK74867	Human immune/haema	c 304	21	4.3	365	24	ABL84956	Human ovarian canc
232	22	4.5	21724	22	AAK26629	Human genomic DNA	c 305	21	4.3	366	24	ABO56337	Human colon cancer
233	22	4.5	21724	22	AAK86125	Human immune/haema	c 306	21	4.3	370	22	AAI83153	Human polynucleoti
234	22	4.5	21727	22	AAK26630	Human genomic DNA	c 307	21	4.3	378	22	AAI88343	Human polynucleoti
235	22	4.5	21727	22	AAK86126	Human immune/haema	c 308	21	4.3	380	22	AAI91393	Human polynucleoti
236	22	4.5	22299	22	AAK40317	Human immune/haema	c 309	21	4.3	392	22	AAI92469	Human polynucleoti
237	22	4.5	22299	22	AAK03917	DNA encoding novel	c 310	21	4.3	393	22	AAI92804	Human polynucleoti
238	22	4.5	23378	22	AAK89555	Human reproductive	c 311	21	4.3	393	22	AAI92804	Human polynucleoti
239	22	4.5	23378	23	ABK42627	Human digestive sy	c 312	21	4.3	393	22	AAI92804	Human polynucleoti
240	22	4.5	23378	23	ABK42627	Human digestive sy	c 313	21	4.3	393	22	AAI92804	Human polynucleoti
241	22	4.5	23457	22	AAK74866	Human immune/haema	c 314	21	4.3	394	22	AAI92804	Human polynucleoti
242	22	4.5	26427	22	ABA20762	Human nervous syst	c 315	21	4.3	397	24	ABK46028	CDNA encoding colo
243	22	4.5	26427	22	ABA20763	Human nervous syst	c 316	21	4.3	400	23	AAK75460	DNA encoding novel
244	22	4.5	31405	22	AAK7293	Human immune/haema	c 317	21	4.3	401	22	AAK96184	Human neurogulin g
245	22	4.5	31405	22	AAK74865	Human immune/haema	c 318	21	4.3	401	22	AAK96185	Human neurogulin g
246	22	4.5	31405	22	AAK83153	Human immune/haema	c 319	21	4.3	401	22	AAK96186	Human neurogulin g
247	22	4.5	32134	22	ABA15354	Human nervous syst	c 320	21	4.3	401	22	AAK96666	Human neurogulin g
248	22	4.5	32134	22	ABA15813	Human nervous syst	c 321	21	4.3	401	22	AAK97677	Human neurogulin g
249	22	4.5	32134	22	AAK04075	Human reproductive	c 322	21	4.3	401	22	AAK97678	Human neurogulin g
250	22	4.5	32170	22	AAK28674	Genomic sequence #	c 323	21	4.3	401	22	AAK97679	Human neurogulin g
251	22	4.5	32196	22	ABA18857	Human nervous syst	c 324	21	4.3	401	22	AAK98159	Human neurogulin g
252	22	4.5	33147	22	AAK67282	Human immune/haema	c 325	21	4.3	402	22	AAK98679	Human ovarian canc
253	22	4.5	35501	22	AAK64829	Human immune/haema	c 326	21	4.3	404	23	ABK43752	Human prostate exp
254	22	4.5	39328	24	ABL51800	Human lipase endoc	c 327	21	4.3	405	22	AAI84155	Human polynucleoti
255	22	4.5	47090	22	AAK68725	Human immune/haema	c 328	21	4.3	405	22	AAI91879	Human polynucleoti
256	22	4.5	47090	22	AAK78219	Human immune/haema	c 329	21	4.3	405	23	ABK34903	Human prostate exp
257	22	4.5	48203	22	AAK70161	Human immune/haema	c 330	21	4.3	408	20	AAK56607	Human W32430. RC DN
258	22	4.5	48203	22	AAK81663	Human immune/haema	c 331	21	4.3	408	22	AAI85328	Human polynucleoti
259	22	4.5	48204	22	AAK70164	Human immune/haema	c 332	21	4.3	409	22	AAI82369	Human polynucleoti
260	22	4.5	48204	22	AAK81666	Human immune/haema	c 333	21	4.3	414	21	AAH30988	Human colon cancer
261	22	4.5	48204	22	AAK82630	Human immune/haema	c 334	21	4.3	414	23	ABK43358	Human prostate exp
262	22	4.5	49312	21	AAH51594	Human immune/haema	c 335	21	4.3	422	23	ABK19990	Human prostate exp
263	22	4.5	50575	23	ABL29244	Human genomic sequ	c 336	21	4.3	424	20	AAK56588	Human R87078. DNA f
264	22	4.5	58708	22	AAK64739	Drosophila melanog	c 337	21	4.3	431	22	AAK65038	Human immune/haema
265	22	4.5	59065	24	ABL42416	Human immune/haema	c 338	21	4.3	442	20	AAK56600	Human AAI96824. RC
266	22	4.5	122186	22	AAK89560	Human serine/threo	c 339	21	4.3	451	24	ABQ89572	Human prostate exp
267	22	4.5	128978	24	ABK83459	Human histone deac	c 340	21	4.3	458	23	ABK49750	Human prostate exp
268	22	4.5	145831	24	ABL62309	Colon adenocarcino	c 341	21	4.3	463	22	AAK79697	Human immune/haema
269	22	4.5	145831	24	ABL62309	Colon adenocarcino	c 342	21	4.3	463	22	AAK89409	Human digestive sy
270	22	4.5	145831	24	ABL68588	Lung cancer relate	c 343	21	4.3	475	22	AAK79696	Human immune/haema
271	22	4.5	145831	24	ABL69213	Kidney cancer rela	c 344	21	4.3	475	23	ABK52632	Human prostate exp
272	22	4.5	145831	24	ABL69213	Prostate cancer re	c 345	21	4.3	477	23	AAI88018	Human polynucleoti
273	22	4.5	149480	24	ABL61947	Colon adenocarcino	c 346	21	4.3	477	23	ABK49750	Human polynucleoti
274	22	4.5	149480	24	ABL61948	Colon adenocarcino	c 347	21	4.3	481	22	AAK83080	Human prostate exp
275	22	4.5	149480	24	ABL68365	Kidney cancer rela	c 348	21	4.3	482	20	AAK56596	Human immune/haema
276	22	4.5	175737	24	ABK83571	Human cDNA differe	c 349	21	4.3	482	24	ABL67344	Thyroid cancer rel
277	21	4.3	111	22	ABN86810	Human gas vacuole	c 350	21	4.3	511	23	ABK57220	Human prostate exp
278	21	4.3	111	22	AAK68344	Human immune/haema	c 351	21	4.3	529	23	ABK18570	Human prostate exp
279	21	4.3	111	22	AAK85110	Human immune/haema	c 352	21	4.3	552	22	ABA17597	Human nervous syst
280	21	4.3	194	21	AAK04989	Human secreted pro	c 353	21	4.3	555	22	AAK82704	Human immune/haema
281	21	4.3	208	21	AAK21550	Human secreted pro	c 354	21	4.3	565	22	AAK82705	Human immune/haema
282	21	4.3	243	22	AAK83640	Human immune/haema	c 355	21	4.3	570	23	ABK51378	Human prostate exp
283	21	4.3	252	20	AAK56612	Human 689191 DNA f	c 356	21	4.3	622	23	ABK48353	Human prostate exp
284	21	4.3	263	15	AAK77248	Human genome fragm	c 357	21	4.3	626	24	ABK63700	Human cancer relat
285	21	4.3	263	20	AAK56611	Human 840069 DNA f	c 358	21	4.3	631	21	AAA16349	Human colon cancer
286	21	4.3	286	22	AAK60210	Human immune/haema	c 359	21	4.3	639	23	ABK51454	Human prostate exp
287	21	4.3	292	22	AAI81021	Human polynucleoti	c 360	21	4.3	662	24	ABK61073	Human cancer relat
288	21	4.3	296	22	ABA18375	Human nervous syst	c 361	21	4.3	700	22	AAH92917	Human inflammatory
289	21	4.3	300	21	AAA00667	Human colon cancer	c 362	21	4.3	724	21	AAA01956	Human colon cancer
290	21	4.3	309	22	AAI88715	Human polynucleoti	c 363	21	4.3	725	22	AAK22964	Human prostate can
291	21	4.3	309	22	AAK59144	Human immune/haema	c 364	21	4.3	745	21	AAA47443	Human TANGO 222 co
292	21	4.3	319	22	AAK37530	Human musculoskele	c 365	21	4.3	760	24	ABQ88854	Human prostate exp
293	21	4.3	329	21	AAK13305	Human secreted pro	c 366	21	4.3	795	22	AAH05002	Human cDNA clone (
294	21	4.3	334	22	AAK55819	Human immune/haema	c 367	21	4.3	797	23	ABK13790	Human prostate exp
295	21	4.3	337	22	AAK38182	Novel human diagn	c 368	21	4.3	801	22	ABH03746	Human cDNA clone (
296	21	4.3	343	22	AAK74601	Human immune/haema	c 369	21	4.3	801	24	ABQ89387	Human prostate exp
297	21	4.3	351	22	AAK62549	Human immune/haema	c 370	21	4.3	847	22	AAH07714	Human cDNA clone (
298	21	4.3	351	22	AAK64729	Novel human polynu	c 371	21	4.3	856	22	AAH03627	Human cDNA clone (
299	21	4.3	354	23	ABK56004	Human prostate exp	c 372	21	4.3	941	22	AAK78948	Human immune/haema
300	21	4.3	356	22	AAK61263	Human immune/haema	c 373	21	4.3	963	23	AAK68860	DNA encoding novel
301	21	4.3	357	20	AAK56610	Human HUMGS02649 D	c 374	21	4.3	1001	21	AAH51395	DNA encoding s-acy

375	21	4.3	1001	21	AAH51396	Human PGDH related	C 448	21	4.3	7373	22	AA541749	Genomic sequence #
376	21	4.3	1002	22	AAH06938	Human reproductive	C 449	21	4.3	7417	22	AAK70374	Human immune/haema
377	21	4.3	1092	22	AAV31336	Mortierella alpina	C 450	21	4.3	7885	22	AAK70210	Human immune/haema
C 378	21	4.3	1095	24	ABL99927	Human secretory po	C 451	21	4.3	8140	22	ABA20556	Human nervous syst
C 380	21	4.3	1231	20	AAH97867	Human secreted pro	C 452	21	4.3	8167	22	AAK05420	Human reproductive
C 381	21	4.3	1231	24	ABN86805	Human gas vacuole	C 453	21	4.3	8223	22	AAK65546	Human immune/haema
C 382	21	4.3	1352	22	AAH08423	Human secreted pro	C 454	21	4.3	8253	22	AA540470	DNA encoding human
C 383	21	4.3	1370	20	AAH97820	Human secreted pro	C 455	21	4.3	8253	22	AAK04087	Human reproductive
C 384	21	4.3	1450	24	ABL41337	Human TFIIID subuni	C 456	21	4.3	8326	22	AA539819	Genomic sequence #
C 385	21	4.3	1496	22	AAK03200	Human reproductive	C 457	21	4.3	8326	22	AAK90175	Human digestive sy
C 386	21	4.3	1496	22	AAK06934	Human reproductive	C 458	21	4.3	8349	23	AA580324	DNA encoding novel
C 387	21	4.3	1496	22	AAH06941	Human reproductive	C 459	21	4.3	8418	22	AA541906	Genomic sequence #
C 388	21	4.3	1511	22	AAH15324	Human cDNA sequenc	C 460	21	4.3	8448	22	AA540680	DNA encoding human
C 389	21	4.3	1572	22	AAH08366	Human secreted pro	C 461	21	4.3	8448	22	AAK06568	Human reproductive
C 390	21	4.3	1598	22	ABA13401	Human nervous syst	C 462	21	4.3	8487	22	AAK37089	Human musculoskele
C 391	21	4.3	1614	22	AAH17079	Human cDNA sequenc	C 463	21	4.3	8535	22	AAK77167	Human immune/haema
C 392	21	4.3	1671	22	AA541905	Genomic sequence #	C 464	21	4.3	8807	22	AA535915	Human cardiovascular
C 393	21	4.3	1672	23	ABK42296	Genomic sequence #	C 465	21	4.3	9192	22	AAK35853	Human musculoskele
C 394	21	4.3	1765	22	AAH14927	Human cDNA sequenc	C 466	21	4.3	9192	23	ABK42359	Genomic sequence #
C 395	21	4.3	1793	22	AAK66938	Human immune/haema	C 467	21	4.3	9397	22	AAK78065	Human immune/haema
C 396	21	4.3	1965	22	AAI60430	Human polynucleoti	C 468	21	4.3	9439	22	AAI99373	Human excretory re
C 397	21	4.3	2022	22	AAH73397	Human G protein co	C 469	21	4.3	9439	22	AAK35859	Human musculoskele
C 398	21	4.3	2061	19	AAV63173	cDNA from clone da	C 470	21	4.3	9439	22	AAI63723	Human kidney relat
C 399	21	4.3	2066	20	AAH37716	Human cDNA clone D	C 471	21	4.3	9474	24	ABK50462	Human histamine re
C 400	21	4.3	2092	22	AA536430	Human cardiovascular	C 472	21	4.3	9566	22	AA540682	DNA encoding human
C 401	21	4.3	2320	21	AAK77434	Human ORFX ORF2989	C 473	21	4.3	9566	22	AAK06570	Human reproductive
C 402	21	4.3	2469	22	AAK87105	Human immune/haema	C 474	21	4.3	9629	22	AAK97855	Human neuroblastom
C 403	21	4.3	2473	22	AAK87106	Human immune/haema	C 475	21	4.3	9799	22	AAK97860	Human neuroblastom
C 404	21	4.3	2516	21	AA559323	DNA encoding a hum	C 476	21	4.3	10053	22	AAK73765	Human immune/haema
C 405	21	4.3	2566	22	AAH17845	Human cDNA sequenc	C 477	21	4.3	10053	24	ABN79990	Human chemically m
C 406	21	4.3	2702	22	AAK72621	Human immune/haema	C 478	21	4.3	10091	22	AAK69350	Human immune/haema
C 407	21	4.3	2713	22	AAK72622	Human immune/haema	C 479	21	4.3	10351	24	ABK88932	Human CD1e cDNA
C 408	21	4.3	2713	22	AAK72625	Human immune/haema	C 480	21	4.3	10388	22	AAI98966	Human excretory re
C 409	21	4.3	2713	22	AAK85252	Human immune/haema	C 481	21	4.3	10388	22	AAI63316	Human kidney relat
C 410	21	4.3	2749	22	AAH18717	Human cDNA sequenc	C 482	21	4.3	10388	21	AAK66549	Human kinesin-like
C 411	21	4.3	2813	22	AAK77165	Human immune/haema	C 483	21	4.3	10989	22	AAK69531	Human immune/haema
C 412	21	4.3	2813	22	AAK77166	Human immune/haema	C 484	21	4.3	11283	22	AAK82965	Human immune/haema
C 413	21	4.3	2904	22	AAH17918	Human cDNA sequenc	C 485	21	4.3	11294	22	AAK82968	Human immune/haema
C 414	21	4.3	3009	22	AAI98965	Human excretory re	C 486	21	4.3	11453	22	AA542059	Genomic sequence #
C 415	21	4.3	3011	22	AA541928	Human kidney relat	C 487	21	4.3	11453	22	AA542060	Genomic sequence #
C 416	21	4.3	3011	22	AA535102	Genomic sequence h	C 488	21	4.3	11453	22	AAK70914	Human immune/haema
C 417	21	4.3	3284	19	AAV31337	DNA #52 encoding #	C 489	21	4.3	11453	22	AAK70915	Human immune/haema
C 418	21	4.3	3598	22	AAI64774	Mortierella alpina	C 490	21	4.3	11742	22	ABA20557	Human nervous syst
C 419	21	4.3	3806	22	AAK75099	Human Glucose tran	C 491	21	4.3	11742	22	AAK70609	Human immune/haema
C 420	21	4.3	3851	21	AAK77558	Human immune/haema	C 492	21	4.3	12774	22	ABA15302	Human nervous syst
C 421	21	4.3	4066	19	AAV59181	Human ORFX ORF3113	C 493	21	4.3	12774	22	AAK72738	Human immune/haema
C 422	21	4.3	4106	22	AAK05051	Human bak gene pro	C 494	21	4.3	13216	22	AAK73092	Human immune/haema
C 423	21	4.3	4106	23	ABL97944	Human reproductive	C 495	21	4.3	13216	22	AAK87561	Human immune/haema
C 424	21	4.3	4192	20	AAK00725	Human testicular a	C 496	21	4.3	13309	22	AAK83380	Human immune/haema
C 425	21	4.3	4224	22	AAI99372	Human aggregan deg	C 497	21	4.3	13392	22	AA540469	DNA encoding human
C 426	21	4.3	4224	22	AAI99372	Human excretory re	C 498	21	4.3	13392	22	AAK04086	Human reproductive
C 427	21	4.3	4300	22	AAI63722	Human kidney relat	C 499	21	4.3	14221	22	AA540881	DNA encoding human
C 428	21	4.3	4300	22	AAK82193	Human immune/haema	C 500	21	4.3	14221	22	AAK06569	Human reproductive
C 429	21	4.3	4301	22	AAI68146	Human aggrcanase-	C 501	21	4.3	14486	22	AA527844	DNA encoding novel
C 430	21	4.3	4303	21	AA595826	Human metalloprote	C 502	21	4.3	15254	22	AAK83135	Human immune/haema
C 431	21	4.3	4406	22	AA546100	Human DNA encoding	C 503	21	4.3	15254	22	AAK83137	Human immune/haema
C 432	21	4.3	4407	21	AA537111	Human PRO1563 (UNQ	C 504	21	4.3	15255	22	AAK83136	Human immune/haema
C 433	21	4.3	4407	22	AA544426	Probe #46 used in	C 505	21	4.3	15256	22	AAK83134	Human immune/haema
C 434	21	4.3	4430	22	AAH18210	Human cDNA sequenc	C 506	21	4.3	15275	22	AAK53975	Human cardiovascular
C 435	21	4.3	4688	22	ABA18600	Human nervous syst	C 507	21	4.3	15812	22	ABA18253	Human cardiovascular
C 436	21	4.3	4688	22	AAI99654	Human expressed po	C 508	21	4.3	15843	22	AA536896	Human immune/haema
C 437	21	4.3	4758	22	AAK83279	Human immune/haema	C 509	21	4.3	15843	22	AAK67635	Human immune/haema
C 438	21	4.3	5000	24	ABK86965	Human immune/haema	C 510	21	4.3	16106	22	AAK83468	Human immune/haema
C 439	21	4.3	5159	22	AAK73342	Human STG genomic	C 511	21	4.3	16161	22	AAK83469	Human immune/haema
C 440	21	4.3	5281	22	AAK05101	Human musculoskele	C 512	21	4.3	16488	24	AAK25856	Human diptheria t
C 441	21	4.3	5281	23	ABL97994	Human reproductive	C 513	21	4.3	16488	24	AAD25895	Human diptheria t
C 442	21	4.3	5284	22	AAK05100	Human testicular a	C 514	21	4.3	16596	22	AAK90993	Human digestive sy
C 443	21	4.3	5284	23	ABL97993	Human reproductive	C 515	21	4.3	16596	22	AA532028	Human liver associ
C 444	21	4.3	5460	24	ABK51683	Human testicular a	C 516	21	4.3	16596	22	ABN90383	Human liver antige
C 445	21	4.3	5805	22	AAK05695	Human ABCG5 upstre	C 517	21	4.3	16772	22	ABA20862	Human nervous syst
C 446	21	4.3	6534	22	AAK02766	Human reproductive	C 518	21	4.3	16774	22	AA536895	Human cardiovascular
C 447	21	4.3	7373	22	ABA06810	Human genomic DNA	C 519	21	4.3	16774	22	AAK36898	Human cardiovascular
	21	4.3					C 520	21	4.3	16774	22	AAK67634	Human immune/haema

521	21	4.3	16774	22	AAK67637	Human immune/haema
522	21	4.3	16817	22	AAK87099	Human immune/haema
C 523	21	4.3	16852	22	AAK72507	Human immune/haema
C 524	21	4.3	16852	22	AAK84641	Human immune/haema
C 525	21	4.3	16876	22	AAK65624	Human immune/haema
C 526	21	4.3	16876	22	AAK56685	Human immune/haema
C 527	21	4.3	17165	22	AAK72506	Human immune/haema
C 528	21	4.3	17165	22	AAK84640	Human immune/haema
C 529	21	4.3	17761	22	AAK79415	Human immune/haema
C 530	21	4.3	17761	23	ABK42709	Genomic sequence #
C 531	21	4.3	18878	22	AAK37441	Human musculoskele
C 532	21	4.3	18925	22	ABA81553	Human phospholipid
C 533	21	4.3	18925	24	AAS94565	Human phospholipid
C 534	21	4.3	18925	24	AAS94692	Human phospholipid
C 535	21	4.3	19387	22	AAK65412	Human DNA for a no
C 536	21	4.3	19497	22	AAK85311	Human immune/haema
C 537	21	4.3	19965	22	AAK73166	Human immune/haema
C 538	21	4.3	19965	24	ABK69932	Human secreted pro
C 539	21	4.3	20261	22	ABA07368	Human pancreatic c
C 540	21	4.3	20261	22	AAS30061	Human lung antigen
C 541	21	4.3	20261	22	AAK65412	Human immune/haema
C 542	21	4.3	20261	22	AAK91099	Human digestive sy
C 543	21	4.3	20420	22	AAK73165	Human immune/haema
C 544	21	4.3	20420	24	ABK69933	Human secreted pro
C 545	21	4.3	20433	22	AAK65626	Human immune/haema
C 546	21	4.3	20991	22	AAK87545	Human immune/haema
C 547	21	4.3	21732	22	AAS39820	Genomic sequence #
C 548	21	4.3	21732	22	AAK90176	Human digestive sy
C 549	21	4.3	21855	22	AAK79678	Human immune/haema
C 550	21	4.3	22161	23	ABK42133	Genomic sequence #
C 551	21	4.3	22467	22	AAS33423	DNA encoding human
C 552	21	4.3	22467	22	AAS33425	DNA encoding human
C 553	21	4.3	23109	22	AAK62298	Human immune/haema
C 554	21	4.3	23164	22	AAK79678	Human immune/haema
C 555	21	4.3	23855	22	AAI99411	Human excretory re
C 556	21	4.3	23855	22	AAI63761	Human kidney relat
C 557	21	4.3	23934	22	AAI36090	Human musculoskele
C 558	21	4.3	24279	22	AAK74999	Human immune/haema
C 559	21	4.3	24329	22	AAK75000	Human immune/haema
C 560	21	4.3	24329	22	AAK75856	Human immune/haema
C 561	21	4.3	24740	21	AAK87743	Human LMP-1 (HIMP-
C 562	21	4.3	24993	22	AAK65726	Human immune/haema
C 563	21	4.3	25131	22	AAK84544	Human immune/haema
C 564	21	4.3	25837	22	AAK85952	Human immune/haema
C 565	21	4.3	25895	22	AAK77832	Human immune/haema
C 566	21	4.3	26110	22	AAK65036	Human immune/haema
C 567	21	4.3	26110	22	AAK78526	Human immune/haema
C 568	21	4.3	26657	24	AAI72317	Human transporter
C 569	21	4.3	26657	24	AAI72317	Human transporter
C 570	21	4.3	26664	21	AAK60207	Human prostate can
C 571	21	4.3	26664	24	AAS98942	Human prostate can
C 572	21	4.3	26928	20	AAZ32184	Human prothrombin
C 573	21	4.3	26928	22	ABA82620	Human HBM gene reg
C 574	21	4.3	26928	24	ABN95780	Gene #2278 used to
C 575	21	4.3	27571	22	ABK22779	Human high bone ma
C 576	21	4.3	27571	22	ABA19222	Human nervous syst
C 577	21	4.3	27572	22	ABA19221	Human nervous syst
C 578	21	4.3	27869	22	ABA19635	Human nervous syst
C 579	21	4.3	27869	22	AAK66517	Human immune/haema
C 580	21	4.3	30222	24	ABL39412	Human electron-tra
C 581	21	4.3	30620	22	AAK66931	Human immune/haema
C 582	21	4.3	30709	24	ABK87217	Human lipase, horm
C 583	21	4.3	31584	22	AAK81054	Human immune/haema
C 584	21	4.3	31741	22	ABA21231	Human nervous syst
C 585	21	4.3	31766	24	AAK22781	Human sulphate tra
C 586	21	4.3	32134	22	ABA07813	Human ovarian and
C 587	21	4.3	32134	22	AAK03615	Human reproductive
C 588	21	4.3	32152	22	AAS39621	Genomic sequence #
C 589	21	4.3	32152	22	AAK89020	Human digestive sy
C 590	21	4.3	32152	22	AAK91534	Human digestive sy
C 591	21	4.3	32152	22	AAI57791	Human colorectal c
C 592	21	4.3	32169	22	ABK43076	Genomic sequence #
C 593	21	4.3	32189	22	AAK04670	Human reproductive
521	23	4.3	32189	23	ABL97577	Human testicular a
522	23	4.3	32191	22	ABA07814	Human ovarian and
523	23	4.3	32191	22	AAK03616	Human reproductive
524	23	4.3	32194	22	AAK04340	Human amyloid beta
525	23	4.3	35973	24	ABK13076	Human immune/haema
526	23	4.3	36485	22	AAK68958	Human immune/haema
527	23	4.3	36485	22	AAK74751	Human immune/haema
528	23	4.3	36933	22	AAK66362	Human immune/haema
529	23	4.3	37959	22	AAK81763	Human immune/haema
530	23	4.3	38358	22	AAK73535	Human immune/haema
531	23	4.3	39746	22	ABL13398	Drosophila melanog
532	23	4.3	41159	22	AAK65631	Human immune/haema
533	23	4.3	43089	21	AAK36335	Genomic sequence o
534	23	4.3	43950	24	AAK36022	Human kinase genom
535	23	4.3	44211	22	AAK85974	Human immune/haema
536	23	4.3	44354	22	AAK77833	Human immune/haema
537	23	4.3	44354	22	AAK77836	Human immune/haema
538	23	4.3	44354	22	AAK77837	Human immune/haema
539	23	4.3	47090	22	AAK68725	Human immune/haema
540	23	4.3	47090	22	AAK78219	Human immune/haema
541	23	4.3	50000	21	AAK96364	Polymorphic repeat
542	23	4.3	50442	22	AAK73083	Human immune/haema
543	23	4.3	50442	22	AAK87551	Human immune/haema
544	23	4.3	51474	22	AAK97846	Human neuroblastom
545	23	4.3	52216	22	AAK28355	Nucleotide sequenc
546	23	4.3	52216	24	ABL50307	Human musashi prom
547	23	4.3	54863	22	AAK86025	Human immune/haema
548	23	4.3	54877	22	AAK86026	Human immune/haema
549	23	4.3	74962	22	AAK15256	Human phosphatase
550	23	4.3	81800	24	ABK84756	Human CDNA differe
551	23	4.3	84495	24	AAS20588	Human methionine a
552	23	4.3	86080	24	ABQ88164	Human osteoblast d
553	23	4.3	86080	24	ABK83561	Human CDNA differe
554	23	4.3	112460	24	ABK83567	Human CDNA differe
555	23	4.3	119950	20	AAK90201	Human yes1 gene
556	23	4.3	121162	21	AAK66548	Human kinesin-like
557	23	4.3	121162	21	AAK66548	Human kinesin-like
558	23	4.3	121724	24	ABQ88143	Human osteoblast d
559	23	4.3	123219	23	AAH88703	Human DNA sequence
560	23	4.3	129722	24	ABQ88117	Human osteoblast d
561	23	4.3	139389	24	ABK84795	Human CDNA differe
562	23	4.3	145831	24	ABL62309	Colon adenocarcino
563	23	4.3	145831	24	ABL66806	Lung cancer relate
564	23	4.3	145831	24	ABL66806	Lung cancer relate
565	23	4.3	145831	24	ABL66806	Lung cancer relate
566	23	4.3	145831	24	ABL66806	Lung cancer relate
567	23	4.3	145831	24	ABL66806	Lung cancer relate
568	23	4.3	145831	24	ABL66806	Lung cancer relate
569	23	4.3	145831	24	ABL66806	Lung cancer relate
570	23	4.3	145831	24	ABL66806	Lung cancer relate
571	23	4.3	145831	24	ABL66806	Lung cancer relate
572	23	4.3	145831	24	ABL66806	Lung cancer relate
573	23	4.3	145831	24	ABL66806	Lung cancer relate
574	23	4.3	145831	24	ABL66806	Lung cancer relate
575	23	4.3	145831	24	ABL66806	Lung cancer relate
576	23	4.3	145831	24	ABL66806	Lung cancer relate
577	23	4.3	145831	24	ABL66806	Lung cancer relate
578	23	4.3	145831	24	ABL66806	Lung cancer relate
579	23	4.3	145831	24	ABL66806	Lung cancer relate
580	23	4.3	145831	24	ABL66806	Lung cancer relate
581	23	4.3	145831	24	ABL66806	Lung cancer relate
582	23	4.3	145831	24	ABL66806	Lung cancer relate
583	23	4.3	145831	24	ABL66806	Lung cancer relate
584	23	4.3	145831	24	ABL66806	Lung cancer relate
585	23	4.3	145831	24	ABL66806	Lung cancer relate
586	23	4.3	145831	24	ABL66806	Lung cancer relate
587	23	4.3	145831	24	ABL66806	Lung cancer relate
588	23	4.3	145831	24	ABL66806	Lung cancer relate
589	23	4.3	145831	24	ABL66806	Lung cancer relate
590	23	4.3	145831	24	ABL66806	Lung cancer relate
591	23	4.3	145831	24	ABL66806	Lung cancer relate
592	23	4.3	145831	24	ABL66806	Lung cancer relate
593	23	4.3	145831	24	ABL66806	Lung cancer relate

c 667	20	4.1	289	23	ABV56681	Human prostate exp
c 668	20	4.1	300	20	AA212665	Human gene express
c 669	20	4.1	300	20	AA398294	Human cancer cell
c 670	20	4.1	301	22	AAK65518	Human immune/haema
c 671	20	4.1	301	22	AAK82056	Human immune/haema
c 672	20	4.1	301	22	AAI62855	Human genomic DNA
c 673	20	4.1	301	22	AAV90033	EST clone DA390
c 674	20	4.1	303	20	AAAC21259	Human secreted pro
c 675	20	4.1	304	21	AAK95258	Human immune/haema
c 676	20	4.1	309	22	AAK95258	Human immune/haema
c 677	20	4.1	321	22	AAK37285	Novel human diagno
c 678	20	4.1	334	23	ABV07716	Human prostate exp
c 679	20	4.1	335	22	AAI89622	Human polynucleoti
c 680	20	4.1	337	22	AAI88453	Human polynucleoti
c 681	20	4.1	340	24	ABN63483	Human cancer relat
c 682	20	4.1	342	22	AAI36458	Human musculoskele
c 683	20	4.1	351	23	ABV01239	Human prostate exp
c 684	20	4.1	352	23	ABV10408	Human prostate exp
c 685	20	4.1	354	22	AAI20745	Human breast cance
c 686	20	4.1	359	22	AAK64316	Novel human polynu
c 687	20	4.1	360	22	AAI28945	Colon tumour relat
c 688	20	4.1	360	22	AAK65560	Novel human polynu
c 689	20	4.1	361	22	AAI90764	Human polynucleoti
c 690	20	4.1	361	22	AAK64709	Novel human polynu
c 691	20	4.1	365	22	AAI87820	Human polynucleoti
c 692	20	4.1	365	22	AAK60894	Human immune/haema
c 693	20	4.1	372	22	AAI86592	Human polynucleoti
c 694	20	4.1	381	24	ABL08195	Human breast cance
c 695	20	4.1	381	24	ABL84961	Human ovarian can
c 696	20	4.1	382	24	ABN96516	Gene #3014 used to
c 697	20	4.1	384	22	AAI89017	Human polynucleoti
c 698	20	4.1	385	22	AAK62104	Human immune/haema
c 699	20	4.1	385	22	AAI81318	Human polynucleoti
c 700	20	4.1	391	24	ABL86195	Human ovarian can
c 701	20	4.1	392	23	AAK64572	DNA encoding novel
c 702	20	4.1	397	24	ABL86202	Human ovarian can
c 703	20	4.1	398	23	ABV31579	Human prostate exp
c 704	20	4.1	398	23	ABV40547	Human prostate exp
c 705	20	4.1	399	22	AAI84258	Human polynucleoti
c 706	20	4.1	399	24	ABL77510	Human ovarian can
c 707	20	4.1	401	24	ABL84120	Human ovarian can
c 708	20	4.1	403	22	AAI83109	Human polynucleoti
c 709	20	4.1	403	24	ABN63060	Human cancer relat
c 710	20	4.1	404	24	ABL84531	Human ovarian can
c 711	20	4.1	405	23	ABV17327	Human prostate exp
c 712	20	4.1	406	22	AAI93723	Human polynucleoti
c 713	20	4.1	408	22	AAI83505	Human polynucleoti
c 714	20	4.1	410	22	AAI89973	Human prostate exp
c 715	20	4.1	413	24	ABL87596	Human polynucleoti
c 716	20	4.1	414	23	ABV10882	Human prostate exp
c 717	20	4.1	416	22	AAI81524	Human polynucleoti
c 718	20	4.1	416	22	AAI92116	Human polynucleoti
c 719	20	4.1	419	22	ABAI3362	Human nervous syst
c 720	20	4.1	420	22	AAI85418	Human polynucleoti
c 721	20	4.1	421	22	AAI81436	Human polynucleoti
c 722	20	4.1	425	22	AAI93694	Human polynucleoti
c 723	20	4.1	430	22	AAI25940	Human breast cance
c 724	20	4.1	432	24	AAK65338	Human cancer relat
c 725	20	4.1	436	22	ABN58087	Human immune/haema
c 726	20	4.1	437	22	AAK67734	Human immune/haema
c 727	20	4.1	437	24	ABN65227	Human cancer relat
c 728	20	4.1	438	23	ABV01713	Human prostate exp
c 729	20	4.1	441	23	ABV32037	Human prostate exp
c 730	20	4.1	441	23	ABV40976	Human prostate exp
c 731	20	4.1	445	22	AAH04811	Human cDNA clone (
c 732	20	4.1	448	22	AAK81752	Human immune/haema
c 733	20	4.1	448	22	AAK81753	Human immune/haema
c 734	20	4.1	449	23	ABV57279	Human prostate exp
c 735	20	4.1	449	24	ABL77420	Human ovarian can
c 736	20	4.1	450	22	AAK86068	Human immune/haema
c 737	20	4.1	450	22	AAK86070	Human immune/haema
c 738	20	4.1	451	24	ABL87595	Human ovarian can
c 739	20	4.1	452	22	AAI92040	Human polynucleoti
c 740	20	4.1	454	23	ABV00376	Human prostate exp
c 741	20	4.1	456	22	AAI84703	Human polynucleoti
c 742	20	4.1	457	23	ABV30721	Human prostate exp
c 743	20	4.1	457	23	ABV39689	Human prostate exp
c 744	20	4.1	462	23	ABV47122	Human prostate exp
c 745	20	4.1	464	22	AAI91243	Human polynucleoti
c 746	20	4.1	465	23	ABV48386	Human prostate exp
c 747	20	4.1	469	23	ABV09545	Human prostate exp
c 748	20	4.1	473	21	AAK43406	Rat secreted expre
c 749	20	4.1	476	24	ABL80655	Human ovarian can
c 750	20	4.1	478	23	ABV51118	Human prostate exp
c 751	20	4.1	479	22	AAK71910	Human immune/haema
c 752	20	4.1	483	22	ABAI4579	Human nervous syst
c 753	20	4.1	483	22	ABAO7465	Human ovarian and
c 754	20	4.1	483	22	AAI19105	Human breast cance
c 755	20	4.1	483	22	AAI00081	Human reproductive
c 756	20	4.1	483	22	AAK69290	Human immune/haema
c 757	20	4.1	483	22	AAK69291	Human immune/haema
c 758	20	4.1	496	24	ABN64038	Human cancer relat
c 759	20	4.1	497	22	AAI91133	Human polynucleoti
c 760	20	4.1	499	22	ABAO7691	Human ovarian and
c 761	20	4.1	499	22	ABL02849	Human reproductive
c 762	20	4.1	503	24	ABN60560	Human cancer relat
c 763	20	4.1	507	22	AAH08989	Human cDNA clone (
c 764	20	4.1	507	23	ABV58334	Human prostate exp
c 765	20	4.1	510	23	ABV47571	Human prostate exp
c 766	20	4.1	511	24	ABN65132	Human cancer relat
c 767	20	4.1	513	23	ABV17834	Human prostate exp
c 768	20	4.1	518	22	ABN63432	Human DNA for a no
c 769	20	4.1	521	24	ABN63327	Human cancer relat
c 770	20	4.1	522	24	ABN64650	Human cancer relat
c 771	20	4.1	531	24	ABN61496	Human cancer relat
c 772	20	4.1	537	24	ABL83489	Human ovarian can
c 773	20	4.1	538	22	AAK86407	Human immune/haema
c 774	20	4.1	556	22	AAH10063	Human cDNA clone (
c 775	20	4.1	558	22	AAH13225	Human cDNA clone (
c 776	20	4.1	563	24	ABN64556	Human cancer relat
c 777	20	4.1	564	24	ABL92350	Human secreted pro
c 778	20	4.1	576	22	AAI12299	Human breast cance
c 779	20	4.1	584	22	AAI05762	Human reproductive
c 780	20	4.1	584	22	AAH12123	Human cDNA clone (
c 781	20	4.1	584	24	ABN61136	Human cancer relat
c 782	20	4.1	587	22	AAI21175	Human breast cance
c 783	20	4.1	587	23	ABV55967	Human prostate exp
c 784	20	4.1	591	24	ABN15908	Human OREF polynuc
c 785	20	4.1	593	24	ABN65447	Human cancer relat
c 786	20	4.1	600	23	ABV53819	Human prostate exp
c 787	20	4.1	601	23	ABV47625	Human prostate exp
c 788	20	4.1	605	23	ABV58501	Human prostate exp
c 789	20	4.1	605	24	ABN62272	Human cancer relat
c 790	20	4.1	628	22	AAH98619	Human EST-derived
c 791	20	4.1	655	22	AAK69148	Human immune/haema
c 792	20	4.1	655	22	AAK71307	Human immune/haema
c 793	20	4.1	668	22	ABAI4738	Human nervous syst
c 794	20	4.1	681	24	ABL92374	Human secreted pro
c 795	20	4.1	695	22	AAH04791	Human cDNA clone (
c 796	20	4.1	708	22	AAH98981	Human EST-derived
c 797	20	4.1	708	22	ABQ89406	Human prostate exp
c 798	20	4.1	740	22	ABQ89406	Human EST-derived
c 799	20	4.1	745	22	AAH99140	Human gene express
c 800	20	4.1	754	20	AAI215610	Human gene express
c 801	20	4.1	755	20	AAI215590	Human gene express
c 802	20	4.1	755	20	AAI215589	Human gene express
c 803	20	4.1	757	19	AAV16883	Human prostate can
c 804	20	4.1	757	20	AAI26018	Prostate disease m
c 805	20	4.1	757	21	AAZ87503	Prostate, breast a
c 806	20	4.1	757	22	AAI93722	Biomarker UC band
c 807	20	4.1	768	22	AAI97377	Human neuroblastom
c 808	20	4.1	769	22	AAI95545	Human neuroblastom
c 809	20	4.1	771	24	ABQ89896	Human prostate exp
c 810	20	4.1	787	20	AAI217095	Human gene express
c 811	20	4.1	787	20	AAI217096	Human gene express
c 812	20	4.1	787	24	ABQ89025	Human prostate exp







D	b	7268	ATTTTTACTGTAGCACACGCTCGTGTCTCAGGCAGCATCCCTTTCCCAATGSCCTGGC	7329
Q	y	181	CCTGCTGCCCTGTGAGATGAGGAGGGAGCGTCTTGGAACCTTCGAGTCCAAAGGCCAGTC	240
D	b	7328	CCTGCTGCCCTGTGAGATGAGGAGGGAGGGTCTGGAACCTTCGAGTCCAAAGGCCAGTC	7387
Q	y	241	CCCATTTCTGCCCTGCTCACCGCTGSGCCCTTAGAGACC CGCAGGTAGGGGTGGGAGATG	300
D	b	7388	CCCATTTCTGCCCTGCTCACCGCTGSGCCCTTAGAGACC CGCAGGTAGGGGTGGGAGATG	7447
Q	y	301	CTTCTCTCTTGCCCCCGCCCTCATGGTCTTAGCCCTTCCCTGAGTCGGGCTGAGGC	360
D	b	7448	CTTCTCTCTTGCCCCCGCCCTCATGGTCTTAGCCCTTCCCTGAGTCGGGCTGAGGC	7507
Q	y	361	CAGAGTCACCTTTTCTGTGGCTGGCTCTACCTTCTCTGTCCCTGAGGTAAACCGTGC CCA	420
D	b	7508	CAGAGTCACCTTTTCTGTGGCTGGCTCTACCTTCTCTGTCCCTGAGGTAAACCGTGC CCA	7567
Q	y	421	TCTTGCATCCTCAAACGACAGAGGAGCTTTTCTGGAAATTTCAAACAATTTGCTCTTAGTC	480
D	b	7568	TCTTGCATCCTCAAACGACAGAGGAGCTTTTCTGGAAATTTCAAACAATTTGCTCTTAGTC	7627
Q	y	481	CCAAGC 486	
D	b	7628	CCAAGC 7633	
 RESULT 3 AAI81887/c				
ID	XX	AAI81887 standard; cDNA; 1855 BP.		
AC	AAI81887;			
DT	06-NOV-2001 (first entry)			
DE	Human polynucleotide SEQ ID NO 1947.			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.			
OS	Homo sapiens.			
PN	WO200164835-A2.			
PD	07-SEP-2001.			
PF	26-FEB-2001; 2001WO-US04927.			
PR	28-FEB-2000; 2000US-0515126.			
PR	18-MAY-2000; 2000US-0577409.			
PA	(HYSE-) HYSEQ INC.			
PI	Tang YT, Liu C, Drmanac RT;			
WP	WI; 2001-514838/56.			
P	-PSDB; AAO01956.			
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -			
PS	Claim 1; SEQ ID NO 1947; 1399pp + Sequence Listing; English.			
CC	The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities.			

RESULT 2	
AAA64507	
ID	AAA64507 standard; DNA; 9048 BP.
XX	
AC	AAA64507;
XX	
DT	02-JAN-2001 (first entry)
XX	
DE	Nucleotide sequence comprising the human FEZ1 gene.
XX	
KW	Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
KW	tumour proliferation; tubulin; microtubule; protein EF1-gamma;
KW	tubulin polymerisation disorder; mitosis initiation; cell proliferation;
KW	cell growth; cell shape; cell rigidity; cell motility; DNA replication;
KW	tumorigenesis; tumour survival; metastasis; ss.
XX	
OS	Homo sapiens.
XX	
WO	WO200005065-A2.
PN	
XX	31-AUG-2000.
PD	
XX	25-FEB-2000; 2000WO-US04950.
XX	
PR	25-FEB-1999; 99US-0121537.
XX	
PA	(UYJE-) UNIV JEFFERSON THOMAS.
XX	
PI	Croce CM, Ishii H;
XX	
DR	WPI; 2000-558396/51.
XX	
PT	New polynucleotide homologous with a portion of one strand of the human
PT	FEZ1 gene, useful for alleviating abnormal cell proliferation such as
PT	cancer -
XX	
PS	Claim 2; Fig 5A; 255pp; English.
XX	
CC	The present sequence comprises the human FEZ1 gene. FEZ1 is a tumour
CC	suppressor gene, located at chromosome location 8p22. Decreased or no
CC	expression of FEZ1 is detected in a variety of cancer cells. Expression
CC	of FEZ1 inhibits tumour growth and proliferation. FEZ1 also interacts
CC	with tubulin, with microtubules, and with protein EF1-gamma.
CC	Post-translational phosphorylation and dephosphorylation modulates the
CC	effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are
CC	useful for inducing cells to proliferate. Compounds which modulate FEZ1
CC	association with tubulin are useful for alleviating tubulin hyper- or
CC	hypo- polymerisation disorders, such as those associated with aberrant
CC	initiation of mitosis, modulation of the initiation and rate of cell
CC	proliferation and cell growth, modulation of cell shape, cell rigidity,
CC	cell motility, rate and stage of cellular DNA replication, intracellular
CC	distribution of organelles, metastatic potential of cell and cellular
CC	transformation from a non-cancerous to cancerous phenotype. Compounds
CC	which modulate FEZ1 binding and phosphorylation are also useful for
CC	alleviating a disorder, such as tumorigenesis, tumour survival, growth
CC	and metastasis.
XX	
SQ	Sequence 9048 BP; 2011 A; 2605 C; 2490 G; 1939 T; 3 other;
Query Match	100.0%; Score 486; DB 21; Length 9048;
Best Local Similarity	100.0%; Pred. No. 4, 4e-221;
Matches	486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AGATTCCAGATGTGAGCCACCGTGGCGCTGTGGCCAGATTTTCTTTTATCTCTCTCTTTT 60
Db	7148 AGATTCCAGATGTGAGCCACCGTGGCGCTGTGGCCAGATTTTCTTTTATCTCTCTTTT 7207
QY	61 CTTTCTTTTGGCTTCTGTCTTTTCAGAAAGCAAGCCAGACCTAGCAGAGCTGTTCATGTTCT 120
Db	7208 CTTTCTTTTGGCTTCTGTCTTTTCAGAAAGCAAGCCAGACCTAGCAGAGCTGTTCATGTTCT 7267
QY	121 ATTTTGGACTGTAGCCACAGCTGCTGTTCTCTCAGGACAGCATCCCTTCCACATGCTGGG 180



```
XX PA (FARB ) BAYER CORP.
XX PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
XX PI Thiagalingam A, Lewis ME;
XX XX WPI; 2002-426115/45.
XX XX New isolated nucleic acid that is differentially expressed in cancer
XX PT tissues useful for determining the presence of colon cancer in a cell
XX PT or tissue type, and in antisense therapy -
XX PS Claim 1; Fig 1; 796pp; English.
XX CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
XX CC expressed in cancer tissues. ABQ78993 to ABQ79004 represent proteins
XX CC expressed by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
XX CC used in antisense therapy. An antibody immunoreactive with a polypeptide
XX CC encoded by (I) is useful for detecting cancer in a patient sample, and
XX CC for detecting the presence or absence of a polynucleotide encoded by a
XX CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
XX CC from (I) can be used for determining the presence of a nucleic acid which
XX CC hybridizes to (I), and for determining the phenotype of cells in a sample
XX CC of cells from a patient. (I) is useful for determining the presence of
XX CC colon cancer in a cell or tissue type, for determining the presence or
XX CC state of other type of cancer, in antisense therapy, to generate
XX CC macroarrays on a solid surface, to identify a chromosome on which the
XX CC corresponding gene resides, and in tissue profiling, forensics, genetic
XX CC analysis, mapping and diagnostic applications. (I) can be used to raise
XX CC antibodies, and to screen for peptide analogues and antagonists.
XX SQ Sequence 547 BP; 163 A; 112 C; 127 G; 130 T; 15 other;

Query Match 5.8%; Score 28; DB 24; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAGA 34
Db 92 CAGATGTGAGCCACCGTGCCTGGCCAGA 65

RESULT 6
AAH98314
ID AAH98314 standard; cDNA; 1660 BP.
XX AC AAH98314;
XX DT 12-OCT-2001 (first entry)
XX DE Human EST-derived coding sequence SEQ ID NO: 171.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX KW diagnostics; forensic test; gene mapping; genetic disorder;
XX KW biodiversity; gene therapy; nutrition; ss.
XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX OS (HYSE-) HYSEQ INC.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX XX WPI; 2001-476164/51.
XX XX P-PSDB; AAM24166.
XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX XX antibodies and research use -
XX XX Claim 1; Page 629; 1275pp; English.
XX XX The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a cDNA
XX CC of the invention.
XX SQ Sequence 1660 BP; 526 A; 308 C; 270 G; 555 T; 1 other;

Query Match 5.8%; Score 28; DB 22; Length 1660;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAGA 34
Db 1185 CAGATGTGAGCCACCGTGCCTGGCCAGA 1212

RESULT 7
AAH98825
ID AAH98825 standard; cDNA; 1660 BP.
XX AC AAH98825;
XX DT 12-OCT-2001 (first entry)
XX DE Human EST-derived coding sequence SEQ ID NO: 682.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX KW diagnostics; forensic test; gene mapping; genetic disorder;
XX KW biodiversity; gene therapy; nutrition; ss.
XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX OS (HYSE-) HYSEQ INC.
XX PN Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX XX WPI; 2001-476164/51.
XX XX P-PSDB; AAM24166.
XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX XX antibodies and research use -
XX XX Claim 1; Page 629; 1275pp; English.
XX XX The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
```

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.

SQ Sequence 1660 BP; 526 A; 308 C; 270 G; 555 T; 1 other;

Query Match 5.8%; Score 28; DB 22; Length 1660;  
 Best Local Similarity 100.0%; Pred. No. 0.002;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CAGATGTGAGCCACCGTGGCCGACAGA 34  
 DB 1185 CAGATGTGAGCCACCGTGGCCGACAGA 1212

## RESULT 8

AXX22304/c

ID AAX22304 standard; DNA; 28866 BP.

XX AC AAX22304;

XX 22-JUN-1999 (first entry)

XX Human IL-1ra BAC contiguous DNA sequence 97.

XX Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition;  
 KW interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis;  
 KW chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease;  
 KW growth factors; treatment; IL-1 receptor complex; BAC; ss.

XX Homo sapiens.

XX W09906426-A1.

XX 11-FEB-1999.

XX 03-AUG-1998; 98WO-US16102.

XX 02-JUL-1998; 98US-0091650.

XX 04-AUG-1997; 97US-0054646.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Pan Y;

XX WPI; 1999-153692/13.

XX New isolated nucleic acid encoding the new human cytokine Tango-77 -  
 PT used to inhibit inflammation and to screen for specific modulators

XX Example 5; Figure 4; 226pp; English.

XX AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic  
 CC sequences containing alternatively spliced forms of human IL-1ra. Such  
 CC fragments are used in the method of the invention which describes the  
 CC isolation of a novel human TANGO-77 encoding nucleic acid and protein.  
 CC Tango-77 is a member of the cytokine superfamily that is expected to  
 CC inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). It  
 CC may also bind to a new receptor so could regulate other cellular  
 CC processes associated with acute or chronic inflammation, e.g. asthma,  
 CC chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and  
 CC inflammatory bowel disease. It may also induce or suppress interleukins,  
 CC cytokines and growth factors. Modulators of this protein are used to  
 CC treat or prevent conditions associated with abnormal levels of  
 CC inflammation, or activity of IL-1 or its receptor complex.

XX Sequence: 28866 BP; 8044 A; 6348 C; 6742 G; 7729 T; 3 other;

Query Match 5.6%; Score 27; DB 20; Length 28866;  
 Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CAGATGTGAGCCACCGTGGCCGACAGA 33  
 DB 21411 CAGATGTGAGCCACCGTGGCCGACAGA 21385

## RESULT 9

ABL85166

ID ABL85166 standard; cDNA; 251 BP.

XX AC ABL85166;

XX 17-MAY-2002 (first entry)

XX Human ovarian cancer related cDNA clone SEQ ID NO:8144.

XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

XX W0200192581-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide

XX Claim 1; SEQ ID 8144; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.

XX Sequence 251 BP; 59 A; 62 C; 54 G; 76 T; 0 other;

Query Match 5.3%; Score 26; DB 24; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGAGCCACCGTGGCCGACAGATTTT 38

DB 137 TGAGCCACCGTGGCCGACAGATTTT 162

```

RESULT 10
ABL84945
ID ABL84945 standard; cDNA; 371 BP.
XX
XX ABL84945;
AC
XX 17-MAY-2002 (first entry)
DT
XX Human ovarian cancer related cDNA clone SEQ ID NO:7923.
DE
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
KW
XX Homo sapiens.
OS
XX WO200192581-A2.
PN
XX 06-DEC-2001.
PD
XX 29-MAY-2001; 2001WO-US17756.
PF
XX 26-MAY-2000; 2000US-207484P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Algate PA, Harlocker SL, Jones R;
PI
XX WPI; 2002-122075/16.
DR
XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide
XX
XX Claim 1; SEQ ID 7923; 489bp; English.
PS
XX
XX The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (SI) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
XX Sequence 371 BP; 100 A; 83 C; 81 G; 107 T; 0 other;
SQ
Query Match 5.3%; Score 26; DB 24; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGAGCCACCGTGGCTGCCAGATTTT 38
| | | | | | | | | | | | | | | | | |
Db 137 TGAGCCACCGTGGCTGCCAGATTTT 162

RESULT 11
AAC75926
ID AAC75926 standard; cDNA; 434 BP.

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XX AAC75926;
AC
XX 08-FEB-2001 (first entry)
DT
XX Human ORFX ORF1481 polynucleotide sequence SEQ ID NO:2961.
DE
XX
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoziatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
XX Homo sapiens.
OS
XX WO200058473-A2.
PN
XX 05-OCT-2000.
PD
XX 31-MAR-2000; 2000WO-US08621.
PF
XX 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI WPI; 2000-602362/57.
DR P-PSDB; AAB41717.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 2198-2199; 5507pp; English.
PS
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnary;
XX antipsoziatic; antiparkinsonian; nootropic; neuroprotective;
XX osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
XX antidiabetic; hypotensive; dermatological; antifungal; antirheumatic;
XX antinflammatory; antibacterial; antiviral; antitumour; antihypertensive;
XX antithyroid; and antianemic. The sequences can be used for determining
XX the presence of or predisposition to or preventing or treating
XX pathological conditions associated with an ORFX-associated disorder. The
XX nucleic acids can be used to express ORFX proteins in gene therapy
XX vectors. The proteins and nucleic acids may be used to treat cancers,
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,
XX graft vs host disease, cardiovascular disease, diabetes mellitus,
XX hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,
XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
XX nocturnal haemoglobinuria, antinflammatory disease; to enhance
XX coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 434 BP; 75 A; 132 C; 123 G; 103 T; 1 other;
SQ
Query Match 5.3%; Score 26; DB 21; Length 434;

```

Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGAGCCACCGTGCTGCCAGATTTT 38  
| | | | | | | | | | | | | | | | | |  
Db 321 TGAGCCACCGTGCTGCCAGATTTT 346

RESULT 12

AAD16646  
ID- AAD16646 standard; DNA; 29449 BP.

XX AC AAD16646;

DT 19-NOV-2001 (first entry)

XX DE Human novel protein-encoding gene 22, SRQ ID NO:73.

XX KW Human; lipid metabolism protein; nootropic; neuroprotective; cardiant;  
KW cerebroprotective; hepatotropic; antidiabetic; ophthalmic; nephrotropic;  
KW immune disorder; autoimmune disease; rheumatoid arthritis; glossitis;  
KW systemic lupus erythematosus; conjunctivitis; inflammatory disorder;  
KW respiratory disorder; asthma; allergy; CNS disorder; Alzheimer's disease;  
KW Parkinson's disease; atherosclerosis; cardiovascular disorder; cancer;  
KW coronary disease; familial hypercholesterolaemia; hyperlipidaemia;  
KW haematopoietic disorder; hypolipidaemia; lipodosis; Gaucher's disease;  
KW Tay-sach's disease; mental retardation; gene therapy; antisense therapy;  
KW ds.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT exon	1..1785
FT exon	/*tag= a
FT intron	1786..1847
FT exon	/*tag= b
FT exon	1848..1971
FT intron	/*tag= c
FT exon	1972..2125
FT exon	/*tag= d
FT intron	2126..2475
FT exon	/*tag= e
FT intron	2476..2895
FT exon	/*tag= f
FT exon	2896..2980
FT intron	/*tag= g
FT exon	2981..3325
FT intron	/*tag= h
FT exon	3326..3786
FT intron	/*tag= i
FT exon	3787..5007
FT intron	/*tag= j
FT exon	5008..5343
FT intron	/*tag= k
FT exon	5344..5789
FT intron	/*tag= l
FT exon	5790..5928
FT intron	/*tag= m
FT exon	5929..6133
FT intron	/*tag= n
FT exon	6134..6205
FT intron	/*tag= o
FT exon	6206..6261
FT intron	/*tag= p
FT exon	6262..7861
FT intron	/*tag= q
FT exon	7862..8072
FT intron	/*tag= r
FT exon	8073..8186
FT intron	/*tag= s
FT exon	8187..8253
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FT exon	8253..8359
FT intron	/*tag= u
FT exon	8360..9085
FT intron	/*tag= v
FT exon	9086..10377
FT intron	/*tag= w
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FT intron	/*tag= y
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FT intron	/*tag= z
FT exon	12643..13123
FT intron	/*tag= aa
FT exon	13124..15128
FT intron	/*tag= ab
FT exon	15129..15284
FT intron	/*tag= ac
FT exon	15285..16827
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FT exon	16828..16879
FT intron	/*tag= ae
FT exon	16880..18110
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FT exon	21723..23308
FT intron	/*tag= an
FT exon	23309..23420
FT intron	/*tag= ao
FT exon	23421..25352
FT intron	/*tag= ap
FT exon	25353..25943
FT intron	/*tag= aq
FT exon	25944..26008
FT intron	/*tag= ar
FT exon	26009..26133
FT intron	/*tag= as
FT exon	26134..26521
FT intron	/*tag= at
FT exon	26522..27709
FT intron	/*tag= au
FT exon	27710..29385
FT intron	/*tag= av
FT exon	29386..29449
FT intron	/*tag= aw
XX	WO200155203-A1.
XX	02-AUG-2001.
XX	17-JAN-2001; 2001WO-US01327.
XX	31-JAN-2000; 2000US-0179065.
XX	04-FEB-2000; 2000US-0180628.
XX	24-FEB-2000; 2000US-0184664.
XX	02-MAR-2000; 2000US-0186350.
XX	16-MAR-2000; 2000US-0189874.
XX	17-MAR-2000; 2000US-0190076.
XX	18-APR-2000; 2000US-0198123.
XX	19-MAY-2000; 2000US-0205515.
XX	07-JUN-2000; 2000US-0209467.



PR	28-JUN-2000;	2000US-0214886.	
PR	30-JUN-2000;	2000US-0215135.	
PR	07-JUL-2000;	2000US-0216647.	
PR	07-JUL-2000;	2000US-0216880.	
PR	11-JUL-2000;	2000US-0217487.	
PR	11-JUL-2000;	2000US-0217496.	
PR	14-JUL-2000;	2000US-0218290.	
PR	26-JUL-2000;	2000US-0220963.	
PR	14-AUG-2000;	2000US-0224518.	
PR	14-AUG-2000;	2000US-0224519.	
PR	14-AUG-2000;	2000US-0225213.	
PR	14-AUG-2000;	2000US-0225214.	
PR	14-AUG-2000;	2000US-0225266.	
PR	14-AUG-2000;	2000US-0225267.	
PR	14-AUG-2000;	2000US-0225268.	
PR	14-AUG-2000;	2000US-0225270.	
PR	14-AUG-2000;	2000US-0225275.	
PR	14-AUG-2000;	2000US-0225758.	
PR	14-AUG-2000;	2000US-0225759.	
PR	18-AUG-2000;	2000US-0226279.	
PR	22-AUG-2000;	2000US-0226681.	
PR	22-AUG-2000;	2000US-0226868.	
PR	22-AUG-2000;	2000US-0227182.	
PR	23-AUG-2000;	2000US-0227009.	
PR	30-AUG-2000;	2000US-0228924.	
PR	01-SEP-2000;	2000US-0229287.	
PR	01-SEP-2000;	2000US-0229343.	
PR	01-SEP-2000;	2000US-0229344.	
PR	01-SEP-2000;	2000US-0229345.	
PR	05-SEP-2000;	2000US-0229509.	
PR	05-SEP-2000;	2000US-0229513.	
PR	06-SEP-2000;	2000US-0230437.	
PR	06-SEP-2000;	2000US-0230438.	

Query Match

Best Local Similarity 5.3%; Score 26; DB 22; Length 29449;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

11 TGTGAGCCACCGTCCTGGCCAGATT 36

|||||

Db

8497 TGTGAGCCACCGTCCTGGCCAGATT 8522

|||||

RESULT 13  
AAS30243/c  
ID AAS30243 standard; DNA; 29449 BP.

XX  
AC AAS30243;  
XX

DT 21-NOV-2001 (first entry)

XX DNA encoding renal and cardiovascular-associated protein, Seq ID 161.  
XX Human; antiinflammatory; neuroprotective; immunomodulator; vulnery;  
KW cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis;  
KW immunosuppressive; kidney disorder; renal failure; hypertension;  
KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;  
KW blood coagulation disorder; electrolyte imbalance disorder; cancer;  
KW hyponatraemia; hyperkalaemia; neoplastic disorder; nephroma;  
KW autoimmune disease; inflammatory disease; reproductive system disorder;  
KW endocrine disorder; neural activity; neurological disorder;  
KW wound healing; respiratory disorder; ss.

OS Homo sapiens.

XX  
PN WO200155328-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01359.

XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216847.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.



osteoporosis; osteopathic; ss.  
Homo sapiens.  
WO200250301-A2.  
27-JUN-2002.  
18-DEC-2001; 2001WO-US48276.  
18-DEC-2000; 2000US-255882P.  
24-APR-2001; 2001US-285691P.  
(GENE-) GENE LOGIC INC.  
(PROC ) PROCTER & GAMBLE CO.  
Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A, Mertz L;  
WPI; 2002-557663/59.  
Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation process -  
Claim 1; SEQ ID NO 93; 78pp + Sequence Listing; English.  
The invention relates to genes and their expression profiles are used for:  
(a) screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition;  
(b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or  
(c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.  
Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention.  
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
Sequence 169739 BP; 49809 A; 35660 C; 35715 G; 48555 T; 0 other;  
Query Match 5.3%; Score 26; DB 24; Length 169739;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CAGATGTGAGCCACCGTGGCCCA 32  
DB 58155 CAGATGTGAGCCACCGTGGCCCA 58130  
RESULT 15  
ABV51351/c  
ID ABV51351 standard; cDNA; 603 BP.  
AC ABV51351;  
XX  
DT 17-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 51342.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX

PN WO200160860-A2.  
XX 23-AUG-2001.  
PD  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
PI  
XX WPI; 2001-662795/76.  
DR  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 9979; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 603 BP; 172 A; 148 C; 149 G; 133 T; 1 other;  
Query Match 5.1%; Score 25; DB 23; Length 603;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CAGATGTGAGCCACCGTGGCCCTGGCC 31  
DB 414 CAGATGTGAGCCACCGTGGCCCTGGCC 390  
Search completed: June 16, 2003, 20:04:12  
Job time : 103.798 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:03 ; Search time 19.0245 Seconds  
(without alignments)  
7834.381 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_7148\_7633

Perfect score: 486

Sequence: 1 agattgcagatgagccac.....cattgtcttagtcccaagc 486

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfilesi.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	6.8	2688	2	US-08-909-965C-1
2	27	5.6	176373	3	US-09-128-155-17
3	25	5.1	819	4	US-09-605-785-571
4	25	5.1	36651	4	US-09-738-894A-3
5	23	4.7	3807	4	US-08-482-918-43
6	23	4.7	3807	4	US-09-224-681-43
7	23	4.7	3807	4	US-08-336-728A-43
8	23	4.7	5864	4	US-08-482-918-47
9	23	4.7	5864	4	US-09-224-681-47
10	23	4.7	5864	4	US-08-336-728A-47
11	23	4.7	55827	4	US-09-813-133A-3
12	23	4.7	81001	4	US-09-750-580-1
13	22	4.5	7042	4	US-09-092-508-1
14	22	4.5	7042	4	US-09-435-110-1
15	22	4.5	7042	4	US-09-098-310-1
16	22	4.5	7042	4	US-09-690-364-21
17	22	4.5	7075	4	US-09-092-508-15
18	22	4.5	7075	4	US-09-435-115-15
19	22	4.5	59065	4	US-09-813-817-3
20	22	4.5	59065	4	US-09-978-197-3
21	21	4.3	631	4	US-09-385-982-354
22	21	4.3	2061	2	US-08-960-022-11
23	21	4.3	4066	4	US-09-367-750-11
24	21	4.3	4192	4	US-09-122-126B-1
25	21	4.3	26664	4	US-09-564-805-28
26	21	4.3	43950	4	US-09-735-934A-3
27	21	4.3	55827	4	US-09-813-133A-3

Sequence 3, Appli	4	US-09-784-316-3	65042	4.3	21	28
Sequence 3, Appli	4	US-09-797-906-3	84495	4.3	21	29
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Sequence 3, Appli	2	US-09-097-199-3	757	4.1	20	31
Sequence 6, Appli	4	US-09-305-639-6	2125	4.1	20	32
Sequence 85, Appli	4	US-09-097-199-85	2125	4.1	20	33
Sequence 1, Appli	4	US-09-799-345-1	2532	4.1	20	34
Sequence 4, Appli	4	US-09-305-639-4	6038	4.1	20	35
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Sequence 20, Appli	1	US-08-488-0118-20	6769	4.1	20	40
Sequence 20, Appli	1	US-08-850-727-20	6769	4.1	20	41
Sequence 20, Appli	5	PCT-US95-10203-20	6769	4.1	20	42
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Sequence 20, Appli	5	PCT-US95-10220-20	6769	4.1	20	44
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Sequence 3, Appli	4	US-09-851-896-3	70000	4.1	20	48
Sequence 3, Appli	4	US-09-741-150-3	112132	4.1	20	49
Sequence 1, Appli	4	US-09-345-882-1	162450	4.1	20	50
Sequence 166, App	4	US-09-345-882-1	162450	4.1	20	51
Sequence 14, Appli	4	US-08-971-089-1	763	3.9	19	52
Sequence 17, Appli	4	US-09-091-725-14	1298	3.9	19	53
Sequence 17, Appli	2	US-09-018-628-17	2907	3.9	19	54
Sequence 11, Appli	3	US-09-273-378-17	2907	3.9	19	55
Sequence 26, Appli	4	US-09-018-635-26	2907	3.9	19	56
Sequence 3, Appli	4	US-09-467-642-3	2907	3.9	19	57
Sequence 771, App	4	US-09-221-0178-771	5351	3.9	19	58
Sequence 20, Appli	3	US-08-471-058-20	5408	3.9	19	59
Sequence 20, Appli	3	US-08-471-057-20	5408	3.9	19	60
Sequence 45, Appli	4	US-09-167-681-45	8453	3.9	19	61
Sequence 1, Appli	4	US-09-345-217-1	11970	3.9	19	62
Sequence 1, Appli	1	US-08-076-011-1	17041	3.9	19	63
Sequence 6, Appli	4	US-09-078-294-6	18443	3.9	19	64
Sequence 3, Appli	4	US-09-810-671-3	21234	3.9	19	65
Sequence 3, Appli	4	US-09-734-673-3	38564	3.9	19	66
Sequence 5, Appli	4	US-08-965-048-5	45716	3.9	19	67
Sequence 4, Appli	4	US-08-965-048-6	45989	3.9	19	68
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Sequence 7, Appli	4	US-09-857-474-7	72604	3.9	19	72
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Sequence 16, Appli	3	US-09-128-155-16	152331	3.9	19	76
Sequence 4, Appli	1	US-08-004-552-4	24	3.7	18	77
Sequence 286, App	3	US-09-009-913-286	86	3.7	18	78
Sequence 287, App	2	US-09-009-913-287	86	3.7	18	79
Sequence 21, Appli	2	US-08-435-149-21	103	3.7	18	80
Sequence 30, Appli	4	US-09-475-460A-30	106	3.7	18	81
Sequence 27, Appli	4	US-09-748-061A-30	106	3.7	18	82
Sequence 1, Appli	1	US-08-026-145-1	928	3.7	18	83
Sequence 8, Appli	1	US-08-446-646-8	928	3.7	18	84
Sequence 7, Appli	1	US-08-321-658B-7	945	3.7	18	85
Sequence 1, Appli	3	US-08-854-764-1	1065	3.7	18	86
Sequence 1, Appli	5	PCT-US95-09377-1	1065	3.7	18	87
Patent No. 5466783	6	US-09-054-782-1	1431	3.7	18	88
Sequence 3, Appli	4	US-08-812-204-1	1613	3.7	18	89
Sequence 3, Appli	2	US-09-431-470-3	1931	3.7	18	90
Sequence 7, Appli	4	US-09-078-294-7	11811	3.7	18	91
Sequence 1, Appli	1	US-08-550-715-1	12847	3.7	18	92
Sequence 6, Appli	4	US-09-173-914-6	14636	3.7	18	93
Sequence 3, Appli	4	US-09-741-154-3	16389	3.7	18	94
Sequence 3, Appli	4	US-09-810-347-3	42571	3.7	18	95

101	18	3.7	246240	2	US-08-724-394A-20	Sequence 20, Appl	174	16	3.3	276	3	US-08-787-739-62	Sequence 62, Appl
102	18	3.7	246240	2	US-08-724-394A-21	Sequence 21, Appl	175	16	3.3	276	3	US-08-487-077A-62	Sequence 62, Appl
103	18	3.7	246240	2	US-08-724-394A-22	Sequence 22, Appl	176	16	3.3	276	3	US-08-485-863A-62	Sequence 62, Appl
104	17	3.5	139	4	US-09-084-120-18	Sequence 18, Appl	177	16	3.3	276	4	US-08-485-049D-62	Sequence 62, Appl
105	17	3.5	414	1	US-08-592-126-98	Sequence 98, Appl	178	16	3.3	276	4	US-09-178-115-62	Sequence 62, Appl
106	17	3.5	454	2	US-08-623-906A-6	Sequence 6, Appl	179	16	3.3	276	4	US-09-177-776-62	Sequence 62, Appl
107	17	3.5	980	4	US-09-171-209-8	Sequence 8, Appl	C 180	16	3.3	279	1	US-08-623-906A-3	Sequence 3, Appl
108	17	3.5	1192	2	US-08-380-916-2	Sequence 2, Appl	C 181	16	3.3	291	1	US-07-922-723A-7	Sequence 7, Appl
109	17	3.5	1192	2	US-08-182-247-1	Sequence 2, Appl	C 182	16	3.3	291	1	US-07-799-828C-7	Sequence 7, Appl
110	17	3.5	1192	3	US-08-721-690-2	Sequence 2, Appl	C 183	16	3.3	291	1	US-08-074-275-7	Sequence 7, Appl
111	17	3.5	1192	3	US-08-891-581-2	Sequence 2, Appl	C 184	16	3.3	291	1	US-08-480-366-7	Sequence 7, Appl
112	17	3.5	1766	1	US-07-991-587A-6	Sequence 6, Appl	C 185	16	3.3	333	4	US-07-952-277A-7	Sequence 7, Appl
113	17	3.5	1766	1	US-08-309-985-6	Sequence 6, Appl	C 186	16	3.3	333	4	US-09-018-584A-27	Sequence 27, Appl
114	17	3.5	2071	4	US-09-816-088-1	Sequence 1, Appl	C 187	16	3.3	415	4	US-09-018-584A-18	Sequence 18, Appl
115	17	3.5	2072	4	US-09-446-047A-19	Sequence 19, Appl	C 188	16	3.3	461	3	US-09-188-930-245	Sequence 245, App
116	17	3.5	2088	1	US-08-164-839-7	Sequence 7, Appl	C 189	16	3.3	480	4	US-09-082-092-1	Sequence 1, Appl
117	17	3.5	2088	1	US-08-583-799-7	Sequence 7, Appl	C 190	16	3.3	555	3	US-09-109-205-8	Sequence 8, Appl
118	17	3.5	2921	1	US-08-164-839-9	Sequence 9, Appl	C 191	16	3.3	583	4	US-08-991-789A-36	Sequence 36, Appl
119	17	3.5	2921	1	US-08-583-799-9	Sequence 9, Appl	C 192	16	3.3	583	4	US-09-062-451-36	Sequence 36, Appl
120	17	3.5	3507	1	US-08-832-883-67	Sequence 67, Appl	C 193	16	3.3	583	4	US-09-598-326-36	Sequence 36, Appl
121	17	3.5	3507	2	US-08-832-877-67	Sequence 67, Appl	C 194	16	3.3	633	4	US-09-134-001C-834	Sequence 834, App
122	17	3.5	3627	2	US-08-232-087A-1	Sequence 1, Appl	C 195	16	3.3	707	4	US-09-328-111-702	Sequence 702, App
123	17	3.5	5253	2	US-08-290-731C-3	Sequence 3, Appl	C 196	16	3.3	769	4	US-09-404-879A-39	Sequence 39, Appl
124	17	3.5	5835	4	US-09-033-333-3	Sequence 3, Appl	C 197	16	3.3	774	2	US-08-467-603-71	Sequence 71, Appl
125	17	3.5	5835	4	US-09-033-333-2	Sequence 2, Appl	C 198	16	3.3	774	2	US-08-467-603-71	Sequence 71, Appl
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127	17	3.5	5836	1	US-08-380-916-1	Sequence 1, Appl	C 200	16	3.3	791	2	US-08-466-793-67	Sequence 67, Appl
128	17	3.5	5836	3	US-08-721-690-1	Sequence 1, Appl	C 201	16	3.3	791	2	US-08-466-793-67	Sequence 67, Appl
129	17	3.5	5836	3	US-08-891-581-1	Sequence 1, Appl	C 202	16	3.3	791	2	US-08-491-861A-67	Sequence 67, Appl
130	17	3.5	5836	3	US-09-033-333-2	Sequence 2, Appl	C 203	16	3.3	793	2	US-08-467-603-69	Sequence 69, Appl
131	17	3.5	5836	4	US-09-033-333-1	Sequence 1, Appl	C 204	16	3.3	793	2	US-08-466-793-69	Sequence 69, Appl
132	17	3.5	5836	4	US-09-614-956-2	Sequence 2, Appl	C 205	16	3.3	793	2	US-08-491-861A-69	Sequence 69, Appl
133	17	3.5	6254	4	US-08-927-219-126	Sequence 126, App	C 206	16	3.3	911	4	US-09-270-391-21	Sequence 21, Appl
134	17	3.5	7301	4	US-09-816-088-3	Sequence 3, Appl	C 207	16	3.3	988	2	US-08-467-603-73	Sequence 73, Appl
135	17	3.5	34303	2	US-08-735-609-4	Sequence 4, Appl	C 208	16	3.3	988	2	US-08-466-793-73	Sequence 73, Appl
136	17	3.5	34303	2	US-08-735-609-4	Sequence 4, Appl	C 209	16	3.3	988	2	US-08-491-861A-73	Sequence 73, Appl
137	17	3.5	34303	2	US-09-315-372-4	Sequence 4, Appl	C 210	16	3.3	998	4	US-09-641-638-282	Sequence 282, App
138	17	3.5	34303	3	US-09-244-752-4	Sequence 4, Appl	C 211	16	3.3	1001	4	US-09-641-638-194	Sequence 194, App
139	17	3.5	34303	3	US-08-245-919-4	Sequence 4, Appl	C 212	16	3.3	1001	4	US-09-641-638-195	Sequence 195, App
140	17	3.5	34303	3	US-09-562-917-4	Sequence 4, Appl	C 213	16	3.3	1001	4	US-09-641-638-283	Sequence 283, App
141	17	3.5	34382	2	US-08-374-483-6	Sequence 6, Appl	C 214	16	3.3	1001	4	US-09-641-638-318	Sequence 318, App
142	17	3.5	35060	3	US-08-814-095-7	Sequence 7, Appl	C 215	16	3.3	1001	4	US-09-641-638-322	Sequence 322, App
143	17	3.5	35408	4	US-09-973-334-3	Sequence 3, Appl	C 216	16	3.3	1090	5	PCT-US96-03940-4	Sequence 4, Appl
144	17	3.5	35408	4	US-09-563-869A-3	Sequence 3, Appl	C 217	16	3.3	1225	1	US-09-734-675-1	Sequence 1, Appl
145	17	3.5	35408	4	US-08-549-489-3	Sequence 3, Appl	C 218	16	3.3	1269	3	US-09-109-205-3	Sequence 3, Appl
146	17	3.5	35935	2	US-08-735-609-1	Sequence 1, Appl	C 219	16	3.3	1338	1	US-08-485-216-1	Sequence 1, Appl
147	17	3.5	35935	2	US-08-735-609-1	Sequence 1, Appl	C 220	16	3.3	1338	2	US-09-003-245-1	Sequence 1, Appl
148	17	3.5	35935	3	US-08-379-452-43	Sequence 43, Appl	C 221	16	3.3	1338	1	US-08-853-552-1	Sequence 1, Appl
149	17	3.5	35935	3	US-09-315-372-1	Sequence 1, Appl	C 222	16	3.3	1392	1	US-08-144-602B-6	Sequence 6, Appl
150	17	3.5	35935	3	US-09-244-752-1	Sequence 1, Appl	C 223	16	3.3	1400	2	US-08-481-658B-43	Sequence 43, Appl
151	17	3.5	35935	3	US-08-245-437-1	Sequence 1, Appl	C 224	16	3.3	1400	2	US-08-477-504A-43	Sequence 43, Appl
152	17	3.5	35935	3	US-09-409-670-43	Sequence 43, Appl	C 225	16	3.3	1400	2	US-08-486-756A-43	Sequence 43, Appl
153	17	3.5	35935	4	US-09-562-919-1	Sequence 1, Appl	C 226	16	3.3	1400	2	US-08-485-862B-43	Sequence 43, Appl
154	17	3.5	44453	4	US-09-146-053-5	Sequence 5, Appl	C 227	16	3.3	1400	2	US-08-787-739-43	Sequence 43, Appl
155	17	3.5	50000	4	US-09-146-053-4	Sequence 4, Appl	C 228	16	3.3	1400	3	US-08-487-077A-43	Sequence 43, Appl
156	17	3.5	50065	4	US-09-813-817-3	Sequence 3, Appl	C 229	16	3.3	1400	3	US-08-485-863A-43	Sequence 43, Appl
157	17	3.5	53065	4	US-09-813-817-3	Sequence 3, Appl	C 230	16	3.3	1400	4	US-08-485-049D-43	Sequence 43, Appl
158	17	3.5	99500	4	US-09-978-137-3	Sequence 10, Appl	C 231	16	3.3	1400	4	US-09-178-115-43	Sequence 43, Appl
159	17	3.5	168575	4	US-09-798-096-10	Sequence 10, Appl	C 232	16	3.3	1400	4	US-09-177-776-43	Sequence 43, Appl
160	16	3.3	40	4	US-09-426-230-1	Sequence 1, Appl	C 233	16	3.3	1404	1	US-08-144-602B-7	Sequence 7, Appl
161	16	3.3	54	3	US-08-369-822C-30	Sequence 30, Appl	C 234	16	3.3	1422	1	US-09-387-574-7	Sequence 7, Appl
162	16	3.3	54	3	US-08-582-776C-45	Sequence 45, Appl	C 235	16	3.3	1422	1	US-09-668-096-7	Sequence 7, Appl
163	16	3.3	54	3	US-08-434-831B-42	Sequence 42, Appl	C 236	16	3.3	1800	5	PCT-US93-11310-11	Sequence 11, Appl
164	16	3.3	71	4	US-09-275-850-132	Sequence 132, App	C 237	16	3.3	1800	5	PCT-US93-11310-11	Sequence 11, Appl
165	16	3.3	209	3	US-08-063-893A-2	Sequence 2, Appl	C 238	16	3.3	1945	4	US-09-082-092-3	Sequence 3, Appl
166	16	3.3	260	4	US-08-991-789A-231	Sequence 231, App	C 239	16	3.3	1974	1	US-08-413-135-3	Sequence 3, Appl
167	16	3.3	260	4	US-09-062-451-231	Sequence 231, App	C 240	16	3.3	1974	4	US-08-971-395-3	Sequence 3, Appl
168	16	3.3	260	4	US-09-598-326-231	Sequence 231, App	C 241	16	3.3	1976	3	US-09-165-042-2	Sequence 2, Appl
169	16	3.3	267	2	US-08-687-080-85	Sequence 85, Appl	C 242	16	3.3	1993	1	US-08-487-890A-108	Sequence 108, App
170	16	3.3	276	2	US-08-481-658B-62	Sequence 62, Appl	C 243	16	3.3	1993	2	US-08-478-435-108	Sequence 108, App
171	16	3.3	276	2	US-08-477-504A-62	Sequence 62, Appl	C 244	16	3.3	1993	2	US-08-337-483-108	Sequence 108, App
172	16	3.3	276	2	US-08-486-756A-62	Sequence 62, Appl	C 245	16	3.3	1993	2	US-08-478-373-108	Sequence 108, App
173	16	3.3	276	2	US-08-485-862B-62	Sequence 62, Appl	C 246	16	3.3	1993	3	US-08-474-671-108	Sequence 108, App

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C 249	16	3.3	1993	4	US-08-637-654-108	Sequence 108, App	C 322	16	3.3	6755	3	US-08-931-999-4	Sequence 1, Appli
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C 254	16	3.3	2115	1	US-08-395-800A-7	Sequence 7, Appli	C 327	16	3.3	7452	5	FCT-US94-0764A-1	Sequence 1, Appli
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C 268	16	3.3	2808	3	US-08-870-126-7	Sequence 7, Appli	C 341	16	3.3	10898	2	US-08-486-756A-5	Sequence 5, Appli
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C 300	16	3.3	4129	4	US-09-224-834-12	Sequence 12, Appli	C 373	16	3.3	40328	3	US-08-742-185-102	Sequence 102, App
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C 303	16	3.3	4697	4	US-08-979-608A-17	Sequence 17, Appli	C 376	16	3.3	45546	4	US-09-146-053-6	Sequence 6, Appli
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C 307	16	3.3	4818	3	US-08-817-926-37	Sequence 27, Appli	C 380	16	3.3	46204	4	US-09-800-960-3	Sequence 3, Appli
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C 311	16	3.3	5629	1	US-08-241-387-2	Sequence 2, Appli	C 384	16	3.3	84495	3	US-09-797-906-3	Sequence 3, Appli
C 312	16	3.3	5643	1	US-08-144-602B-4	Sequence 4, Appli	C 385	16	3.3	84495	3	US-08-781-891-79	Sequence 79, Appli
C 313	16	3.3	5648	5	FCT-US96-03940-1	Sequence 1, Appli	C 386	16	3.3	87350	3	US-08-781-891-79	Sequence 79, Appli
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C 318	16	3.3	6091	4	US-09-221-017B-803	Sequence 803, App	C 391	16	3.3	11182	4	US-09-754-250-3	Sequence 3, Appli
C 319	16	3.3	6124	4	US-08-213-419B-3	Sequence 3, Appli	C 392	16	3.3	152331	3	US-09-128-155-16	Sequence 16, Appli

393	16	3.3	169998	4	US-09-676-610B-24	Sequence 24, Appl	466	15	3.1	372	5	PCT-US95-17111A-35	Sequence 35, Appl
394	16	3.3	176373	3	US-09-128-155-17	Sequence 17, Appl	C 467	15	3.1	376	2	US-08-623-906A-18	Sequence 18, Appl
395	16	3.3	246240	2	US-08-724-394A-20	Sequence 20, Appl	C 468	15	3.1	386	4	US-08-905-223-113	Sequence 113, Appl
396	16	3.3	246240	2	US-08-724-394A-21	Sequence 21, Appl	C 469	15	3.1	396	4	US-09-134-001C-1320	Sequence 1320, Appl
397	16	3.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	C 470	15	3.1	417	3	US-08-714-918-106	Sequence 106, Appl
398	15	3.1	21	2	US-08-740-215B-1	Sequence 1, Appl	C 471	15	3.1	417	4	US-09-265-315-106	Sequence 106, Appl
399	15	3.1	21	2	US-08-740-215B-4	Sequence 4, Appl	C 472	15	3.1	417	4	US-09-265-315-106	Sequence 106, Appl
400	15	3.1	21	2	US-08-740-215B-6	Sequence 6, Appl	C 473	15	3.1	417	4	US-09-266-417-106	Sequence 106, Appl
401	15	3.1	30	2	US-08-902-623B-6	Sequence 31, Appl	C 474	15	3.1	502	4	US-09-084-120-19	Sequence 19, Appl
402	15	3.1	30	2	US-08-902-623B-34	Sequence 34, Appl	C 475	15	3.1	503	4	US-09-370-838-165	Sequence 165, Appl
403	15	3.1	35	2	US-08-173-489C-19	Sequence 19, Appl	C 476	15	3.1	522	1	US-08-672-569-3	Sequence 3, Appl
404	15	3.1	35	2	US-08-701-124-44	Sequence 44, Appl	C 477	15	3.1	529	4	US-09-222-575-100	Sequence 100, Appl
405	15	3.1	39	2	US-08-701-124-45	Sequence 45, Appl	C 478	15	3.1	559	4	US-09-328-111-456	Sequence 111, Appl
406	15	3.1	39	2	US-08-130-225-44	Sequence 44, Appl	C 479	15	3.1	565	4	US-09-385-982-20	Sequence 20, Appl
407	15	3.1	39	3	US-09-130-225-45	Sequence 45, Appl	C 480	15	3.1	600	5	PCT-US93-1041B-1	Sequence 1, Appl
408	15	3.1	39	4	US-09-455-061-44	Sequence 44, Appl	C 481	15	3.1	629	4	US-09-328-111-395	Sequence 395, Appl
409	15	3.1	39	4	US-09-455-061-45	Sequence 45, Appl	C 482	15	3.1	670	4	US-09-040-984-7	Sequence 7, Appl
410	15	3.1	39	4	US-09-101-751A-68	Sequence 68, Appl	C 483	15	3.1	670	4	US-09-123-912-7	Sequence 7, Appl
411	15	3.1	39	4	US-09-101-751A-79	Sequence 79, Appl	C 484	15	3.1	670	4	US-09-643-597-7	Sequence 7, Appl
412	15	3.1	39	4	US-09-101-751A-80	Sequence 80, Appl	C 485	15	3.1	672	1	US-08-599-252-102	Sequence 102, Appl
413	15	3.1	42	4	US-09-101-751A-69	Sequence 69, Appl	C 486	15	3.1	672	5	PCT-US96-06352-102	Sequence 102, Appl
414	15	3.1	45	2	US-08-701-124-42	Sequence 42, Appl	C 487	15	3.1	672	5	PCT-US96-06583-102	Sequence 102, Appl
415	15	3.1	45	3	US-09-130-225-42	Sequence 42, Appl	C 488	15	3.1	764	4	US-08-858-207A-224	Sequence 224, Appl
416	15	3.1	45	4	US-09-455-061-42	Sequence 42, Appl	C 489	15	3.1	780	4	US-09-385-982-32	Sequence 32, Appl
417	15	3.1	45	4	US-09-101-751A-77	Sequence 77, Appl	C 490	15	3.1	807	2	US-08-531-927B-9	Sequence 9, Appl
418	15	3.1	52	4	US-09-208-966-28	Sequence 28, Appl	C 491	15	3.1	817	1	US-08-672-569-2	Sequence 2, Appl
419	15	3.1	57	4	US-09-101-751A-35	Sequence 35, Appl	C 492	15	3.1	859	4	US-09-535-008-58	Sequence 58, Appl
420	15	3.1	60	4	US-09-208-966-19	Sequence 19, Appl	C 493	15	3.1	937	3	US-08-860-368B-10	Sequence 10, Appl
421	15	3.1	63	5	PCT-US91-03680-8	Sequence 8, Appl	C 494	15	3.1	984	4	US-09-583-492-9	Sequence 9, Appl
422	15	3.1	71	4	US-09-254-968B-113	Sequence 113, Appl	C 495	15	3.1	984	4	US-08-642-274D-53	Sequence 53, Appl
423	15	3.1	86	4	US-09-101-751A-27	Sequence 27, Appl	C 496	15	3.1	988	4	US-08-952-014C-53	Sequence 53, Appl
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c 704	15	3.1	4699	1	US-08-487-890A-1	Sequence 1, Appli	c 777	15	3.1	8342	5	PCT-US94-04496-63	Sequence 63, Appli
c 705	15	3.1	4699	2	US-08-478-435-1	Sequence 1, Appli	c 778	15	3.1	8382	1	US-08-080-255-6	Sequence 6, Appli
c 706	15	3.1	4699	2	US-08-337-483-1	Sequence 1, Appli	c 779	15	3.1	8392	3	US-08-465-713-6	Sequence 6, Appli
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c 710	15	3.1	4699	4	US-08-897-438-1	Sequence 1, Appli	c 783	15	3.1	8494	4	US-08-961-527-163	Sequence 163, App
c 711	15	3.1	4699	4	US-08-637-654-1	Sequence 1, Appli	c 784	15	3.1	8722	4	US-09-221-017B-263	Sequence 263, App
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716	15	3.1	4757	4	US-08-374-219B-12	Sequence 12, Appli	c 789	15	3.1	9207	3	US-08-488-551B-800	Sequence 800, App
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c 722	15	3.1	5009	2	US-08-478-373-3	Sequence 3, Appli	795	15	3.1	10079	2	US-08-476-866-20	Sequence 20, Appli
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c 727	15	3.1	5009	4	US-08-649-518-3	Sequence 3, Appli	c 800	15	3.1	10825	3	US-08-652-265-7	Sequence 7, Appli
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c 746	15	3.1	5537	1	US-08-483-852-9	Sequence 9, Appli	c 819	15	3.1	11340	4	US-08-961-527-147	Sequence 147, App
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c 749	15	3.1	5537	1	US-08-187-453-32	Sequence 32, Appli	c 822	15	3.1	12146	4	US-09-277-457-27	Sequence 27, Appli
c 750	15	3.1	5537	1	US-08-562-985A-5	Sequence 5, Appli	823	15	3.1	12665	4	US-08-961-527-134	Sequence 134, App
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753	15	3.1	5599	2	US-08-477-451-13	Sequence 13, Appli	826	15	3.1	14747	4	US-09-608-285A-42	Sequence 42, Appli
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C 834	15	3.1	19736	4	US-09-740-035-3	Sequence 3, Appl	907	14	2.9	394	2	US-08-623-906A-7	Sequence 7, Appl
C 835	15	3.1	19932	2	US-08-477-451-25	Sequence 25, Appl	908	14	2.9	414	2	US-08-347-563A-22	Sequence 22, Appl
C 836	15	3.1	20598	4	US-09-593-995-10	Sequence 10, Appl	909	14	2.9	414	3	US-08-485-942A-22	Sequence 22, Appl
C 837	15	3.1	22481	4	US-08-367-841A-43	Sequence 43, Appl	910	14	2.9	414	3	US-08-488-214A-22	Sequence 22, Appl
C 838	15	3.1	22481	5	PCT-US95-07201-43	Sequence 43, Appl	911	14	2.9	414	3	US-08-488-208A-22	Sequence 22, Appl
C 839	15	3.1	22484	4	US-09-875-223-2	Sequence 2, Appl	912	14	2.9	414	4	US-08-483-211A-22	Sequence 22, Appl
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C 842	15	3.1	29629	4	US-09-729-995-3	Sequence 3, Appl	915	14	2.9	420	4	US-09-641-638-229	Sequence 229, App
C 843	15	3.1	31571	1	US-08-323-443B-1	Sequence 1, Appl	c 916	14	2.9	422	4	US-09-397-787-186	Sequence 186, App
C 844	15	3.1	32042	4	US-09-245-281-44	Sequence 44, Appl	917	14	2.9	427	4	US-09-556-877-46	Sequence 46, Appl
C 845	15	3.1	35060	3	US-08-814-095-7	Sequence 7, Appl	918	14	2.9	427	4	US-09-620-412C-46	Sequence 46, Appl
C 846	15	3.1	36741	4	US-09-301-665-3	Sequence 3, Appl	c 919	14	2.9	427	4	US-09-397-787-206	Sequence 206, App
C 847	15	3.1	40352	3	US-08-846-111D-15	Sequence 15, Appl	920	14	2.9	432	5	PCT-US94-00545-11	Sequence 11, Appl
C 848	15	3.1	40352	4	US-08-443-077-15	Sequence 15, Appl	c 921	14	2.9	443	4	US-09-397-787-194	Sequence 194, App
C 849	15	3.1	48974	4	US-08-920-422-17	Sequence 17, Appl	922	14	2.9	447	4	US-08-875-533-40	Sequence 40, Appl
C 850	15	3.1	49136	4	US-09-422-869-1	Sequence 1, Appl	923	14	2.9	447	4	US-08-875-533-48	Sequence 48, Appl
C 851	15	3.1	51259	3	US-08-781-891-209	Sequence 209, App	924	14	2.9	447	4	US-08-875-533-49	Sequence 49, Appl
C 852	15	3.1	53526	3	US-08-658-136-2	Sequence 2, Appl	925	14	2.9	447	4	US-08-875-533-50	Sequence 50, Appl
C 853	15	3.1	53577	3	US-08-658-136-1	Sequence 1, Appl	c 926	14	2.9	457	1	US-08-039-364-17	Sequence 17, Appl
C 854	15	3.1	81001	4	US-08-750-580-1	Sequence 1, Appl	c 927	14	2.9	457	4	US-09-158-710-17	Sequence 17, Appl
C 855	15	3.1	98844	4	US-08-791-211-10	Sequence 10, Appl	928	14	2.9	459	4	US-08-875-533-58	Sequence 58, Appl
C 856	15	3.1	112132	4	US-09-741-150-3	Sequence 3, Appl	929	14	2.9	465	3	US-08-469-318-180	Sequence 180, App
C 857	14	2.9	20	1	US-08-418-859-22	Sequence 22, Appl	930	14	2.9	465	3	US-08-468-609A-180	Sequence 180, App
C 858	14	2.9	20	2	US-08-643-181-22	Sequence 22, Appl	931	14	2.9	465	3	US-08-471-045-54	Sequence 54, Appl
C 859	14	2.9	21	4	US-08-943-731-328	Sequence 328, App	932	14	2.9	465	3	US-08-469-712A-54	Sequence 54, Appl
C 860	14	2.9	23	3	US-08-975-688A-12	Sequence 12, Appl	933	14	2.9	465	4	US-08-446-871-54	Sequence 54, Appl
C 861	14	2.9	23	4	US-09-417-090-12	Sequence 12, Appl	934	14	2.9	465	4	US-08-446-872A-180	Sequence 180, App
C 862	14	2.9	23	4	US-09-727-578-12	Sequence 12, Appl	935	14	2.9	465	4	US-08-468-910-54	Sequence 54, Appl
C 863	14	2.9	25	1	US-08-469-005A-8	Sequence 8, Appl	936	14	2.9	465	4	US-08-761-907-54	Sequence 54, Appl
C 864	14	2.9	33	1	US-08-591-070A-24	Sequence 24, Appl	937	14	2.9	465	4	US-08-762-227A-180	Sequence 180, App
C 865	14	2.9	33	2	US-08-927-855-24	Sequence 24, Appl	938	14	2.9	465	5	PCT-US95-01185-180	Sequence 180, App
C 866	14	2.9	33	3	US-08-768-859A-3	Sequence 3, Appl	939	14	2.9	465	6	5496550-9	Patent No. 5496550
C 867	14	2.9	33	3	US-08-767-820A-3	Sequence 3, Appl	940	14	2.9	466	6	5496550-7	Patent No. 5496550
C 868	14	2.9	33	3	US-08-622-046B-9	Sequence 9, Appl	c 941	14	2.9	471	4	US-08-875-533-55	Sequence 55, Appl
C 869	14	2.9	33	5	PCT-US95-06157-3	Sequence 3, Appl	c 942	14	2.9	471	4	US-09-134-001C-395	Sequence 395, App
C 870	14	2.9	53	4	US-09-275-850-289	Sequence 289, App	943	14	2.9	474	4	US-08-875-533-56	Sequence 56, Appl
C 871	14	2.9	60	4	US-09-101-751A-33	Sequence 33, Appl	c 944	14	2.9	490	3	US-09-042-426-2	Sequence 2, Appl
C 872	14	2.9	82	1	US-08-477-530-24	Sequence 24, Appl	c 945	14	2.9	490	4	US-09-231-238-2	Sequence 2, Appl
C 873	14	2.9	82	1	US-08-477-530-24	Sequence 24, Appl	c 946	14	2.9	490	4	US-09-330-760-2	Sequence 2, Appl
C 874	14	2.9	82	1	US-08-477-830-24	Sequence 24, Appl	c 947	14	2.9	490	4	US-09-328-473-2	Sequence 2, Appl
C 875	14	2.9	87	2	US-08-631-751A-4	Sequence 4, Appl	c 948	14	2.9	490	4	US-09-330-737-2	Sequence 2, Appl
C 876	14	2.9	100	1	US-08-145-705A-5	Sequence 5, Appl	c 949	14	2.9	490	4	US-09-329-169-2	Sequence 2, Appl
C 877	14	2.9	130	2	US-08-631-751A-1	Sequence 1, Appl	c 950	14	2.9	490	4	US-09-330-714B-2	Sequence 2, Appl
C 878	14	2.9	137	4	US-08-991-789A-68	Sequence 68, Appl	c 951	14	2.9	490	4	US-09-328-826-2	Sequence 2, Appl
C 879	14	2.9	137	4	US-09-062-451-68	Sequence 68, Appl	952	14	2.9	492	5	PCT-US95-08295-9	Sequence 9, Appl
C 880	14	2.9	137	4	US-09-598-326-68	Sequence 68, Appl	953	14	2.9	494	4	US-09-040-984-54	Sequence 54, Appl
C 881	14	2.9	231	4	US-09-605-990-5	Sequence 5, Appl	954	14	2.9	494	4	US-09-123-912-54	Sequence 54, Appl
C 882	14	2.9	231	4	US-09-420-797B-5	Sequence 5, Appl	955	14	2.9	494	4	US-09-643-597-54	Sequence 54, Appl
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C 884	14	2.9	240	1	US-08-222-177A-9	Sequence 9, Appl	957	14	2.9	513	4	US-08-642-274D-48	Sequence 48, Appl
C 885	14	2.9	270	4	US-09-530-378A-8	Sequence 8, Appl	c 958	14	2.9	513	4	US-08-642-274D-48	Sequence 48, Appl
C 886	14	2.9	270	4	US-09-404-879A-130	Sequence 130, App	959	14	2.9	513	4	US-08-952-014C-48	Sequence 48, Appl
C 887	14	2.9	272	4	US-09-071-035-439	Sequence 439, App	c 960	14	2.9	513	4	US-08-952-014C-48	Sequence 48, Appl
C 888	14	2.9	279	3	US-08-952-670-5	Sequence 5, Appl	961	14	2.9	513	4	US-09-288-143-31	Sequence 31, Appl
C 889	14	2.9	281	4	US-09-488-295-10	Sequence 10, Appl	c 962	14	2.9	516	4	US-09-134-001C-729	Sequence 729, App
C 890	14	2.9	301	4	US-08-605-785-234	Sequence 234, App	963	14	2.9	532	4	US-09-404-879A-24	Sequence 24, Appl
C 891	14	2.9	301	4	US-09-439-313-234	Sequence 234, App	c 964	14	2.9	532	4	US-09-280-116-137	Sequence 137, App
C 892	14	2.9	301	4	US-09-352-616A-234	Sequence 234, App	965	14	2.9	536	4	US-09-385-982-347	Sequence 347, App
C 893	14	2.9	301	4	US-08-232-149A-234	Sequence 234, App	c 966	14	2.9	541	4	US-09-227-357-23	Sequence 23, Appl
C 894	14	2.9	312	4	US-09-526-935B-9	Sequence 9, Appl	967	14	2.9	544	4	US-09-221-017B-303	Sequence 303, App
C 895	14	2.9	313	1	US-08-365-981-5	Sequence 6, Appl	968	14	2.9	545	4	US-09-397-212-4	Sequence 4, Appl
C 896	14	2.9	321	4	US-08-385-982-366	Sequence 366, App	c 969	14	2.9	545	4	US-09-948-802-4	Sequence 4, Appl
C 897	14	2.9	333	1	US-08-594-031-57	Sequence 57, Appl	c 970	14	2.9	546	4	US-08-729-601A-84	Sequence 84, Appl
C 898	14	2.9	340	4	US-09-006-353A-17	Sequence 17, Appl	971	14	2.9	549	4	US-09-522-433B-19	Sequence 19, Appl
C 899	14	2.9	340	4	US-09-573-986-17	Sequence 17, Appl	c 972	14	2.9	573	4	US-08-906-156A-67	Sequence 67, Appl
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C 902	14	2.9	372	4	US-09-018-584A-15	Sequence 15, Appl	c 975	14	2.9	599	4	US-09-385-982-74	Sequence 74, Appl
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783 14 2.9 606 4 US-08-247-946A-5  
784 14 2.9 615 1 US-08-247-946A-5  
785 14 2.9 615 5 PCT-US95-06420-5  
786 14 2.9 621 4 US-09-643-597-209  
787 14 2.9 622 4 US-09-385-982-46  
788 14 2.9 624 1 US-07-782-113B-1  
789 14 2.9 624 4 US-09-181-974-1  
790 14 2.9 624 4 US-09-518-950-1  
791 14 2.9 625 4 US-09-328-111-507  
792 14 2.9 627 3 US-08-718-904-99  
793 14 2.9 628 4 US-09-385-982-383  
794 14 2.9 634 4 US-08-642-274D-26  
795 14 2.9 634 4 US-08-952-014C-26  
796 14 2.9 663 4 US-09-134-001C-2236  
797 14 2.9 674 4 US-09-129-030-23  
798 14 2.9 675 4 US-08-134-001C-2605  
799 14 2.9 692 1 US-08-592-126-123  
800 14 2.9 697 4 US-09-488-295-3  
801 14 2.9 703 4 US-09-071-035-339

ALIGNMENTS

RESULT 1  
US-08-909-965C-1  
; Sequence 1, Application US/08909965C  
; Patent No. 5936078  
; GENERAL INFORMATION:  
; APPLICANT: Kuga Tetsuo  
; APPLICANT: Nakagawa Satoshi  
; APPLICANT: Sakaki Yoshiyuki  
; APPLICANT: Zhao Nanding  
; APPLICANT: Hashida Hideji  
; TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE  
; TITLE OF INVENTION: AND NOVEL ANTIBODY  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO  
; STREET: 277 Park Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10172-0194  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/909,965C  
; FILING DATE: August 12, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 322745/95  
; APPLICATION NUMBER: PCT/J96/03630  
; FILING DATE: 12-Dec-1996  
; FILING DATE: 12-Dec-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lawrence S. Perry  
; REGISTRATION NUMBER: 31865  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-2400  
; TELEFAX: 212-758-2982  
; TELEX: 236262  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2688 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: human  
; IMMEDIATE SOURCE:  
; CLONE: F55  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 358 to 486  
; LOCATION: 560 to 799  
; LOCATION: 1042 to 1182  
; LOCATION: 2105 to 2269  
; LOCATION: 2370 to 2462  
; IDENTIFICATION METHOD: by experiment  
; US-08-909-965C-1  
Query Match 6.8%; Score 33; DB 2; Length 2688;  
Best Local Similarity 100.0%; Pred. No. 4.2e-07;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GATTGAGATGTGAGCCACCGTGCCTGGCCAGA 34  
Db 286 GATTGAGATGTGAGCCACCGTGCCTGGCCAGA 318  
RESULT 2  
US-09-128-155-17/c  
; Sequence 17, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 176373  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(176373)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-17  
Query Match 5.6%; Score 27; DB 3; Length 176373;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAG 33  
Db 168918 CAGATGTGAGCCACCGTGCCTGGCCAG 168892  
RESULT 3  
US-09-605-785-571/c  
; Sequence 571, Application US/09605785  
; Patent No. 6321716  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C16  
; CURRENT APPLICATION NUMBER: US/09/605,785  
; CURRENT FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 835  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 571  
; LENGTH: 819  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-605-785-571

Query Match 5.1%; Score 25; DB 4; Length 819;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31  
Db 481 CAGATGTGAGCCACCGTGGCC 457

RESULT 4  
US-09-738-894A-3/c  
; Sequence 3, Application US/09738894A  
; Patent No. 6331423  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL000636  
; CURRENT APPLICATION NUMBER: US/09/738,894A  
; CURRENT FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 36651  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(36651)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-738-894A-3

Query Match 5.1%; Score 25; DB 4; Length 36651;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31  
Db 29888 CAGATGTGAGCCACCGTGGCC 29864

RESULT 5  
US-08-482-918-43/c  
; Sequence 43, Application US/08482918  
; Patent No. 6207417  
; GENERAL INFORMATION:  
; APPLICANT: Zsebo, Krisztina M.

; APPLICANT: Bosselman, Robert A.  
; APPLICANT: Suggs, Sidney V.  
; APPLICANT: Martin, Francis H.  
; TITLE OF INVENTION: Stem Cell Factor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/482,918  
; APPLICATION NUMBER: US/08/482,918  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 01017/33005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3807 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Join(905..1018, 1914..1976, 2572..2742, 3152  
; LOCATION: ..3307, 3513..3595)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: Join(965..1018, 1914..1976, 2572..2742, 3152  
; LOCATION: ..3307, 3513..3595)  
US-08-482-918-43  
Query Match 4.7%; Score 23; DB 4; Length 3807;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 CCACCGTGCCTGGCCAGATTTT 39  
Db 2292 CCACCGTGCCTGGCCAGATTTT 2270  
RESULT 6  
US-09-224-681-43/c  
; Sequence 43, Application US/09224681  
; Patent No. 6207454  
; GENERAL INFORMATION:  
; APPLICANT: Zsebo, Krisztina M.  
; APPLICANT: Bosselman, Robert A.  
; APPLICANT: Suggs, Sidney V.  
; APPLICANT: Martin, Francis H.  
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene  
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America

ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/224,681  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/005,893  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/449,653  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/35199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3807 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152  
LOCATION: ..3307, 3513..3595)  
NAME/KEY: mat peptide  
LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152  
LOCATION: ..3307, 3513..3595)  
US-09-224-681-43

Query Match 4.7%; Score 23; DB 4; Length 3807;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CCACCGTGCCTGGCCAGATTTT 39  
Db 2292 CCACCGTGCCTGGCCAGATTTT 2270

## RESULT 7

US-08-336-728A-43/c  
; Sequence 43, Application US/08336728A  
; Patent No. 6207802  
; GENERAL INFORMATION:  
; APPLICANT: Zeebo, Krisztina M.

APPLICANT: Bosselman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,728A  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/32956  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3807 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152  
LOCATION: ..3307, 3512..3597)  
NAME/KEY: mat peptide  
LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152  
LOCATION: ..3307, 3512..3597)  
US-08-336-728A-43

Query Match 4.7%; Score 23; DB 4; Length 3807;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CCACCGTGCCTGGCCAGATTTT 39  
Db 2292 CCACCGTGCCTGGCCAGATTTT 2270

## RESULT 8

US-08-482-918-47/c  
; Sequence 47, Application US/08482918



## RESULT 10

US-08-336-728A-47/c  
; Sequence 47, Application US/08336728A  
; Patent No. 6207802  
; GENERAL INFORMATION:  
; APPLICANT: Zsebo, Krisztina M.  
; APPLICANT: Bosselman, Robert A.  
; APPLICANT: Sugrue, Sidney V.  
; APPLICANT: Martin, Francis H.  
; TITLE OF INVENTION: Stem Cell Factor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/336,728A  
; FILING DATE: 09-NOV-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/982,255  
; FILING DATE: 25-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/589,701  
; FILING DATE: 01-OCT-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/573,616  
; FILING DATE: 24-AUG-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/537,198  
; FILING DATE: 11-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/422,383  
; FILING DATE: 16-OCT-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 01017/32956  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5864 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521,  
; LOCATION: 3932..4088, 4314..4397, 4778..4887, 5208..5275,  
; LOCATION: 5677..5713)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932  
; LOCATION: ..4088, 4314..4397, 4778..4887, 5208..5275, 5677  
; LOCATION: ..5713)  
US-08-336-728A-47

Query Match 4.7%; Score 23; DB 4; Length 5864;  
Best Local Similarity 100.0%; Pred.No. 0.038;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 17

CCACCGTGCTGGCCAGATTTT 39  
|||||  
Db 3071 CCACCGTGCTGGCCAGATTTT 3049

## RESULT 11

US-09-813-133A-3/c  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-3

Query Match 4.7%; Score 23; DB 4; Length 55827;  
Best Local Similarity 100.0%; Pred.No. 0.043;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 11

TGTGAGCCACCGTGCTGGCCAG 33  
|||||  
Db 10867 TGTGAGCCACCGTGCTGGCCAG 10845

## RESULT 12

US-09-750-580-1  
; Sequence 1, Application US/09750580  
; Patent No. 6455280  
; GENERAL INFORMATION:  
; APPLICANT: Yen, Frances  
; APPLICANT: Denison, Blake  
; APPLICANT: Bour, Barbara  
; APPLICANT: Bihain, Bernard  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Ebbets-Reed, Dana  
; APPLICANT: Salter-Cid, Luisa  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH  
; FILE REFERENCE: 89 US2.CIP  
; CURRENT APPLICATION NUMBER: US/09/750,580  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 09/599,362  
; PRIOR FILING DATE: 2000-06-21  
; PRIOR APPLICATION NUMBER: PCT/IB00/0101  
; PRIOR FILING DATE: 2000-06-21  
; PRIOR APPLICATION NUMBER: PCT/IB99/02058  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 49/469/099  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: US 60/113,686  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: US 60/141,032  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1  
; LENGTH: 81001  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature



LOCATION: 10946..12946  
; OTHER INFORMATION: 5'regulatory region  
; NAME/KEY: exon  
LOCATION: 12947..12958  
; OTHER INFORMATION: exon 1  
; NAME/KEY: exon  
LOCATION: 13470..13526  
; OTHER INFORMATION: exon 2  
; NAME/KEY: exon  
LOCATION: 13641..13752  
; OTHER INFORMATION: exon 3  
; NAME/KEY: exon  
LOCATION: 14271..15968  
; OTHER INFORMATION: exon 4  
; NAME/KEY: misc feature  
LOCATION: 15969..17969  
; OTHER INFORMATION: 3'regulatory region  
; NAME/KEY: allele  
LOCATION: 1239  
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T  
; NAME/KEY: allele  
LOCATION: 12347  
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T  
; NAME/KEY: allele  
LOCATION: 15241  
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T  
; NAME/KEY: allele  
LOCATION: 42218  
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G  
; NAME/KEY: allele  
LOCATION: 45442  
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G  
; NAME/KEY: allele  
LOCATION: 77058  
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T  
; NAME/KEY: primer\_bind  
LOCATION: 929..949  
; OTHER INFORMATION: 20-828.pu  
; NAME/KEY: primer\_bind  
LOCATION: 1357..1377  
; OTHER INFORMATION: 20-828.rp complement  
; NAME/KEY: primer\_bind  
LOCATION: 12029..12050  
; OTHER INFORMATION: 17-42.pu  
; NAME/KEY: primer\_bind  
LOCATION: 12581..12603  
; OTHER INFORMATION: 17-42.rp complement  
; NAME/KEY: primer\_bind  
LOCATION: 14992..15012  
; OTHER INFORMATION: 17-41.pu  
; NAME/KEY: primer\_bind  
LOCATION: 15460..15482  
; OTHER INFORMATION: 17-41.rp complement  
; NAME/KEY: primer\_bind  
LOCATION: 42070..42090  
; OTHER INFORMATION: 20-841.pu  
; NAME/KEY: primer\_bind  
LOCATION: 42572..42591  
; OTHER INFORMATION: 20-841.rp complement  
; NAME/KEY: primer\_bind  
LOCATION: 45328..45347  
; OTHER INFORMATION: 20-842.pu  
; NAME/KEY: primer\_bind  
LOCATION: 45863..45883  
; OTHER INFORMATION: 20-842.rp complement  
; NAME/KEY: primer\_bind  
LOCATION: 76644..76664  
; OTHER INFORMATION: 20-853.pu  
; NAME/KEY: primer\_bind  
LOCATION: 77166..77185  
; OTHER INFORMATION: 20-853.rp complement  
; NAME/KEY: primer\_bind  
LOCATION: 1220..1238

; OTHER INFORMATION: 20-828-311.mis  
; NAME/KEY: primer\_bind  
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US-09-750-580-1

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Qy 12 GTGAGCCACCGTCGCTGCCAGCA 34  
Db 30139 GTGAGCCACCGTCGCTGCCAGCA 30161

## RESULT 13

US-09-092-508-1  
; Sequence 1, Application US/09092508  
; Patent No. 6291643  
; GENERAL INFORMATION:  
; APPLICANT: Henzel, William J.  
; TITLE OF INVENTION: APAP-1, AN ACTIVATOR OF C ASPASE-3  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

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STREET: 3100 No. 6291643west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092.508
FILING DATE: 05-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,807
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: 60/055,258
FILING DATE: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11669.6USU1
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7042 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 578...4159
OTHER INFORMATION:
US-09-092-508-1

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Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGGCCGAG 33
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; Sequence 1, Application US/09435115
; Patent No. 6346607
; GENERAL INFORMATION:
; APPLICANT: Henzel, William J.
; TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6346607west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/435,115
; FILING DATE:
; CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/092,508
FILING DATE:
APPLICATION NUMBER: 60/055,258
FILING DATE: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11669.6USU1
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7042 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 578...4159
OTHER INFORMATION:
US-09-435-115-1

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Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGGCCGAG 33
Db 5007 GTGAGCCACCGTGGCCGAG 5028

RESULT 15
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; Sequence 1, Application US/09098310
; Patent No. 6403765
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF USE
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 480140.438
; CURRENT APPLICATION NUMBER: US/09/098,310
; CURRENT FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7042
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (578)...(4159)
US-09-098-310-1

Query Match 4.5%; Score 22; DB 4; Length 7042;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGGCCGAG 33
Db 5007 GTGAGCCACCGTGGCCGAG 5028

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	26	5.3	29449	9	Sequence 161, App
6	26	5.3	29449	9	Sequence 73, Appl
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537	22	4.5	14040	9	US-09-764-891-10205	Sequence 10205, A	610	21	4.3	4407	9	US-10-180-557-351	Sequence 351, App
538	22	4.5	20444	9	US-09-764-891-9422	Sequence 9422, Ap	611	21	4.3	4407	9	US-10-173-700-351	Sequence 351, App
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893	21	4.3	4407	9	US-10-198-767-351	Sequence 351, App	966	21	4.3	4407	9	US-10-201-323-351	Sequence 351, App
894	21	4.3	4407	9	US-10-199-307-351	Sequence 351, App	967	21	4.3	4407	9	US-10-205-510-351	Sequence 351, App
895	21	4.3	4407	9	US-10-199-307-351	Sequence 351, App	968	21	4.3	4407	9	US-10-205-891-351	Sequence 351, App

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969 21 4.3 4407 9 US-10-205-904-351 Sequence 351, App
970 21 4.3 4407 9 US-10-206-917-351 Sequence 351, App
971 21 4.3 4407 9 US-10-207-923-351 Sequence 351, App
972 21 4.3 4407 9 US-10-207-924-351 Sequence 351, App
973 21 4.3 4407 9 US-10-208-028-351 Sequence 351, App
974 21 4.3 4407 9 US-10-121-062-351 Sequence 351, App
975 21 4.3 4407 9 US-10-175-753-351 Sequence 351, App
976 21 4.3 4407 9 US-10-180-553-351 Sequence 351, App
977 21 4.3 4407 9 US-10-201-327-351 Sequence 351, App
978 21 4.3 4407 9 US-10-006-116A-316 Sequence 316, App
979 21 4.3 4407 9 US-10-006-117A-316 Sequence 316, App
980 21 4.3 4407 9 US-10-013-913A-316 Sequence 316, App
981 21 4.3 4407 9 US-10-017-527A-316 Sequence 351, App
982 21 4.3 4407 9 US-10-173-696-351 Sequence 351, App
983 21 4.3 4407 9 US-10-183-003-351 Sequence 351, App
984 21 4.3 4407 9 US-10-183-016-351 Sequence 351, App
985 21 4.3 4407 9 US-10-125-923A-351 Sequence 351, App
986 21 4.3 4407 9 US-10-176-491-351 Sequence 351, App
987 21 4.3 4407 9 US-10-176-979-351 Sequence 351, App
988 21 4.3 4407 9 US-10-187-592-351 Sequence 351, App
989 21 4.3 4407 9 US-10-007-194A-316 Sequence 316, App
990 21 4.3 4407 9 US-10-013-430A-316 Sequence 351, App
991 21 4.3 4407 9 US-10-197-691-351 Sequence 351, App
992 21 4.3 4407 9 US-10-198-771-351 Sequence 351, App
993 21 4.3 4407 9 US-10-011-671A-316 Sequence 316, App
994 21 4.3 4407 9 US-10-012-755A-316 Sequence 351, App
995 21 4.3 4407 9 US-10-174-575A-351 Sequence 351, App
996 21 4.3 4407 9 US-10-179-520-351 Sequence 351, App
997 21 4.3 4407 9 US-10-201-325-351 Sequence 351, App
998 21 4.3 4407 9 US-10-202-941-351 Sequence 351, App
999 21 4.3 4407 9 US-10-205-910-351 Sequence 351, App
1000 21 4.3 4407 9 US-10-015-386A-316 Sequence 316, App
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## ALIGNMENTS

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RESULT 1
US-09-918-995-27892
; Sequence 27892, Application US/09918995
; Publication No.: US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27892
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(470)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27892

Query Match 31.1%; Score 151; DB 9; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.8e-68;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 336 CCCTTCCTCCTGAGTGGGGCTGAGGCCAGAGTCACCTTTCTGTGGCTGGCTCTACCTTCC 395
|
|
|
Db 73 CCCTTCCTCCTGAGTGGGGCTGAGGCCAGAGTCACCTTTCTGTGGCTGGCTCTACCTTCC 132
|
|
|
Qy 396 TGTCCTCCTGAGTTAAACGGTGCCCATCTGCGCATCTCAACACGACAGAGGAGCTTTCTG 455
|
|
|
Db 133 TGTCCTCCTGAGTTAAACGGTGCCCATCTGCGCATCTCAACACGACAGAGGAGCTTTCTG 192
|
|
|
```

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Qy 456 GAATTTCAACACCATTCCTCTTACTGCCAAGC 486
|
|
|
Db 193 GAATTTCAACACCATTCCTCTTACTGCCAAGC 223
|
|
|
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## RESULT 2

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US-10-095-407-17/c
; Sequence 17, Application US/10095407
; Patent No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17
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Query Match 5.6%; Score 27; DB 9; Length 176373;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 7 CAGATGTGAGCCACCGTGGCTGGCCAG 33
|
|
|
Db 168918 CAGATGTGAGCCACCGTGGCTGGCCAG 168892
|
|
|
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## RESULT 3

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US-09-867-701-8144
; Sequence 8144, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8144
; LENGTH: 251
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8144
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Query Match 5.3%; Score 26; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 13 TGAGCCACCGTGGCTGGCCAGATTTT 38
|
|
|
Db 137 TGAGCCACCGTGGCTGGCCAGATTTT 162
|
|
|
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## RESULT 4

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US-09-867-701-7923
; Sequence 7923, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7923
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7923

Query Match      5.3%; Score 26; DB 10; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TGAGCCACCGTGGCTGCGCCAGATTTT 38
Db      137 TGAGCCACCGTGGCTGCGCCAGATTTT 162

RESULT 5
US-09-989-442-161/c
; Sequence 161, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
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; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
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; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
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; PRIOR FILING DATE: 2000-11-17  
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; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,080  
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; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/233,063  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,397  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065  
; PRIOR FILING DATE: 2000-09-14

Query Match 5.3%; Score 26; DB 9; Length 29449;

Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGTGAGCCACCGTGCCTGGCCAGATT 36  
|||||

Db 20953 TGTGAGCCACCGTGCCTGGCCAGATT 20928  
|||||

#### RESULT 6

US-10-074-045-73  
; Sequence 73, Application US/10074045  
; Publication No. US20030092102A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT221C1  
; CURRENT APPLICATION NUMBER: US/10/074,045  
; CURRENT FILING DATE: 2002-02-14  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 29449  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-074-045-73

Query Match 5.3%; Score 26; DB 9; Length 29449;

Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGTGAGCCACCGTGCCTGGCCAGATT 36  
|||||

Db 8497 TGTGAGCCACCGTGCCTGGCCAGATT 8522  
|||||

#### RESULT 7

US-10-012-896-571/c  
; Sequence 571, Application US/10012896  
; Publication No. US20020183251A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.

```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-571

Query Match      5.1%; Score 25; DB 9; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGGCC 31
Db      481 CAGATGTGAGCCACCGTGGCC 457

RESULT 8
US-09-895-793-571/c
; Sequence 571, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895, 814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-571

Query Match      5.1%; Score 25; DB 9; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGGCC 31
Db      481 CAGATGTGAGCCACCGTGGCC 457

RESULT 9
US-09-895-814-571/c
; Sequence 571, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895, 814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-571

Query Match      5.1%; Score 25; DB 9; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGGCC 31
Db      481 CAGATGTGAGCCACCGTGGCC 457

RESULT 10
US-09-759-143-571/c
; Sequence 571, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun

```

```
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-571

Query Match          5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
      |||||||||||||||||||||||||||
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 11
US-09-780-669-571/c
; Sequence 571, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurlal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-571

Query Match          5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
      |||||||||||||||||||||||||||
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 12
US-09-822-827-571/c
; Sequence 571, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-571

Query Match          5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
      |||||||||||||||||||||||||||
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 13
US-10-012-896-881/c
; Sequence 881, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinala de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeline Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-881

Query Match          5.1%; Score 25; DB 9; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
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; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-571

Query Match          5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
      |||||||||||||||||||||||||||
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 11
US-09-780-669-571/c
; Sequence 571, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurlal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-571

Query Match          5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
      |||||||||||||||||||||||||||
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 12
US-09-822-827-571/c
; Sequence 571, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-571

Query Match          5.1%; Score 25; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
      |||||||||||||||||||||||||||
Db      481 CAGATGTGAGCCACCGTGCCTGGCC 457

RESULT 13
US-10-012-896-881/c
; Sequence 881, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinala de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeline Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-881

Query Match          5.1%; Score 25; DB 9; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CAGATGTGAGCCACCGTGCCTGGCC 31
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Db 481 CAGATGTGAGCCACCGTGGCC 457

## RESULT 14

US-10-012-896-882/c

; Sequence 882, Application US/10012896

; Publication No. US20020183251A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; APPLICANT: Wantanabe, Yoshihiro

; APPLICANT: Meagher, Madeleine Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C27

; CURRENT APPLICATION NUMBER: US/10/012.896

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 1011

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 882

; LENGTH: 2455

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-896-882

Query Match 5.1%; Score 25; DB 9; Length 2455;  
Best Local Similarity 100.0%; Pred. No. 0.0057;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31

Db 481 CAGATGTGAGCCACCGTGGCC 457

## RESULT 15

US-09-895-793-881/c

; Sequence 881, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C2  
; CURRENT APPLICATION NUMBER: US/09/895,793  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 881  
; LENGTH: 2455  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-895-793-881

Query Match 5.1%; Score 25; DB 9; Length 2455;  
Best Local Similarity 100.0%; Pred. No. 0.0057;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGGCC 31

Db 481 CAGATGTGAGCCACCGTGGCC 457

Search completed: June 17, 2003, 09:59:34  
Job time : 57.3786 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 552.273 Seconds  
(without alignments)

14252.028 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_7148\_7633

Perfect score: 486

Sequence: 1 agattgcagatgtgagccac.....cattgtctttagtcccaagc 486

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vrt: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rod: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	240	49.4	294	13	BI061867
4	239	49.2	331	12	BF819430
5	200	41.2	713	13	BI226587
6	155	31.9	319	14	BQ345812

c	7	87	17.9	204	12	BF934192
	8	64	13.2	306	12	BF947854
	9	64	13.2	435	14	T65465
	10	46	9.5	302	14	F11822
	11	28	5.8	362	9	AI684794
	12	28	5.8	399	9	AA651660
	13	28	5.8	499	10	AW974922
	14	27	5.6	344	12	BE826708
	15	27	5.6	350	17	AQ043261
	16	27	5.6	364	12	BE826581
	17	27	5.6	508	17	AQ319687
	18	27	5.6	527	17	AQ723378
	19	27	5.6	541	10	BE014383
	20	26	5.3	251	9	AA847103
	21	26	5.3	351	17	AQ008494
	22	26	5.3	371	9	AA837683
	23	26	5.3	426	10	AW265498
	24	26	5.3	484	13	EG977956
	25	26	5.3	466	17	B33966
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	27	26	5.3	486	17	AQ384959
	28	26	5.3	489	17	AQ193515
	29	26	5.3	520	17	AQ473430
	30	26	5.3	554	9	AA682840
	31	26	5.3	562	17	AQ892343
	32	26	5.3	641	10	AW979242
	33	26	5.3	647	17	AG049716
	34	26	5.3	662	17	AG065702
	35	26	5.3	899	14	BQ216612
	36	26	5.3	931	12	EG104754
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	39	25	5.1	286	13	BI010653
	40	25	5.1	321	10	AW326884
	41	25	5.1	342	17	B80341
	42	25	5.1	346	10	BF072026
	43	25	5.1	361	12	BF858962
	44	25	5.1	396	9	AA626829
	45	25	5.1	412	17	AQ593490
	46	25	5.1	437	17	AG075803
	47	25	5.1	440	12	BG230544
	48	25	5.1	451	17	AQ476459
	49	25	5.1	466	17	AQ695146
	50	25	5.1	527	17	AQ494356
	51	25	5.1	531	17	AQ210269
	52	25	5.1	563	17	AQ382242
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	54	25	5.1	604	14	BQ777619
	55	25	5.1	659	17	AG119978
	56	25	5.1	718	17	AG000721
	57	25	5.1	757	17	AG000135
	58	25	5.1	758	17	AG000136
	59	25	5.1	775	17	AG000154
	60	25	5.1	776	17	AG000153
	61	24	4.9	180	17	AQ383311
	62	24	4.9	320	17	AQ081806
	63	24	4.9	425	9	AI037914
	64	24	4.9	447	17	AQ134180
	65	24	4.9	452	14	T67519
	66	24	4.9	474	17	BI242335
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	68	24	4.9	498	10	AW996821
	69	24	4.9	505	10	AV707864
	70	24	4.9	525	17	AQ485774
	71	24	4.9	533	17	AQ511433
	72	24	4.9	545	17	AQ666891
	73	24	4.9	579	17	AQ576617
	74	24	4.9	614	17	AZ055831
	75	24	4.9	654	17	BM991838
	76	24	4.9	657	17	AG039054
	77	24	4.9	683	17	AG160445
	78	24	4.9	945	17	AQ690721
	79	23	4.7	195	17	AQ554471

c	80	23	4.7	199	13	BI039464	BI039464 IL3-NT028	153	23	4.7	628	17	AG165879	AG165879 Pan trogl
	81	23	4.7	253	12	BF736236	BF736236 PM4-KT000	154	23	4.7	629	17	AG020807	AG020807 Pan trogl
	82	23	4.7	260	12	BF795628	BF795628 602260315	c 155	23	4.7	630	14	BM928802	BM928802 UI-H-DT0-
	83	23	4.7	271	12	BF795628	BF795628 602260315	c 156	23	4.7	631	10	BM636885	BM636885 CIT-HSP-2
	84	23	4.7	271	14	H27289	H27289 y116f01.s1	c 157	23	4.7	632	17	AQ012852	AQ012852 CIT-HSP-2
	85	23	4.7	273	17	AQ633853	AQ633853 RPI-11-4	c 158	23	4.7	633	10	BB217077	BB217077 Pan trogl
	86	23	4.7	273	10	BE505213	BE505213 dcl9c12.x	c 159	23	4.7	634	10	BB217077	BB217077 Pan trogl
	87	23	4.7	279	10	BE505213	BE505213 dcl9c12.x	c 160	23	4.7	635	17	AZ361301	AZ361301 IM0104L24
	88	23	4.7	296	9	AA889097	AA889097 am38g07.s	c 161	23	4.7	636	17	AA126814	AA126814 zn87c10.r
	89	23	4.7	298	9	AA434120	AA434120 zw24d02.s	c 162	23	4.7	637	17	AQ055741	AQ055741 CIT-HSP-2
	90	23	4.7	330	9	AA455282	AA455282 zx80b09.s	c 163	23	4.7	638	17	AQ069900	AQ069900 Pan trogl
	91	23	4.7	330	10	AA8556425	AA8556425 PM0-CT028	c 164	23	4.7	639	17	AQ071009	AQ071009 CITBI-E1-
	92	23	4.7	335	10	AV688511	AV688511 AV688511	c 165	23	4.7	640	17	AG131706	AG131706 Pan trogl
	93	23	4.7	354	10	AW078821	AW078821 xag9h09.x	c 166	23	4.7	641	17	AG096721	AG096721 Pan trogl
	94	23	4.7	355	10	AW511507	AW511507 xus7a01.x	c 167	23	4.7	642	12	EG481182	EG481182 602528502
	95	23	4.7	359	14	H39839	H39839 ypo1f12.s1	c 168	23	4.7	643	12	EG480433	EG480433 602529652
	96	23	4.7	363	10	AW390284	AW390284 CM2-ST018	c 169	23	4.7	644	17	AG111647	AG111647 Pan trogl
	97	23	4.7	366	9	A1347665	A1347665 qp01c06.x	c 170	23	4.7	645	12	EG209884	EG209884 RST29412
	98	23	4.7	373	17	AQ521750	AQ521750 HS 5239.A	c 171	23	4.7	646	12	BF107316	BF107316 601823721
	99	23	4.7	376	9	AA644223	AA644223 ab63e10.s	c 172	23	4.7	647	12	BF674925	BF674925 602138003
	100	23	4.7	381	9	A1581433	A1581433 to71h07.x	c 173	23	4.7	648	12	AA195059	AA195059 zt35e11.s
	101	23	4.7	381	9	AA581498	AA581498 nd8f02.s	c 174	23	4.7	649	12	EG702736	EG702736 602684289
	102	23	4.7	382	17	AQ0207950	AQ0207950 HS 3145.B	c 175	23	4.7	650	17	AQ740017	AQ740017 HS 5503.A
	103	23	4.7	382	17	AQ041505	AQ041505 CIT-HSP-2	c 176	23	4.7	651	14	BQ653001	BQ653001 AGENCOURT
	104	23	4.7	393	9	A1472736	A1472736 tal3c04.x	c 177	23	4.7	652	14	BQ708999	BQ708999 AGENCOURT
	105	23	4.7	398	12	BF475466	BF475466 nac30h01.	c 178	23	4.7	653	14	BQ721541	BQ721541 AGENCOURT
	106	23	4.7	399	9	AA079350	AA079350 zm96d01.s	c 179	23	4.7	654	13	BM547130	BM547130 AGENCOURT
	107	23	4.7	407	10	AW103674	AW103674 x82d07.x	c 180	23	4.7	655	14	BM904665	BM904665 AGENCOURT
	108	23	4.7	411	14	BQ101225	BQ101225 1j25f02.y	c 181	23	4.7	656	14	BQ646064	BQ646064 AGENCOURT
	109	23	4.7	416	13	BM667496	BM667496 UI-E-DX0-	c 182	23	4.7	657	12	BF945953	BF945953 CM0-NN15
	110	23	4.7	420	10	AW316599	AW316599 xw09e04.x	c 183	23	4.7	658	12	BF945953	BF945953 CM0-NN15
	111	23	4.7	421	10	AW440568	AW440568 xt15e04.x	c 184	23	4.7	659	10	BE173452	BE173452 RC2-HT056
	112	23	4.7	421	17	AQ187918	AQ187918 HS 3138.B	c 185	23	4.7	660	10	AW380926	AW380926 CM2-HT028
	113	23	4.7	422	12	BE892611	BE892611 601433420	c 186	23	4.7	661	9	AA318209	AA318209 EST20530
	114	23	4.7	429	9	AA614449	AA614449 nm89d09.s	c 187	23	4.7	662	13	BI017658	BI017658 PM1-ET025
	115	23	4.7	429	14	BQ184116	BQ184116 UI-E-EJ1-	c 188	23	4.7	663	12	BF924053	BF924053 QV4-NT024
	116	23	4.7	438	9	AA678932	AA678932 ah08g03.s	c 189	23	4.7	664	12	BF924053	BF924053 QV4-NT024
	117	23	4.7	440	12	BG611079	BG611079 602612028	c 190	23	4.7	665	9	AA678616	AA678616 ah03c11.s
	118	23	4.7	442	17	AQ836262	AQ836262 HS 5511.A	c 191	23	4.7	666	12	BF767054	BF767054 RC4-CN008
	119	23	4.7	446	17	AZ110237	AZ110237 RPI-23-4	c 192	23	4.7	667	14	BQ376042	BQ376042 RC0-TN007
	120	23	4.7	449	10	AW081610	AW081610 xc32b10.x	c 193	23	4.7	668	17	AZ808053	AZ808053 2M0071B22
	121	23	4.7	453	12	BF846122	BF846122 QV0-EN005	c 194	23	4.7	669	12	BE141341	BE141341 MR0-HT007
	122	23	4.7	455	9	AA181700	AA181700 zp55h01.s	c 195	23	4.7	670	9	AA654485	AA654485 nt62h05.s
	123	23	4.7	456	14	BM679390	BM679390 UI-E-BOO-	c 196	23	4.7	671	14	BQ376041	BQ376041 RC0-TN007
	124	23	4.7	460	10	BE301610	BE301610 bb75e09.x	c 197	23	4.7	672	12	BF950271	BF950271 CM3-NN118
	125	23	4.7	463	14	BQ024670	BQ024670 UI-1-BBIP	c 198	23	4.7	673	12	BF912838	BF912838 IL3-UT011
	126	23	4.7	465	9	AA283753	AA283753 zt19g06.s	c 199	23	4.7	674	12	BF915805	BF915805 IL3-UT011
	127	23	4.7	471	10	BE677244	BE677244 7d82d09.x	c 200	23	4.7	675	14	AW802845	AW802845 IL2-UM007
	128	23	4.7	476	14	N67313	N67313 yz51e02.s1	c 201	23	4.7	676	12	AW972743	AW972743 EST384837
	129	23	4.7	483	17	AQ193028	AQ193028 HS 3055.B	c 202	23	4.7	677	12	BF812870	BF812870 CM2-CI018
	130	23	4.7	495	10	AW080160	AW080160 xc49c05.x	c 203	23	4.7	678	14	BQ185176	BQ185176 UI-E-EJ1-
	131	23	4.7	495	14	N42784	N42784 yz25g12.r1	c 204	23	4.7	679	12	BE932779	BE932779 CM4-HT086
	132	23	4.7	498	14	BM995211	BM995211 UI-H-ED0-	c 205	23	4.7	680	12	BF944142	BF944142 CM0-NN015
	133	23	4.7	500	17	AQ216864	AQ216864 HS 3253.B	c 206	23	4.7	681	12	BF944224	BF944224 CM0-NN115
	134	23	4.7	505	14	BM716303	BM716303 UI-E-COI-	c 207	23	4.7	682	12	BF945947	BF945947 CM0-NN115
	135	23	4.7	511	10	BE464585	BE464585 hg85a05.x	c 208	23	4.7	683	10	BM110091	BM110091 EST557627
	136	23	4.7	511	17	AQ378061	AQ378061 RPI-11-13	c 209	23	4.7	684	14	BQ187986	BQ187986 UI-E-EJ1-
	137	23	4.7	512	17	AQ568405	AQ568405 HS 5239.B	c 210	23	4.7	685	14	F07193	F07193 HSC1VD091.n
	138	23	4.7	520	10	AV718743	AV718743 AV718743	c 211	23	4.7	686	9	AA834891	AA834891 oeo2e08.s
	139	23	4.7	521	17	AQ172248	AQ172248 HS 3179.B	c 212	23	4.7	687	10	T11629	T11629 AL342F Hear
	140	23	4.7	527	17	AQ564404	AQ564404 HS 5355.A	c 213	23	4.7	688	10	AA805449	AA805449 QV1-UM010
	141	23	4.7	536	17	AQ122660	AQ122660 HS 3086.A	c 214	23	4.7	689	9	AA321595	AA321595 EST24203
	142	23	4.7	536	17	AQ628374	AQ628374 CITBI-E1-	c 215	23	4.7	690	9	AI538236	AI538236 tp37h08.x
	143	23	4.7	537	17	B52287	B52287 CIT-HSP-387	c 216	23	4.7	691	12	AG005999	AG005999 PM4-GN023
	144	23	4.7	544	12	BE701335	BE701335 MR0-NN015	c 217	23	4.7	692	9	AA865144	AA865144 oh48c04.s
	145	23	4.7	546	9	AI889995	AI889995 wm80c03.x	c 218	23	4.7	693	10	AA836097	AA836097 odi5b01.s
	146	23	4.7	556	17	AQ589258	AQ589258 CITBI-E1-	c 219	23	4.7	694	9	AA975915	AA975915 'oo33d01.s
	147	23	4.7	557	12	BF817600	BF817600 MR3-CI018	c 220	23	4.7	695	17	AQ177372	AQ177372 HS 2208.A
	148	23	4.7	561	9	AA439758	AA439758 LD14406.5	c 221	23	4.7	696	17	AQ263599	AQ263599 CITBI-E1-
	149	23	4.7	576	9	AU155117	AU155117 AU155117	c 222	23	4.7	697	13	BM662212	BM662212 UI-E-CL0-
	150	23	4.7	581	17	AQ377968	AQ377968 RPI-11-1	c 223	23	4.7	698	17	AQ347796	AQ347796 RPI-11-13
	151	23	4.7	589	9	AA483043	AA483043 ne71b09.s	c 224	23	4.7	699	17	AQ965225	AQ965225 LER1B10TF
	152	23	4.7	606	14	BQ778458	BQ778458 il31d07.x	c 225	23	4.7	700	9	AI233155	AI233155 EST229843

c 226	22	4.5	364	9	AA341813	AA341813 EST47225	c 299	22	4.5	499	17	AQ298446	AQ298446 HS 2231.B
c 227	22	4.5	364	9	AA525293	AA525293 ni53b03.s	c 300	22	4.5	503	17	AQ24830	AQ24830 CITBI-EI-
c 228	22	4.5	366	14	T70937	T70937 yc49a12.r1	c 301	22	4.5	510	17	AQ228412	AQ228412 HS 2014.B
c 229	22	4.5	371	9	AA626404	AA626404 ab49c03.r	c 302	22	4.5	513	13	BI754824	BI754824 603025281
c 230	22	4.5	376	9	AA494960	AA494960 zx05f03.s	c 303	22	4.5	513	14	BM978865	BM978865 UI-CF-DU1
c 231	22	4.5	376	9	AA508036	AA508036 ng92c08.s	c 304	22	4.5	517	12	BF187711	BF187711 EST443998
c 232	22	4.5	377	10	BE062321	BE062321 RC1-BT025	c 305	22	4.5	519	14	BM690164	BM690164 UI-E-CLO-
c 233	22	4.5	386	10	AW961477	AW961477 EST373549	c 306	22	4.5	520	17	AQ127555	AQ127555 HS 3062.B
c 234	22	4.5	388	10	AV691147	AV691147 AV691147	c 307	22	4.5	526	9	AL603305	AL603305 DKF2p6861
c 235	22	4.5	389	17	AQ032744	AQ032744 HS 2213.B	c 308	22	4.5	528	17	B37130	B37130 HS-1042-B1-
c 236	22	4.5	390	12	BF842141	BF842141 RC6-HT084	c 309	22	4.5	528	17	AQ380439	AQ380439 RFC111-16
c 237	22	4.5	392	12	EG057631	EG057631 nan93h05.	c 310	22	4.5	529	17	AQ111124	AQ111124 CIT-HSP-2
c 238	22	4.5	392	17	AQ154533	AQ154533 HS 5429.B	c 311	22	4.5	531	17	AQ961606	AQ961606 EST373678
c 239	22	4.5	396	9	AI273675	AI273675 ql61h01.x	c 312	22	4.5	535	17	AG020061	AG020061 Homo sapi
c 240	22	4.5	397	9	AI887797	AI887797 wml18h12.x	c 313	22	4.5	536	10	AW170332	AW170332 xn59g03.x
c 241	22	4.5	399	10	M271071	M271071 xi48c12.x	c 314	22	4.5	538	12	BG776152	BG776152 602663107
c 242	22	4.5	400	14	M77950	M77950 EST01534.Fe	c 315	22	4.5	539	10	AV685047	AV685047 AV685047
c 243	22	4.5	401	9	AA593535	AA593535 nm28b04.s	c 316	22	4.5	540	10	AW090261	AW090261 xc85h08.x
c 244	22	4.5	402	9	AA318481	AA318481 EST20562	c 317	22	4.5	540	17	AQ477094	AQ477094 CITBI-EI-
c 245	22	4.5	405	17	B40586	B40586 HS-1051-B2-	c 318	22	4.5	542	17	AQ628282	AQ628282 CITBI-EI-
c 246	22	4.5	406	9	AI360521	AI360521 qx18d10.x	c 319	22	4.5	544	17	AQ189519	AQ189519 HS 3203.B
c 247	22	4.5	409	14	BM792401	BM792401 K-EST0072	c 320	22	4.5	546	17	AQ382744	AQ382744 RFC111-16
c 248	22	4.5	410	9	AI278211	AI278211 ql83d09.x	c 321	22	4.5	550	10	BE159081	BE159081 MR0-HT040
c 249	22	4.5	410	17	AQ630370	AQ630370 RFC1-11-4	c 322	22	4.5	550	10	BE548885	BE548885 601073327
c 250	22	4.5	413	9	AI268564	AI268564 qo37e08.x	c 323	22	4.5	551	17	AQ626960	AQ626960 CITBI-EI-
c 251	22	4.5	413	9	AI475798	AI475798 tc94f05.x	c 324	22	4.5	552	14	N79258	N79258 za63h10.s1
c 252	22	4.5	414	9	AI560073	AI560073 tpi2c07.x	c 325	22	4.5	552	17	AQ406908	AQ406908 HS 5113.A
c 253	22	4.5	414	9	BE173615	BE173615 RC2-HT056	c 326	22	4.5	554	17	AQ386113	AQ386113 RFC111-14
c 254	22	4.5	415	9	AA618451	AA618451 nm27f08.s	c 327	22	4.5	556	17	AQ569873	AQ569873 HS-5357.A
c 255	22	4.5	416	12	BG474043	BG474043 602516603	c 328	22	4.5	557	17	AQ611081	AQ611081 HS 5100.B
c 256	22	4.5	417	17	AQ695151	AQ695151 HS 5485.B	c 329	22	4.5	560	17	AQ392493	AQ392493 CITBI-EI-
c 257	22	4.5	419	10	BE173511	BE173511 RC2-HT056	c 330	22	4.5	561	9	AL697074	AL697074 DKF2p6860
c 258	22	4.5	424	9	AI821595	AI821595 nc39a08.x	c 331	22	4.5	561	10	BE300991	BE300991 ba82a12.x
c 259	22	4.5	424	12	BF900891	BF900891 IL2-WT017	c 332	22	4.5	562	17	AQ111084	AQ111084 CIT-HSP-2
c 260	22	4.5	428	9	AI859219	AI859219 wl34c12.x	c 333	22	4.5	563	10	BE674238	BE674238 7877c01.x
c 261	22	4.5	428	10	AW276933	AW276933 xp57g10.x	c 334	22	4.5	573	17	AQ774558	AQ774558 HS 3142.A
c 262	22	4.5	430	9	AL041013	AL041013 DKF2p4340	c 335	22	4.5	575	10	AW817814	AW817814 PMO-ST026
c 263	22	4.5	432	10	AW818004	AW818004 CM3-ST027	c 336	22	4.5	575	13	BE180549	BE180549 RC3-HT062
c 264	22	4.5	434	12	BG483561	BG483561 602503270	c 337	22	4.5	578	10	BE252421	BE252421 601108224
c 265	22	4.5	435	14	N69462	N69462 za18a08.s1	c 338	22	4.5	578	12	BF694257	BF694257 602082888
c 266	22	4.5	438	17	AQ167966	AQ167966 HS 2232.B	c 339	22	4.5	578	12	BE869668	BE869668 60145770
c 267	22	4.5	444	17	AZ626797	AZ626797 IM0467E13	c 340	22	4.5	578	17	AQ679563	AQ679563 HS 5346.A
c 268	22	4.5	444	17	AQ569912	AQ569912 HS 5328.A	c 341	22	4.5	587	17	B68220	B68220 CIT9789K-A-
c 269	22	4.5	445	17	AQ020367	AQ020367 CIT-HSP-2	c 342	22	4.5	592	17	AQ509373	AQ509373 nbxb0096K
c 270	22	4.5	445	17	AZ773462	AZ773462 UP 500-4C	c 343	22	4.5	594	9	AL598913	AL598913 DKF2p313D
c 271	22	4.5	445	17	AQ594759	AQ594759 HS 5413.A	c 344	22	4.5	594	10	BE180543	BE180543 RC3-HT062
c 272	22	4.5	446	9	AA225034	AA225034 nc34b07.F	c 345	22	4.5	596	9	AL707906	AL707906 DKF2p686B
c 273	22	4.5	448	17	AQ734927	AQ734927 HS 3051.A	c 346	22	4.5	597	9	AL134457	AL134457 DKF2p547J
c 274	22	4.5	450	12	BG170524	BG170524 602322914	c 347	22	4.5	597	10	BE148631	BE148631 MR0-HT024
c 275	22	4.5	451	17	AQ129984	AQ129984 HS 2170.A	c 348	22	4.5	599	17	AQ965227	AQ965227 LBR1B10TR
c 276	22	4.5	452	10	AW974897	AW974897 EST387002	c 349	22	4.5	600	9	AL138218	AL138218 DKF2p547A
c 277	22	4.5	453	10	BE173455	BE173455 RC2-HT056	c 350	22	4.5	600	13	BI509736	BI509736 BBI70019B
c 278	22	4.5	456	17	AQ790067	AQ790067 HS 3193.B	c 351	22	4.5	600	17	AQ478963	AQ478963 RFC1-11-2
c 279	22	4.5	456	17	B30904	B30904 HS-1003-A2-	c 352	22	4.5	606	17	AQ632815	AQ632815 RFC1-11-4
c 280	22	4.5	458	17	AQ114900	AQ114900 CIT-HSP-2	c 353	22	4.5	609	10	AW817810	AW817810 PMO-ST026
c 281	22	4.5	459	17	B59129	B59129 CIT-HSP-201	c 354	22	4.5	609	12	BE929451	BE929451 MR0-GN002
c 282	22	4.5	461	13	BM132512	BM132512 iq75e03.y	c 355	22	4.5	613	14	BM722009	BM722009 UI-E-E00
c 283	22	4.5	466	9	AI138918	AI138918 qc56g02.x	c 356	22	4.5	616	10	AW949748	AW949748 EST361818
c 284	22	4.5	469	12	BF955438	BF955438 MR4-WN119	c 357	22	4.5	618	17	AQ543062	AQ543062 RFC1-11-3
c 285	22	4.5	472	14	BM997236	BM997236 UI-H-DHO-	c 358	22	4.5	623	14	BQ778000	BQ778000 l139g03.y
c 286	22	4.5	473	10	AW102811	AW102811 xdg3e05.x	c 359	22	4.5	630	17	AQ152294	AQ152294 Pan trogl
c 287	22	4.5	476	9	AA741020	AA741020 ny99b11.s	c 360	22	4.5	630	17	AQ515606	AQ515606 HS 5237.A
c 288	22	4.5	477	14	BQ018445	BQ018445 UI-H-DH1-	c 361	22	4.5	632	17	AG083897	AG083897 Pan trogl
c 289	22	4.5	477	17	AQ348428	AQ348428 RFC111-13	c 362	22	4.5	640	9	AL044041	AL044041 DKF2p434K
c 290	22	4.5	478	9	AL596189	AL596189 DKF2p313H	c 363	22	4.5	641	17	AG090402	AG090402 Pan trogl
c 291	22	4.5	480	9	AI091282	AI091282 owc2c02.x	c 364	22	4.5	643	17	AG078779	AG078779 Pan trogl
c 292	22	4.5	485	9	AI371804	AI371804 tai2a04.x	c 365	22	4.5	647	12	BE888431	BE888431 601512802
c 293	22	4.5	485	12	BF897789	BF897789 QV1-WT022	c 366	22	4.5	647	14	BM791560	BM791560 K-EST0071
c 294	22	4.5	490	17	AQ893312	AQ893312 HS 3175.A	c 367	22	4.5	648	10	AQ387105	AQ387105 MR0-ST002
c 295	22	4.5	494	17	AQ588960	AQ588960 CITBI-EI-	c 368	22	4.5	648	17	AQ266668	AQ266668 RFC111-74
c 296	22	4.5	496	14	BM720112	BM720112 UI-E-E00-	c 369	22	4.5	652	17	AG064845	AG064845 Pan trogl
c 297	22	4.5	497	9	AA488898	AA488898 aa55h05.s	c 370	22	4.5	656	17	AG142083	AG142083 Pan trogl
c 298	22	4.5	497	17	AQ233463	AQ233463 HS 2045.B	c 371	22	4.5	656	17	AG142083	AG142083 Pan trogl

C 372	22	4.5	658	12	BG530359	602559296	445	21	4.3	148	12	BG003545	CW0-GN010
C 373	22	4.5	660	17	AG045026	Pan trogl	446	21	4.3	153	12	BF930860	CMI-HT087
C 374	22	4.5	663	17	AQ351155	RFC111-12	C 447	21	4.3	189	9	AA337750	EST42322
C 375	22	4.5	664	10	BE395137	601310764	C 448	21	4.3	189	12	BF994645	CW0-GN009
C 376	22	4.5	665	17	AG157485	Pan trogl	C 449	21	4.3	205	12	BF841886	RC6-HT084
C 377	22	4.5	672	10	BE541778	601063746	C 450	21	4.3	208	12	BF810994	CW2-CI017
C 378	22	4.5	672	17	AG134171	Pan trogl	C 451	21	4.3	208	12	BF818609	MR3-CI018
C 379	22	4.5	673	17	AG051795	Pan trogl	C 452	21	4.3	215	12	BF928054	IL5-NT022
C 380	22	4.5	677	17	AG183516	Pan trogl	C 453	21	4.3	216	9	AL601789	DFPZp313G
C 381	22	4.5	681	17	AG129457	Pan trogl	C 454	21	4.3	217	10	AW862049	RC3-CT034
C 382	22	4.5	685	17	AQ423897	CITBI-E1-	C 455	21	4.3	220	10	AW814200	MR3-ST020
C 383	22	4.5	687	12	BG718011	602696017	C 456	21	4.3	225	14	T10591	hbc623 Huma
C 384	22	4.5	688	17	AG107615	Pan trogl	C 457	21	4.3	231	12	BF929538	QV3-NT021
C 385	22	4.5	691	14	BQ181319	UT-H-EUO-	C 458	21	4.3	232	12	BE743332	601573249
C 386	22	4.5	693	10	AV733710	AV733710	C 459	21	4.3	233	14	H86067	YS93C06.s1
C 387	22	4.5	694	17	AZ3354813	IM0094D16	C 460	21	4.3	234	14	T10583	hbc332 Huma
C 388	22	4.5	695	17	AG171499	Pan trogl	C 461	21	4.3	236	10	AW089809	kd13c03.x
C 389	22	4.5	696	17	AG169302	Pan trogl	C 462	21	4.3	242	13	BG951696	MR1-CT073
C 390	22	4.5	706	17	AZ970121	2M0243H09	C 463	21	4.3	248	9	AA669059	ab92f03.s
C 391	22	4.5	707	17	AG096186	Pan trogl	C 464	21	4.3	248	10	BE155313	PM1-HT035
C 392	22	4.5	708	14	BQ004148	UT-H-E10-	C 465	21	4.3	248	10	BE160803	PM1-HT042
C 393	22	4.5	711	17	AG098953	Pan trogl	C 466	21	4.3	249	10	AW895905	QV4-NN003
C 394	22	4.5	717	13	BG965738	602830594	C 467	21	4.3	253	17	AQ281285	RFC111-80
C 395	22	4.5	718	17	AG012676	Homo sapi	C 468	21	4.3	262	9	AI612032	tt63e01.x
C 396	22	4.5	719	17	AG012678	Homo sapi	C 469	21	4.3	263	14	Z21052	HSAADKIG H
C 397	22	4.5	720	17	AG012683	Homo sapi	C 470	21	4.3	264	17	AQ063244	CIT-HSP-2
C 398	22	4.5	721	14	BQ512442	EST619857	C 471	21	4.3	265	9	AA381775	EST94893
C 399	22	4.5	725	17	AG012682	Homo sapi	C 472	21	4.3	268	10	BE152573	CW2-HT032
C 400	22	4.5	725	17	AG172854	Pan trogl	C 473	21	4.3	268	12	BF935802	IL2-NT020
C 401	22	4.5	733	10	AV706448	AV706448	C 474	21	4.3	270	12	BF767026	RC5-CS002
C 402	22	4.5	738	12	AV703460	AV703460	C 475	21	4.3	272	14	BF997339	QV3-GN020
C 403	22	4.5	739	12	BG850644	1024028H1	C 476	21	4.3	272	14	R19542	YG26f03.x1
C 404	22	4.5	746	12	BG2888116	602387914	C 477	21	4.3	276	12	BF834158	RC1-HT022
C 405	22	4.5	746	13	BM013316	603635233	C 478	21	4.3	277	10	AW370083	MR0-BT024
C 406	22	4.5	753	14	BM997063	UT-H-ED0-	C 479	21	4.3	278	17	B57322	CIT-HSP-200
C 407	22	4.5	754	12	BG392602	602410833	C 480	21	4.3	281	10	AW370055	MR0-BT024
C 408	22	4.5	776	17	AQ901643	HS 3203 B	C 481	21	4.3	281	10	AW576662	MR0-BT024
C 409	22	4.5	786	17	BH024116	Gm_UMB001	C 482	21	4.3	283	14	N74177	za76f08.s1
C 410	22	4.5	788	17	AG029909	Pan trogl	C 483	21	4.3	284	17	AZ317123	IM0035F07
C 411	22	4.5	800	12	BG402348	602465934	C 484	21	4.3	285	17	AQ284723	RFC111-89
C 412	22	4.5	812	13	B1116317	602869057	C 485	21	4.3	288	10	AW370099	MR0-BT024
C 413	22	4.5	825	12	BG109294	602281132	C 486	21	4.3	288	10	AW576658	MR0-BT024
C 414	22	4.5	834	17	AQ746306	HS 2277 A	C 487	21	4.3	288	10	AW805113	QV1-UM009
C 415	22	4.5	843	17	BH560119	BOGWH70TF	C 488	21	4.3	288	17	AQ391637	CITBI-E1-
C 416	22	4.5	844	17	AQ891345	HS_5263 A	C 489	21	4.3	290	10	BE069109	QV3-BT037
C 417	22	4.5	844	17	AZ175714	SP_0133 A	C 490	21	4.3	291	10	BE069196	QV3-BT037
C 418	22	4.5	853	10	BE470416	IPRdk0146	C 491	21	4.3	291	12	BF927262	CW1-NT024
C 419	22	4.5	854	13	B1912717	603176374	C 492	21	4.3	291	13	BI050929	CM4-GN036
C 420	22	4.5	854	17	AQ900581	HS 2087 B	C 493	21	4.3	294	12	BF741047	QV1-HB003
C 421	22	4.5	913	12	BG108218	602280101	C 494	21	4.3	294	12	BF741050	QV1-HB003
C 422	22	4.5	920	12	BF982222	60236273	C 495	21	4.3	294	14	BQ301850	QV1-HB003
C 423	22	4.5	921	14	BQ425349	AGENCOURT	C 496	21	4.3	295	9	AA831801	oe21b02.s
C 424	22	4.5	927	12	BF983588	602306578	C 497	21	4.3	297	12	BF766735	RC5-CS002
C 425	22	4.5	931	14	BQ942350	AGENCOURT	C 498	21	4.3	298	17	B78904	CIT-HSP-292
C 426	22	4.5	940	12	BE787771	601482347	C 499	21	4.3	299	9	AA338204	EST43100
C 427	22	4.5	952	14	BQ674594	AGENCOURT	C 500	21	4.3	299	10	AW805314	QV1-UM010
C 428	22	4.5	1002	17	AG031839	Pan trogl	C 501	21	4.3	300	17	AQ106944	HS_3086_A
C 429	22	4.5	1010	13	BM465334	AGENCOURT	C 502	21	4.3	300	17	AQ554436	RPCI-11-4
C 430	22	4.5	1015	12	BF206123	601869480	C 503	21	4.3	302	13	BI051239	CM4-GN036
C 431	22	4.5	1042	12	BG683708	602651731	C 504	21	4.3	304	10	AW935933	QV3-BT001
C 432	22	4.5	1078	13	BM415532	OP20608 M	C 505	21	4.3	305	14	N75715	YV31b02.x1
C 433	22	4.5	1082	10	BE620534	601483796	C 506	21	4.3	306	12	BF848613	IL5-EN008
C 434	22	4.5	1108	12	BG387308	602486058	C 507	21	4.3	307	12	BG059365	nah50c11.
C 435	22	4.5	1124	12	BF981559	602309437	C 508	21	4.3	310	9	AA832016	oe22b10.s
C 436	22	4.5	1133	14	BQ050855	AGENCOURT	C 509	21	4.3	310	10	BE138504	xt76c01.x
C 437	22	4.5	1201	17	CNS016FT	Drosophila	C 510	21	4.3	311	17	AQ530386	RPCI-11-3
C 438	22	4.5	1282	12	BG111360	602281721	C 511	21	4.3	312	10	AW203108	fj08h09.x
C 439	22	4.5	1371	12	BG035008	602325282	C 512	21	4.3	313	13	BI115748	602866202
C 440	22	4.5	1522	13	BM478753	AGENCOURT	C 513	21	4.3	314	9	AA856950	oe03d01.s
C 441	21	4.3	102	10	AW843450	CW0-CN003	C 514	21	4.3	316	9	AI886432	wm94G02.x
C 442	21	4.3	109	17	AQ537311	RPCI-11-3	C 515	21	4.3	316	10	AW024008	d164B04.Y
C 443	21	4.3	122	13	BI024994	CM4-MT028	C 516	21	4.3	319	9	AA669647	ac20f02.s
C 444	21	4.3	145	9	AA320448	EST23157	C 517	21	4.3	319	10	BB085179	BB085179

518	21	4.3	320	12	BF927045	BF927045 CM2-NT019	c 591	21	4.3	378	17	AQ486453	AQ486453 RPCI-11-2
519	21	4.3	326	10	AW339970	AW339970 ha61g10.x	c 592	21	4.3	379	13	BI052200	BI052200 CM4-GN031
520	21	4.3	326	9	AA345399	AA345399 EST51412	c 593	21	4.3	379	13	BI052200	BI052200 CM4-GN031
521	21	4.3	326	17	AQ264626	AQ264626 CITBI-E1-	c 594	21	4.3	381	14	R83702	R83702 YL14309.r1
522	21	4.3	328	9	AA502688	AA502688 ng63a04.b	c 595	21	4.3	382	17	AQ090883	AQ090883 GSSTC0101
523	21	4.3	329	9	AA908540	AA908540 o982g10.b	c 596	21	4.3	382	17	AQ122945	AQ122945 HS_3094_B
524	21	4.3	329	17	AQ594641	AQ594641 HS_2120_B	c 597	21	4.3	383	9	AI417675	AI417675 tg80h05.x
525	21	4.3	331	10	BE150331	BE150331 QV4-HT026	c 598	21	4.3	384	10	AW051333	AW051333 QV0-NN107
526	21	4.3	333	17	AQ094318	AQ094318 HS_3025_B	c 599	21	4.3	384	12	BE934245	BE934245 CM0-HT091
527	21	4.3	334	14	H59346	H59346 Yr27d01.r1	c 600	21	4.3	384	17	AQ062048	AQ062048 CIT-HSP-2
528	21	4.3	335	17	AQ393389	AQ393389 CITBI-E1-	c 601	21	4.3	387	9	AA418048	AA418048 zv97h12.s
529	21	4.3	336	9	AI922115	AI922115 wn88f01.x	c 602	21	4.3	388	9	AI486670	AI486670 tx63h05.x
530	21	4.3	336	13	EG957884	EG957884 IL3-CT067	c 603	21	4.3	389	12	BF897633	BF897633 RCI-MT016
531	21	4.3	337	13	EG953731	EG953731 MR4-CT053	c 604	21	4.3	390	12	BF896026	BF896026 CM2-MT015
532	21	4.3	338	12	BF771418	BF771418 IL5-IT002	c 605	21	4.3	391	14	N44678	N44678 YV22b03.r1
533	21	4.3	338	13	BI032335	BI032335 CM3-NN025	c 606	21	4.3	391	14	N44678	N44678 YV22b03.r1
534	21	4.3	339	17	AQ081573	AQ081573 RPCI11-54	c 607	21	4.3	392	17	AQ243921	AQ243921 HS_2058_B
535	21	4.3	340	9	AA601930	AA601930 np02e04.s	c 608	21	4.3	393	14	H40536	H40536 YP63f02.s1
536	21	4.3	340	14	F09292	F09292 HSC2F032.n	c 609	21	4.3	395	10	BE178609	BE178609 PM3-HT060
537	21	4.3	341	17	AQ113312	AQ113312 CIT-HSP-2	c 610	21	4.3	396	9	AI825372	AI825372 wb17f08.x
538	21	4.3	343	10	AW149882	AW149882 XG30e09.x	c 611	21	4.3	397	9	AI572560	AI572560 tx59a10.x
539	21	4.3	343	13	EG956712	EG956712 MR4-CT053	c 612	21	4.3	398	9	AI224481	AI224481 qx06d09.x
540	21	4.3	343	14	N51140	N51140 YV96a10.r1	c 613	21	4.3	398	9	AA620292	AA620292 af04h06.s
541	21	4.3	346	10	AW370188	AW370188 RC5-BT025	c 614	21	4.3	398	10	AW089796	AW089796 XG08d07.x
542	21	4.3	347	12	BF773101	BF773101 CM3-IT004	c 615	21	4.3	398	10	BE181228	BE181228 CM2-HT063
543	21	4.3	347	12	BF773101	BF773101 CM3-IT004	c 616	21	4.3	398	17	AQ082856	AQ082856 RPCI11-55
544	21	4.3	348	9	AI002398	AI002398 or78b03.b	c 617	21	4.3	399	9	AA877143	AA877143 oh79e03.s
545	21	4.3	348	17	AQ042012	AQ042012 CIT-HSP-2	c 618	21	4.3	399	17	AQ207824	AQ207824 HS_3028_A
546	21	4.3	348	17	AQ554433	AQ554433 RPCI-11-4	c 619	21	4.3	401	9	AI650636	AI650636 wb01h10.x
547	21	4.3	349	9	AI769210	AI769210 wg35c02.x	c 620	21	4.3	401	12	BF855695	BF855695 RC6-FN020
548	21	4.3	349	12	BF732461	BF732461 nael0b06.	c 621	21	4.3	401	13	BI005157	BI005157 PM3-HN007
549	21	4.3	351	9	AI9393740	AI9393740 tg60c09.x	c 622	21	4.3	401	17	AQ354491	AQ354491 CITBI-E1-
550	21	4.3	352	9	AI801690	AI801690 to94a02.x	c 623	21	4.3	402	12	BF771450	BF771450 CM1-IT003
551	21	4.3	352	10	AW088763	AW088763 xd29h02.x	c 624	21	4.3	402	17	AZ755944	AZ755944 ex04c09.r
552	21	4.3	352	12	BF946793	BF946793 CM0-NN115	c 625	21	4.3	403	9	AA468575	AA468575 ne07f03.s
553	21	4.3	352	17	AQ905998	AQ905998 GSSTC0657	c 626	21	4.3	403	9	AA508040	AA508040 ng52d03.s
554	21	4.3	354	9	AA641435	AA641435 nr93c01.s	c 627	21	4.3	403	17	BE609578	BE609578 HVI2C10
555	21	4.3	354	12	BG006166	BG006166 RC5-GN019	c 628	21	4.3	404	17	AQ043406	AQ043406 CIT-HSP-2
556	21	4.3	355	9	AI217536	AI217536 qd43a09.x	c 629	21	4.3	405	17	AQ037934	AQ037934 CIT-HSP-2
557	21	4.3	356	17	AQ068284	AQ068284 HS_2240_B	c 630	21	4.3	405	17	AQ685494	AQ685494 HS_5528_B
558	21	4.3	356	17	AQ0817094	AQ0817094 HS_5553_A	c 631	21	4.3	405	17	AQ182308	AQ182308 HS_2233_B
559	21	4.3	357	9	AA666066	AA666066 ac41c04.s	c 632	21	4.3	407	10	AV762816	AV762816 AV762816
560	21	4.3	357	14	D45476	D45476 HUMGS02649	c 633	21	4.3	407	13	BI002174	BI002174 RC3-IT002
561	21	4.3	357	17	AQ816076	AQ816076 HS_5484_A	c 634	21	4.3	408	13	BI002174	BI002174 RC3-IT002
562	21	4.3	358	9	AI923135	AI923135 wn29a09.x	c 635	21	4.3	408	13	W32430	W32430 zc05d10.s1
563	21	4.3	358	12	BG010509	BG010509 PM4-GN030	c 636	21	4.3	409	13	BI034926	BI034926 QV2-NN200
564	21	4.3	359	17	AQ584200	AQ584200 RPCI-11-4	c 637	21	4.3	409	13	BI513745	BI513745 BS160013B
565	21	4.3	360	9	AI218171	AI218171 qh28c06.x	c 638	21	4.3	410	13	BI036617	BI036617 RC5-NT018
566	21	4.3	360	9	AA470596	AA470596 nc69e11.r	c 639	21	4.3	410	17	AQ220064	AQ220064 HS_3251_B
567	21	4.3	361	13	BG956714	BG956714 MR4-CT053	c 640	21	4.3	411	9	AA837607	AA837607 od68c10.s
568	21	4.3	361	9	AI982522	AI982522 wt21e01.x	c 641	21	4.3	411	9	AA837607	AA837607 od68c10.s
569	21	4.3	363	12	BG012513	BG012513 IL5-GN023	c 642	21	4.3	411	9	AI768879	AI768879 tu70d04.x
570	21	4.3	364	10	AW591402	AW591402 XG35h09.x	c 643	21	4.3	411	9	AI738813	AI738813 wi36h07.x
571	21	4.3	364	14	N47882	N47882 YV96a10.s1	c 644	21	4.3	411	10	AV744364	AV744364 AV744364
572	21	4.3	364	17	AQ242624	AQ242624 CITBI-E1-	c 645	21	4.3	411	10	AW084237	AW084237 xc53f08.x
573	21	4.3	364	17	AQ472259	AQ472259 CITBI-E1-	c 646	21	4.3	412	10	AW074223	AW074223 x509e11.x
574	21	4.3	365	9	AA837709	AA837709 oe06c10.s	c 647	21	4.3	412	10	AW074223	AW074223 x509e11.x
575	21	4.3	365	9	AA601680	AA601680 no01f11.s	c 648	21	4.3	412	17	B30650	B30650 HS-1003-A1-
576	21	4.3	365	10	AW905130	AW905130 QV0-NN107	c 649	21	4.3	412	17	AQ527907	AQ527907 RPCI-11-3
577	21	4.3	367	9	AA634013	AA634013 ac74b02.s	c 650	21	4.3	413	10	AW735885	AW735885 AV735885
578	21	4.3	368	10	BE086702	BE086702 QV1-BT067	c 651	21	4.3	413	10	AW512739	AW512739 XG06g04.x
579	21	4.3	368	14	H65994	H65994 Yr73b11.r1	c 652	21	4.3	413	13	BG950830	BG950830 CM4-CT066
580	21	4.3	369	12	BG012998	BG012998 IL5-GN023	c 653	21	4.3	414	9	AI619953	AI619953 ty45d03.x
581	21	4.3	370	13	BI710741	BI710741 iq90b01.y	c 654	21	4.3	414	12	BF771409	BF771409 IL5-IT002
582	21	4.3	370	9	AA594510	AA594510 nl94e10.s	c 655	21	4.3	415	10	AW516975	AW516975 XG05e08.x
583	21	4.3	370	14	H58688	H58688 Yr20g04.s1	c 656	21	4.3	417	17	AQ264160	AQ264160 CITBI-E1-
584	21	4.3	370	17	AQ192909	AQ192909 HS_3045_B	c 657	21	4.3	418	9	AA418231	AA418231 zv97h12.r
585	21	4.3	371	9	AA084726	AA084726 zn06f08.s	c 658	21	4.3	418	12	BF821769	BF821769 MR1-RT004
586	21	4.3	372	12	BG012983	BG012983 IL5-GN023	c 659	21	4.3	419	9	AI672778	AI672778 we73a03.x
587	21	4.3	372	14	R08853	R08853 Yf21c04.s1	c 660	21	4.3	420	14	N55508	N55508 YV50e05.s1
588	21	4.3	373	9	AI660629	AI660629 wf23a02.x	c 661	21	4.3	422	17	B85693	B85693 RPCI11-20J2
589	21	4.3	373	17	AQ778733	AQ778733 HS_2174_B	c 662	21	4.3	423	10	AW593635	AW593635 X193b03.x
590	21	4.3	377	17	BI3935	BI3935 A-423E9.TP	c 663	21	4.3	423	17	AQ334428	AQ334428 HS_5005_A

C 664	21	4.3	424	9	AA780046	AA780046 zj24f02.s	C 737	21	4.3	467	10	BE504930	BE504930 hz32g08.x
C 665	21	4.3	424	14	R87078	R87078 yq31f04.r1	738	21	4.3	467	17	AQ178246	AQ178246 HS 2217.B
C 666	21	4.3	425	9	AI538779	AI538779 cp66d11.x	739	21	4.3	468	9	AA115656	AA115656 z186c09.s
C 667	21	4.3	425	17	AQ825042	AQ825042 HS 5253.A	740	21	4.3	468	9	AI951698	AI951698 wv38d07.x
C 668	21	4.3	426	12	BF963838	BF963838 QV2-NT004	741	21	4.3	469	10	AW517716	AW517716 xs86h03.x
C 669	21	4.3	426	10	AW008093	AW008093 wv49h04.x	742	21	4.3	469	12	BF034813	BF034813 x01457319
C 670	21	4.3	427	14	R73294	R73294 yj92e02.r1	743	21	4.3	470	14	W45229	W45229 zc23d10.r1
C 671	21	4.3	427	9	AA789350	AA789350 v93b11.x	744	21	4.3	470	17	AQ110647	AQ110647 CIT-HSP-2
C 672	21	4.3	428	17	AQ333433	AQ333433 CITBI-EI-	745	21	4.3	471	10	AW473537	AW473537 hb05e08.x
C 673	21	4.3	434	17	AQ380968	AQ380968 RPI111-16	746	21	4.3	471	13	BI015807	BI015807 PM2-ET025
C 674	21	4.3	435	14	N79243	N79243 za63c09.s1	747	21	4.3	472	13	BI715111	BI715111 ic29a09.y
C 675	21	4.3	436	12	BF771348	BF771348 RC3-TT002	748	21	4.3	472	14	BM710409	BM710409 UT-E-CQ1-
C 676	21	4.3	437	17	AQ589705	AQ589705 HS 2117.B	749	21	4.3	472	17	AQ933785	AQ933785 RPCI-23-2
C 677	21	4.3	438	14	R66831	R66831 y125h06.r1	750	21	4.3	474	10	AW812117	AW812117 RC1-ST017
C 678	21	4.3	439	17	AQ331997	AQ331997 HS 5011.A	751	21	4.3	474	10	AW812124	AW812124 RC1-ST017
C 679	21	4.3	439	17	AQ609456	AQ609456 HS 5078.B	752	21	4.3	476	9	AI889356	AI889356 wms8a12.x
C 680	21	4.3	440	9	AA011367	AA011367 z101c04.f	753	21	4.3	476	14	BQ581554	BQ581554 1110c03.x
C 681	21	4.3	440	14	W01078	W01078 za56b10.r1	754	21	4.3	476	17	AQ708398	AQ708398 HS 5568.A
C 682	21	4.3	441	9	AI928406	AI928406 w096h08.x	755	21	4.3	478	17	AQ229829	AQ229829 HS 2027.A
C 683	21	4.3	441	10	BE162414	BE162414 PM1-HT045	756	21	4.3	479	9	AI814767	AI814767 wk65e05.x
C 684	21	4.3	442	9	AI278896	AI278896 q051b07.x	757	21	4.3	479	12	BF589833	BF589833 rac25f08
C 685	21	4.3	442	9	AI278896	AI278896 q051b07.x	758	21	4.3	479	12	BF589833	BF589833 rac25f08
C 686	21	4.3	442	17	AQ080562	AQ080562 CIT-HSP-2	759	21	4.3	479	17	AQ191881	AQ191881 HS 3223.B
C 687	21	4.3	442	17	AQ550371	AQ550371 RPCI-11-4	760	21	4.3	479	17	AQ191881	AQ191881 HS 3223.B
C 688	21	4.3	442	10	AW117936	AW117936 x639d08.x	761	21	4.3	480	9	AI249735	AI249735 qj64e10.x
C 689	21	4.3	444	14	BM988988	BM988988 UT-H-DIO-	762	21	4.3	480	9	AI924095	AI924095 wn78g10.x
C 690	21	4.3	444	14	R72145	R72145 yj87f08.r1	763	21	4.3	480	14	H98660	H98660 yx17a06.s1
C 691	21	4.3	444	17	AQ706405	AQ706405 HS 5554.A	764	21	4.3	481	12	BF900598	BF900598 W81-WT028
C 692	21	4.3	445	9	AI217123	AI217123 qf47b12.x	765	21	4.3	481	14	R95838	R95838 yq50a11.r1
C 693	21	4.3	445	9	AI559114	AI559114 tq31d12.x	766	21	4.3	481	14	R95838	R95838 yq50a11.r1
C 694	21	4.3	446	17	AQ691848	AQ691848 HS 5385.A	767	21	4.3	482	14	BQ581877	BQ581877 1110c03.y
C 695	21	4.3	447	9	AI799444	AI799444 tw55e03.x	768	21	4.3	482	14	N54909	N54909 yv34e04.s1
C 696	21	4.3	447	17	AQ383758	AQ383758 RPI111-12	769	21	4.3	483	17	AQ814924	AQ814924 HS 5249.B
C 697	21	4.3	448	9	AI346528	AI346528 qp46a05.x	770	21	4.3	484	17	AQ040336	AQ040336 CIT-HSP-2
C 698	21	4.3	448	12	BF880775	BF880775 QV3-ET017	771	21	4.3	485	9	AI523316	AI523316 ar71f11.x
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C 700	21	4.3	450	9	AI079823	AI079823 ox50b05.x	773	21	4.3	485	17	AQ441297	AQ441297 HS 5129.B
C 701	21	4.3	450	9	AI708173	AI708173 DKZp686H	774	21	4.3	486	9	AI889361	AI889361 wms8b08.x
C 702	21	4.3	450	10	AW889893	AW889893 RC5-NT003	775	21	4.3	486	9	AI889361	AI889361 wms8b08.x
C 703	21	4.3	450	12	BF771353	BF771353 RC3-IT002	776	21	4.3	487	13	BI792314	BI792314 ic29a09.x
C 704	21	4.3	450	12	BG06892	BG06892 IL5-GN023	777	21	4.3	488	10	AW058407	AW058407 wx20c11.x
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C 709	21	4.3	453	10	BE675381	BE675381 7f08b04.x	782	21	4.3	491	9	AA642887	AA642887 nr34a01.s
C 710	21	4.3	454	17	AQ627764	AQ627764 CITBI-EI-	783	21	4.3	491	9	AA642887	AA642887 nr34a01.s
C 711	21	4.3	455	10	AW192325	AW192325 x144a02.x	784	21	4.3	492	17	AQ753098	AQ753098 HS 5303.A
C 712	21	4.3	455	10	AQ079438	AQ079438 CIT-HSP-2	785	21	4.3	492	17	AQ475870	AQ475870 CITBI-EI-
C 713	21	4.3	455	17	AQ392348	AQ392348 CITBI-EI-	786	21	4.3	494	17	B80382	B80382 CIT-HSP-204
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C 719	21	4.3	457	17	AQ232321	AQ232321 HS 2009.A	792	21	4.3	499	14	BM990819	BM990819 UT-H-DIO-
C 720	21	4.3	458	9	AI935684	AI935684 w039e04.x	793	21	4.3	500	10	AW889901	AW889901 RC5-NT003
C 721	21	4.3	458	17	AQ232316	AQ232316 HS 2009.A	794	21	4.3	500	10	AW889901	AW889901 RC5-NT003
C 722	21	4.3	460	9	AA988666	AA988666 q08e10.s	795	21	4.3	501	17	AQ470357	AQ470357 CITBI-EI-
C 723	21	4.3	460	9	AA565826	AA565826 nj32a09.s	796	21	4.3	501	17	AQ470357	AQ470357 CITBI-EI-
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C 725	21	4.3	461	14	N73439	N73439 yz31g10.r1	798	21	4.3	504	17	AQ553093	AQ553093 RPCI-11-4
C 726	21	4.3	462	13	BI061800	BI061800 PM4-UT010	799	21	4.3	505	9	AA126271	AA126271 z186g03.s
C 727	21	4.3	462	14	BM983733	BM983733 UT-CF-DU1	800	21	4.3	505	9	AA126271	AA126271 z186g03.s
C 728	21	4.3	462	17	AQ460432	AQ460432 HS 5141.A	801	21	4.3	505	17	AQ062744	AQ062744 CIT-HSP-2
C 729	21	4.3	463	12	BF821941	BF821941 MRI-RT004	802	21	4.3	505	17	AQ43943	AQ43943 HS 3074.A
C 730	21	4.3	463	14	BM729198	BM729198 UT-E-BO1-	803	21	4.3	507	17	AQ792017	AQ792017 HS 5270.A
C 731	21	4.3	464	9	AI793119	AI793119 oo31a01.y	804	21	4.3	507	17	AQ120179	AQ120179 HS 3028.B
C 732	21	4.3	465	9	AI986134	AI986134 wr30g05.x	805	21	4.3	508	9	AI863203	AI863203 tz44f04.x
C 733	21	4.3	465	14	BM672735	BM672735 UT-E-CQ0-	806	21	4.3	510	9	AI844771	AI844771 wk65e12.x
C 734	21	4.3	465	17	AQ754647	AQ754647 HS 5537.B	807	21	4.3	510	14	BM993150	BM993150 UR-H-DIO-
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C 815	21	4.3	515	10	BE170758	HS_2354_A	888	21	4.3	581	17	BG6212	BG6212
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C 823	21	4.3	519	17	AZ517776	RFCI-11-8	896	21	4.3	587	10	AM169118	x118906.x
C 824	21	4.3	520	17	AQ248278	HS_2063_A	897	21	4.3	587	13	BM010302	603631181
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C 826	21	4.3	520	17	AQ387974	RFCI-11-4	899	21	4.3	588	17	AQ268909	RFCI-11-75
C 827	21	4.3	521	12	BE927881	MR3-CT046	900	21	4.3	588	17	AQ347819	RFCI-11-11
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C 831	21	4.3	523	17	AQ019769	CIT-HSP-2	904	21	4.3	593	10	AQ373685	RFCI-11-15
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C 838	21	4.3	529	13	BI085366	BI085366	911	21	4.3	603	13	BI907187	BI907187
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C 845	21	4.3	543	10	AW129741	xz23g06.x	918	21	4.3	616	13	BM478467	BM478467
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C 848	21	4.3	545	10	AW517695	x86604.x	921	21	4.3	619	9	AI982994	AI982994
C 849	21	4.3	546	17	AQ486753	RFCI-11-2	922	21	4.3	621	17	AQ374906	RFCI-11-15
C 850	21	4.3	547	17	AQ829732	HS_4962_A	923	21	4.3	623	9	AI114869	AI114869
C 851	21	4.3	549	17	AQ717342	HS_5494_B	924	21	4.3	623	12	BF818471	MR1-C1018
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C 853	21	4.3	551	17	AQ720386	HS_5856_A	926	21	4.3	624	10	AV705122	AV705122
C 854	21	4.3	551	17	AQ536274	RFCI-11-4	927	21	4.3	626	10	AW816505	PV0-ST023
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C 863	21	4.3	558	12	BG008492	PM4-GN030	936	21	4.3	640	17	AQ536737	RFCI-11-3
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C 865	21	4.3	560	9	AA196339	zp96e03.x	938	21	4.3	644	12	BG491393	602535682
C 866	21	4.3	560	14	BQ267126	1198c02.y	939	21	4.3	644	17	AG057657	Pan trogl
C 867	21	4.3	560	17	AQ764816	HS_3118_A	940	21	4.3	645	12	BE811408	MR3-AN002
C 868	21	4.3	562	12	BF906243	IL3-MT026	941	21	4.3	645	17	AG033429	Pan trogl
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C 871	21	4.3	564	9	AA528688	nfs1d02.s	944	21	4.3	645	17	AQ391374	CITBI-E1
C 872	21	4.3	564	12	BF846742	QV0-EN005	945	21	4.3	647	17	AG176477	Pan trogl
C 873	21	4.3	564	17	AQ358231	HS_5029_A	946	21	4.3	648	17	AZ083477	RFCI-23-3
C 874	21	4.3	566	17	AQ012743	CIT-HSP-2	947	21	4.3	648	17	AG123083	Pan trogl
C 875	21	4.3	566	17	AQ346062	RFCI-11-12	948	21	4.3	649	14	BM998914	UI-H-D10
C 876	21	4.3	566	17	AQ427700	CITBI-E1	949	21	4.3	649	17	AG047653	Pan trogl
C 877	21	4.3	567	10	AV720723	AV720723	950	21	4.3	651	17	AG041720	Pan trogl
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C 879	21	4.3	568	17	AQ531625	RFCI-11-3	952	21	4.3	653	17	AG160435	Pan trogl
C 880	21	4.3	570	17	BH552938	BOHQ622R	953	21	4.3	654	13	BM009397	603629880
C 881	21	4.3	570	17	AQ391603	CITBI-E1	954	21	4.3	655	17	AZ839675	2M0135121
C 882	21	4.3	570	17	AQ425937	CITBI-E1	955	21	4.3	655	17	AQ544656	CITBI-E1











Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

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JOURNAL

MEDLINE

COMMENT

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This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&t2=PM0-NT0314-

280501-004-d08&t3=2001-05-28&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence stop: 319.

Location/Qualifiers

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/db xref="taxon:9606"

/clone lib="NT0314"

/dev stage="Adult"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

68 a 108 c 64 g 78 t 1 others

BASE COUNT

ORIGIN

Query Match 31.9%; Score 155; DB 14; Length 319;

Best Local Similarity 100.0%; Pred. No. 2.3e-60;

Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 CTAGCCCTTCCCTGAGTGGGGCTGAGCCAGAGTCACCTTTTCTGTGGCTGCTTACC 391

Db 16 CTAGCCCTTCCCTGAGTGGGGCTGAGCCAGAGTCACCTTTTCTGTGGCTGCTTACC 75

Qy 392 TTCTGTCCCTGAGGTTAAACGGTGGCCATCTCCATCTCAACGACAGAGGCTTT 451

Db 76 TTCTGTCCCTGAGGTTAAACGGTGGCCATCTCCATCTCAACGACAGAGGCTTT 135

Qy 452 TCTGGATTTCAACACCATGCTCTTAGTCCCAAGC 486

Db 136 TCTGGATTTCAACACCATGCTCTTAGTCCCAAGC 170

RESULT 7

BF934192/c

LOCUS

BF934192

DEFINITION

CM3-NT0245-211200-585-b05 NT0245 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF934192

VERSION

BF934192.1 GI:12351516

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 204)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

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Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

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(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-NT0245-

211200-585-b05&t3=2000-12-21&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 46

High quality sequence stop: 204.

Location/Qualifiers

1..204

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone lib="NT0245"

/dev stage="Adult"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

59 a 46 c 65 g 34 t

BASE COUNT

ORIGIN

Query Match 17.9%; Score 87; DB 12; Length 204;

Best Local Similarity 100.0%; Pred. No. 3.2e-29;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 GAGATGTTCTCTCTTGGCCCCCGCCCTCATGGTCTTCCCTGAGTGGGGC 354

Db 204 GAGATGTTCTCTCTTGGCCCCCGCCCTCATGGTCTTCCCTGAGTGGGGC 145

Qy 355 TGAGGCCAGAGTCACCTTTTCTGTGGC 381

Db 144 TGAGGCCAGAGTCACCTTTTCTGTGGC 118

RESULT 8

BF947854

LOCUS

BF947854

DEFINITION

CM2-NN0212-301000-440-a07 NN0212 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF947854

VERSION

BF947854.1 GI:12365129

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 306)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [astimpson@ludwig.org.br](mailto:astimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM2&t2=CM2-NN0212-301000-440-a07&t3=2000-10-30&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 22  
High quality sequence stop: 306.

FEATURES source

Location/Qualifiers	
1. .306	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_lib="NN0212"	
/dev_stage="Adult"	
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
65 a	97 c 63 g 81 t

BASE COUNT	65 a	97 c	63 g	81 t	Conservative
ORIGIN					
Query Match		13.2%	Score 64;	DB 12;	Length 306;
Best Local Similarity		100.0%;	Pred. NO. 1.1e-18;		
Matches 64;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	423	CTGCCATCTCTCAACGACGAGGAGGCTTTCTGGAAATTC	AAACCAATTCCTTAGTCCC	482	
Db	81	CTGCCATCTCTCAACGACGAGGAGGCTTTCTGGAAATTC	AAACCAATTCCTTAGTCCC	140	
Qy	483	AAGC	486		
Db	141	AAGC	144		

```

RESULT 9
T65465
LOCUS
DEFINITION
T65465 435 bp mRNA linear EST 07-MAR-1995
Y737309.r1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:21528 5', mRNA sequence.
T65465
T65465.1 GI:674510
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 435)
Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman
M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J.,
Rifkin L., Rohlfing T., Soares M., Tan F., Trzaskas E., Waterston
R., Williamson A., Woldmann P. and Wilson R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
Contact: Wilson RK
JOURNAL
Washington University School of Medicine
COMMENT
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1734

```

Seq primer: M13RP1	
High quality sequence stop: 336.	
FEATURES	
source	Location/Qualifiers
	1. .435

```

1. .435
/organism="Homo sapiens"
/db_xref="GDB:393875"
/db_xref="taxon:9606"
/clone="IMAGE:21528"
/clone_lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="PH10B (ampicillin resistant)"
/notes="Organ: whole brain; Vector: Lfamid BA; Site:1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AACTGGAAGAAATTCGGCGCGGAGGAATTTTTTTTTTT 3'];"
double-stranded cDNA was ligated to Hind III adaptors
(pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
94 a 130 c 105 g 103 t 3 others
BASE COUNT

```

BASE COUNT	94	a	130	c	105	g	103	t	3	others
ORIGIN										
Query Match	13.2%; Score 64; DB 14; Length 435;									
Best Local Similarity	100.0%; Pred. No. 1.1e-18;									
Matches	64;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	Gaps
Qy	423	CTGCCATCTCTCAACGACGACGAGGAGCTTTTCTCGAATTTTCAAACCATTTGCTCTTAGTCCC	482							
Db	32	CTGCCATCTCTCAACGACGACGAGGAGCTTTTCTCGAATTTTCAAACCATTTGCTCTTAGTCCC	91							
Qy	483	AAGC	486							
Db	92	AAGC	95							

RESULT	10
FIL1822	
LOCUS	HSC32A091 302 bp mRNA linear EST 12-MAR-1995
DEFINITION	HSC32A091 normalized infant brain cDNA Homo sapiens CDNA clone G-32a09, mRNA sequence.
ACCESSION	Fil1822
VERSION	Fil1822.1 GI:706134
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
AUTHORS	1. (bases 1 to 302) Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Marriage-Samson,R., Pietu,G., Pouliot,Y., Sebastien-Kabakthis,C. and Tessier,A. IMAGE: molecular integration of the analysis of the human genome and its expression
TITLE	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
JOURNAL	95277534
MEDLINE	Contact: Genethon
COMMENT	Genexpress-Genethon Genethon Centre de recherche sur le Genome Humain 1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE Tel: 33169472800 Fax: 33160778698 Email: genexpress@genethon.fr Single read. Genexpress_library_id: C; Genexpress_sequence_id: Ylc-32a09 Seq primer: (-21)M13 universal.

```

FEATURES
  source
    Location/Qualifiers
      1..302
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="C-32a09"

```

/clone\_lib="normalized infant brain cDNA"  
 /sex="Female"  
 /tissue\_type="total brain"  
 /dev\_stage="3 months old"  
 /note="Organ: brain; Vector: lafmid BA; Site\_1: HindIII;  
 Site\_2: NotI; sex:female; dev\_stage=3 months old;  
 isolate-muscular atrophy patient; tissue\_type=total brain  
 ; total mRNA was oligo-(dT) primed and directionally  
 cloned 5' -> 3' into the HindIII -> NotI sites of the  
 lafmid BA vector. Clone library from B.Soaress, Psychiatry  
 Dept. Columbia University, USA. Normalization\_method:  
 Bento Soares, P.N.A.S in press"

BASE COUNT 67 a 97 c 65 g 72 t 1 others  
 ORIGIN

Query Match 9.5%; Score 46; DB 14; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 AGAGAGCTTTCTGGAATTTCAAACCATTCCTCTAGTCCCAAGC 486  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 52 AGAGAGCTTTCTGGAATTTCAAACCATTCCTCTAGTCCCAAGC 97

RESULT 11  
 AI684794 362 bp mRNA linear EST 27-MAY-1999  
 LOCUS wa73905.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 DEFINITION IMAGE:2301848 3' similar to contains Alu repetitive element; mRNA  
 sequence.

ACCESSION AI684794  
 VERSION AI684794.1 GI:4896088  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 362)  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco  
 High quality sequence stop: 252.

FEATURES  
 source  
 1. 362  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2301848"  
 /clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
 /lab\_host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBHL19W, testis NHT, and B-cell  
 NCI-CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682832-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 90 a 86 c 69 g 116 t 1 others  
 ORIGIN

Query Match 5.8%; Score 28; DB 9; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGATGTGAGCCACCGTGCCTGGCCAGA 34  
 ||||||||||||||||||||||||||||||||  
 Db 232 CAGATGTGAGCCACCGTGCCTGGCCAGA 259

RESULT 12  
 AA651660/c 399 bp mRNA linear EST 13-NOV-1997  
 LOCUS ns89d03.e1 NCI CGAP Pr3 Homo sapiens cDNA clone IMAGE:1190789  
 DEFINITION similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AA651660  
 VERSION AA651660.1 GI:2583312  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 399)  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.  
 , Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 503 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES  
 Location/Qualifiers  
 1. 399  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1190789"  
 /clone\_lib="NCI CGAP\_Pr3"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"

/note="vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10  
 ,000 microdissected cells histologically-determined to be  
 fully malignant prostate cancer cells. Double-stranded  
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR  
 applied to the cDNA with an adaptor-specific primer, and  
 the resulting PCR product subcloned into pAMP10 by the  
 UDC-cloning method (life technologies). Average insert  
 size is 600 bp. NOTE: Not directionally cloned. This  
 library was constructed by David Krizman."

BASE COUNT 116 a 93 c 113 g 77 t  
 ORIGIN

Query Match 5.8%; Score 28; DB 9; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTGCCTGGCCAGATTTT 39  
 ||||||||||||||||||||||||||||  
 Db 122 GTGAGCCACCGTGCCTGGCCAGATTTT 95

RESULT 13  
 AW974922/c

LOCUS AW974922 499 bp mRNA linear EST 02-JUN-2000  
 DEFINITION EST387027 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW974922  
 VERSION AW974922.1 GI:8166125

```

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 499) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: john@tigr.org
Plate: 341
Seq primer: Forward.
Location/Qualifiers
1..499
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pluescriptSKm"
BASE COUNT 139 a 116 c 138 g 106 t
ORIGIN
Query Match 5.8%; Score 28; DB 10; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTCTGCGCCAGATTTT 39
|||||
Db 236 GTGAGCCACCGTCTGCGCCAGATTTT 209
|||||

RESULT 14
BE826708/c 344 bp mRNA linear EST 22-SEP-2000
LOCUS QV1-EN0042-130600-237-b05 EN0042 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE826708
ACCESSION BE826708.1 GI:10259086
VERSION BE826708.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 344) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negai,M.A., da Silva,W. Jr., Zagó,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QV1-EN0042-130
600-237-b05&t3=2000-06-13&t4=1)
Seq primer: puc 18 forward

```

```

FEATURES
source
Location/Qualifiers
1..344
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="EN0042"
/dev stage="Adult"
/note="Organ: lung normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 136,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 82 a 87 c 114 g 61 t
ORIGIN
Query Match 5.6%; Score 27; DB 12; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GTGAGCCACCGTCTGCGCCAGATTTT 38
|||||
Db 257 GTGAGCCACCGTCTGCGCCAGATTTT 231
|||||

RESULT 15
AQ043261 350 bp DNA linear GSS 14-JUL-1998
LOCUS CIT-HSP-2329A1.TR CIT-HSP Homo sapiens genomic clone 2329A1, DNA
DEFINITION AQ043261
ACCESSION AQ043261
VERSION AQ043261.1 GI:3312188
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 350) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M., and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2329A1.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..350
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="2329A1"
/clone_lib="CIT-HSP"
/sex="Male"
/cell type="Sperm"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2:
HindIII"
BASE COUNT 76 a 84 c 84 g 106 t
ORIGIN
Query Match 5.6%; Score 27; DB 17; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.1;

```

	Matches	27;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	12	GTGAGCCACCGTGCCTGGCCAGATTTT	38							
Db	314	GTGAGCCACCGTGCCTGGCCAGATTTT	340							

Search completed: June 17, 2003, 06:26:24  
Job time : 594.523 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 1317.49 Seconds  
(without alignments)  
15794.017 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_7806\_8520  
Perfect score: 715  
Sequence: 1 actgcccacgagacagag.....ttccctctagtctctccag 715

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 1000 summaries

Database :				GenEmbl.:			
1:	gb_ba.:	1:	gb_ba.:	1:	gb_ba.:	1:	gb_ba.:
2:	gb_htg.:	2:	gb_htg.:	2:	gb_htg.:	2:	gb_htg.:
3:	gb_in.:	3:	gb_in.:	3:	gb_in.:	3:	gb_in.:
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7:	gb_ph.:	7:	gb_ph.:	7:	gb_ph.:	7:	gb_ph.:
8:	gb_pl.:	8:	gb_pl.:	8:	gb_pl.:	8:	gb_pl.:
9:	gb_pr.:	9:	gb_pr.:	9:	gb_pr.:	9:	gb_pr.:
10:	gb_ro.:	10:	gb_ro.:	10:	gb_ro.:	10:	gb_ro.:
11:	gb_rts.:	11:	gb_rts.:	11:	gb_rts.:	11:	gb_rts.:
12:	gb_sy.:	12:	gb_sy.:	12:	gb_sy.:	12:	gb_sy.:
13:	gb_un.:	13:	gb_un.:	13:	gb_un.:	13:	gb_un.:
14:	gb_vi.:	14:	gb_vi.:	14:	gb_vi.:	14:	gb_vi.:
15:	em_ba.:	15:	em_ba.:	15:	em_ba.:	15:	em_ba.:
16:	em_fun.:	16:	em_fun.:	16:	em_fun.:	16:	em_fun.:
17:	em_hum.:	17:	em_hum.:	17:	em_hum.:	17:	em_hum.:
18:	em_in.:	18:	em_in.:	18:	em_in.:	18:	em_in.:
19:	em_mu.:	19:	em_mu.:	19:	em_mu.:	19:	em_mu.:
20:	em_om.:	20:	em_om.:	20:	em_om.:	20:	em_om.:
21:	em_or.:	21:	em_or.:	21:	em_or.:	21:	em_or.:
22:	em_ov.:	22:	em_ov.:	22:	em_ov.:	22:	em_ov.:
23:	em_pat.:	23:	em_pat.:	23:	em_pat.:	23:	em_pat.:
24:	em_ph.:	24:	em_ph.:	24:	em_ph.:	24:	em_ph.:
25:	em_pi.:	25:	em_pi.:	25:	em_pi.:	25:	em_pi.:
26:	em_ro.:	26:	em_ro.:	26:	em_ro.:	26:	em_ro.:
27:	em_rts.:	27:	em_rts.:	27:	em_rts.:	27:	em_rts.:
28:	em_un.:	28:	em_un.:	28:	em_un.:	28:	em_un.:
29:	em_vi.:	29:	em_vi.:	29:	em_vi.:	29:	em_vi.:
30:	em_htg_hum.:	30:	em_htg_hum.:	30:	em_htg_hum.:	30:	em_htg_hum.:
31:	em_htg_inv.:	31:	em_htg_inv.:	31:	em_htg_inv.:	31:	em_htg_inv.:
32:	em_htg_other.:	32:	em_htg_other.:	32:	em_htg_other.:	32:	em_htg_other.:
33:	em_htg_mus.:	33:	em_htg_mus.:	33:	em_htg_mus.:	33:	em_htg_mus.:
34:	em_htg_pln.:	34:	em_htg_pln.:	34:	em_htg_pln.:	34:	em_htg_pln.:
35:	em_htg_rtd.:	35:	em_htg_rtd.:	35:	em_htg_rtd.:	35:	em_htg_rtd.:
36:	em_htg_man.:	36:	em_htg_man.:	36:	em_htg_man.:	36:	em_htg_man.:
37:	em_htg_vrt.:	37:	em_htg_vrt.:	37:	em_htg_vrt.:	37:	em_htg_vrt.:
38:	em_sy.:	38:	em_sy.:	38:	em_sy.:	38:	em_sy.:
39:	em_htgo_hum.:	39:	em_htgo_hum.:	39:	em_htgo_hum.:	39:	em_htgo_hum.:
40:	em_htgo_mus.:	40:	em_htgo_mus.:	40:	em_htgo_mus.:	40:	em_htgo_mus.:
41:	em_htgo_other.:	41:	em_htgo_other.:	41:	em_htgo_other.:	41:	em_htgo_other.:

Result No.	Score	Query Match	Length	DB ID	Description
1	715	100.0	5492	9	AF123659 Homo sapi
2	715	100.0	9108	9	AF123653 Homo sapi
3	662	92.6	173264	2	AC025853 Homo sapi
4	22	3.1	113331	2	AC107283 Rattus no
5	22	3.1	159838	9	AC073991 Homo sapi
6	22	3.1	251905	2	AC093682 Homo sapi
7	21	2.9	11215	1	AE001783 Thermotog
8	21	2.9	84661	9	AL353695 Human DNA
9	21	2.9	147968	2	AC114256 Rattus no
10	21	2.9	155334	2	AC011156 Homo sapi
11	21	2.9	163315	2	AC120209 Mus muscu
12	21	2.9	164924	9	AC098966 Homo sapi
13	21	2.9	184835	2	AC068091 Homo sapi
14	21	2.9	230879	9	AP003465 Homo sapi
15	20	2.8	6975	10	AF139185 Rattus no
16	20	2.8	61583	2	AC100438 Mus muscu
17	20	2.8	63796	9	AL035660 Human DNA
18	20	2.8	74853	9	AC007900 Homo sapi
19	20	2.8	78438	2	AC095834 Rattus no
20	20	2.8	80484	9	AL511174 Human DNA
21	20	2.8	92095	2	AC107548 Rattus no
22	20	2.8	108605	2	AC103501 Rattus no
23	20	2.8	131570	9	AP002495 Homo sapi
24	20	2.8	133084	2	AC099208 Rattus no
25	20	2.8	135734	2	AC002346 Homo sapi
26	20	2.8	138709	2	AC093395 Bos tauru
27	20	2.8	143968	2	AC108404 Mus muscu
28	20	2.8	166379	9	AC074121 Homo sapi
29	20	2.8	169873	2	AC079881 Homo sapi
30	20	2.8	173269	2	AC068357 Homo sapi
31	20	2.8	178785	9	AC068139 Homo sapi
32	20	2.8	179936	2	AC025491 Homo sapi
33	20	2.8	181168	2	AC055888 Homo sapi
34	20	2.8	183301	2	AC092487 Homo sapi
35	20	2.8	184637	2	AC012043 Homo sapi
36	20	2.8	186731	2	AC073212 Homo sapi
37	20	2.8	187680	9	AC093333 Homo sapi
38	20	2.8	188121	2	AC093394 Bos tauru
39	20	2.8	191306	2	AC130544 Mus muscu
40	20	2.8	193675	2	AC010551 Homo sapi
41	20	2.8	193758	2	AL845440 Mus muscu
42	20	2.8	196245	10	AC092202 Mus muscu
43	20	2.8	197046	9	AC009123 Homo sapi
44	20	2.8	201642	2	AC124727 Mus muscu
45	20	2.8	203484	2	AC010194 Homo sapi
46	20	2.8	205588	9	AC068400 Homo sapi
47	20	2.8	210608	9	AC006028 Homo sapi
48	20	2.8	211438	2	AC122902 Mus muscu
49	20	2.8	220599	2	AL357792 Homo sapi
50	20	2.8	228201	2	AC016814 Mus muscu
51	19	2.7	179	9	HUMEMP07 L06513 Human eryth
52	19	2.7	348	4	AF42526081 AF425260 Equus cab
53	19	2.7	531	6	AX315176 Sequence
54	19	2.7	834	10	AF115410 Cricetulu
55	19	2.7	2335	9	HUMEMP42 M29399 Human eryth
56	19	2.7	2375	9	HUMF42SA M30646 Human eryth
57	19	2.7	2465	9	HUMF42LA M30647 Human eryth
58	19	2.7	2484	4	RAB11A11 L10237 Oryctolagus
59	19	2.7	2652	9	HUMEMP842 M60298 Human eryth
60	19	2.7	2702	9	BC001482 Homo sapi
61	19	2.7	2713	10	AF155144 Cricetulu
62	19	2.7	5246	10	MMIRS1 X69722 M.musculus
63	19	2.7	8331	9	HSU28054 U28054 Homo sapien
64	19	2.7	13110	1	AE012320 Xanthomon
65	19	2.7	36676	9	HSJ858B16 AL096768 Human DNA

Pred. No. is the number of results predicted by chance to have a

66	19	2.7	39203	9	AP001066	AP001066 Homo sapi	c 139	19	2.7	194287	10	AC087899	AC087899 Mus muscu
67	19	2.7	52614	2	AC090899	AC090899 Mus muscu	c 140	19	2.7	194520	10	AL691424	AL691424 Mouse DNA
68	19	2.7	52752	9	AL157773	AL157773 Human DNA	c 141	19	2.7	196496	2	AL805910	AL805910 Mus muscu
69	19	2.7	58145	2	AC125828	AC125828 Rattus no	c 142	19	2.7	197706	2	AL772232	AL772232 Mus muscu
70	19	2.7	62417	2	AC130360	AC130360 Homo sapi	c 143	19	2.7	200237	2	AC113533	AC113533 Mus muscu
71	19	2.7	66127	2	AC130367	AC130367 Homo sapi	c 144	19	2.7	200761	10	AC122140	AC122140 Mus muscu
72	19	2.7	86742	2	AC023223	AC023223 Homo sapi	c 145	19	2.7	200859	2	AC011218	AC011218 Homo sapi
73	19	2.7	89934	2	AC008867	AC008867 Homo sapi	c 146	19	2.7	201444	2	AL807810	AL807810 Mus muscu
74	19	2.7	95655	2	AC110069	AC110069 Homo sapi	c 147	19	2.7	202081	9	AL391987	AL391987 Human DNA
75	19	2.7	99858	9	HSJ1059A9	HSJ1059A9 Human DNA	c 148	19	2.7	205624	2	AC123494	AC123494 Rattus no
76	19	2.7	107880	2	AC129786	AC129786 Rattus no	c 149	19	2.7	208632	2	AC073711	AC073711 Mus muscu
77	19	2.7	108795	2	AC124894	AC124894 Rattus no	c 150	19	2.7	213973	2	AC109509	AC109509 Mus muscu
78	19	2.7	110000	2	AC003656 <sup>4</sup>	Continuation (5 of	c 151	19	2.7	220376	2	AC025579	AC025579 Mus muscu
79	19	2.7	110000	2	AC117408 <sup>1</sup>	Continuation (2 of	c 152	19	2.7	221222	2	AC023794	AC023794 Homo sapi
80	19	2.7	110000	2	HSS171M <sup>2</sup>	Continuation (3 of	c 153	19	2.7	224847	2	AC129569	AC129569 Mus muscu
81	19	2.7	111409	2	AL162741	AL162741 Homo sapi	c 154	19	2.7	225203	2	AC123856	AC123856 Mus muscu
82	19	2.7	114233	9	AF000783	AF000783 Homo sapi	c 155	19	2.7	225254	2	AL713994	AL713994 Mus muscu
83	19	2.7	115137	9	AF252831	AF252831 Homo sapi	c 156	19	2.7	226576	3	CNS07EGE	AL1590447 chromosom
84	19	2.7	121056	8	OSJN00204	AL663006 Oryza sat	c 157	19	2.7	230695	2	AL390719	AL390719 Homo sapi
85	19	2.7	121478	9	AL365229	AL365229 Human DNA	c 158	19	2.7	230760	2	AC073714	AC073714 Mus muscu
86	19	2.7	123843	2	AC128622	AC128622 Rattus no	c 159	19	2.7	230760	2	AC073714	AC073714 Mus muscu
87	19	2.7	129217	2	AC100442	AC100442 Mus muscu	c 160	19	2.7	230884	2	AC079523	AC079523 Mus muscu
88	19	2.7	130268	2	AF005541	AF005541 Oryza sat	c 161	19	2.7	240125	10	AL669982	AL669982 Mouse DNA
89	19	2.7	143334	9	AC005293	AC005293 Homo sapi	c 162	19	2.7	241714	2	AC083834	AC083834 Mus muscu
90	19	2.7	143843	2	AC103633	AC103633 Mus muscu	c 163	19	2.7	249285	2	AC093482	AC093482 Mus muscu
91	19	2.7	148845	9	AP001067	AP001067 Homo sapi	c 164	19	2.7	255345	2	AL807830	AL807830 Mus muscu
92	19	2.7	149574	2	AC109718	AC109718 Rattus no	c 165	19	2.7	256657	2	AC129177	AC129177 Mus muscu
93	19	2.7	152449	9	AC079319	AC079319 Homo sapi	c 166	19	2.7	314146	2	AC073759	AC073759 Mus muscu
94	19	2.7	153987	2	AC094593	AC094593 Rattus no	c 167	19	2.7	319404	2	AC112130	AC112130 Homo sapi
95	19	2.7	154311	2	AC121919	AC121919 Mus muscu	c 168	19	2.7	340000	9	AP001754	AP001754 Homo sapi
96	19	2.7	155111	2	AC119639	AC119639 Rattus no	c 169	19	2.7	340000	9	HS21C102	HS21C102 Homo sapi
97	19	2.7	156207	2	AC025507	AC025507 Homo sapi	c 170	18	2.5	186	9	HS75F2R	Z62942 H.sapiens C
98	19	2.7	157080	2	AC083981	AC083981 Homo sapi	c 171	18	2.5	198	9	HS78A5R	Z66135 H.sapiens C
99	19	2.7	158375	2	AC080039	AC080039 Homo sapi	c 172	18	2.5	204	10	MMBXSB3	U77306 Mus musculus
100	19	2.7	160716	2	AC053475	AC053475 Homo sapi	c 173	18	2.5	296	9	HS75F2F	Z62941 H.sapiens C
101	19	2.7	161407	9	AC010139	AC010139 Homo sapi	c 174	18	2.5	565	11	G59208	G59208 SHGC-110139
102	19	2.7	162446	9	AL137118	AL137118 Human DNA	c 175	18	2.5	583	6	AX390937	AX390937 Sequence
103	19	2.7	164141	2	AC025137	AC025137 Homo sapi	c 176	18	2.5	660	9	HS333658	AL333658 Homo sapi
104	19	2.7	164521	9	HSJ610C12	AL121762 Human DNA	c 177	18	2.5	694	14	AF516390	AF516390 Hepatitis
105	19	2.7	164885	2	AC119594	AC119594 Rattus no	c 178	18	2.5	749	9	HS328750	HS328750 Homo sapi
106	19	2.7	166134	2	AC117059	AC117059 Rattus no	c 179	18	2.5	801	10	RATTH	AL28750 Rat tyrosin
107	19	2.7	166521	9	AC013724	AC013724 Homo sapi	c 180	18	2.5	1110	9	HS3250392	HS3250392 Homo sapi
108	19	2.7	168515	9	AC022260	AC022260 Homo sapi	c 181	18	2.5	1473	8	SOU85200	SOU85200 Scenedemus
109	19	2.7	170981	2	AC129376	AC129376 Rattus no	c 182	18	2.5	1680	6	AR194958	AR194958 Sequence
110	19	2.7	172207	2	AC117698	AC117698 Mus muscu	c 183	18	2.5	1696	10	AF217089	AF217089 Rattus no
111	19	2.7	173438	9	AF003967	AF003967 Homo sapi	c 184	18	2.5	1728	4	AF117757	AF117757 Bos tauru
112	19	2.7	175676	2	AC117691	AC117691 Mus muscu	c 185	18	2.5	1734	10	MMREAR2	X76654 M.musculus
113	19	2.7	175853	2	AC123550	AC123550 Mus muscu	c 186	18	2.5	1741	5	AB042026	AB042026 Oncohync
114	19	2.7	176353	2	AC117106	AC117106 Rattus no	c 187	18	2.5	1774	10	MUSBFCGR3	M63495 Mouse Igg r
115	19	2.7	178660	9	AC009852	AC009852 Homo sapi	c 188	18	2.5	1775	10	AF003926	AF003926 Mus muscu
116	19	2.7	178889	2	AC128923	AC128923 Sus scrof	c 189	18	2.5	1818	10	AF058318	AF058318 Homo sapi
117	19	2.7	180167	2	AC129246	AC129246 Rattus no	c 190	18	2.5	1923	9	AK095213	AK095213 Homo sapi
118	19	2.7	180207	2	AC060802	AC060802 Homo sapi	c 191	18	2.5	2022	9	AK000266	AK000266 Homo sapi
119	19	2.7	181923	2	AC011372	AC011372 Homo sapi	c 192	18	2.5	2175	10	BC013528	BC013528 Mus muscu
120	19	2.7	182366	9	AL591926	AL591926 Human DNA	c 193	18	2.5	2261	9	BC006280	BC006280 Homo sapi
121	19	2.7	182660	2	AC012416	AC012416 Homo sapi	c 194	18	2.5	2318	9	BC030127	BC030127 Homo sapi
122	19	2.7	183982	2	AC009825	AC009825 Homo sapi	c 195	18	2.5	2472	10	AF080452	AF080452 Rattus no
123	19	2.7	186187	2	AC110369	AC110369 Rattus no	c 196	18	2.5	2516	9	AK094159	AK094159 Homo sapi
124	19	2.7	186882	9	AL136307	AL136307 Human DNA	c 197	18	2.5	2600	9	AK096925	AK096925 Homo sapi
125	19	2.7	186947	9	AC091493	AC091493 Homo sapi	c 198	18	2.5	2675	9	AK091639	AK091639 Homo sapi
126	19	2.7	187114	2	AC026998	AC026998 Homo sapi	c 199	18	2.5	3105	10	RATTHA	M23598 Rattus norv
127	19	2.7	187617	2	AC118993	AC118993 Rattus no	c 200	18	2.5	3483	9	HSB802181	HSB802181 Homo sapi
128	19	2.7	187985	2	AL591889	AL591889 Homo sapi	c 201	18	2.5	4066	1	PSEIS4018X	PSEIS4018X Pseudomonas
129	19	2.7	188062	9	AL162731	AL162731 Human DNA	c 202	18	2.5	4382	9	HSB802264	HSB802264 Rattus no
130	19	2.7	189126	2	AC073094	AC073094 Homo sapi	c 203	18	2.5	4518	10	AF069036	AF069036 Rattus no
131	19	2.7	189352	2	AC011967	AC011967 Homo sapi	c 204	18	2.5	4898	9	AF159447	AF159447 Homo sapi
132	19	2.7	189643	9	AL161729	AL161729 Human DNA	c 205	18	2.5	4919	6	AX405811	AX405811 Sequence
133	19	2.7	189648	2	AC118994	AC118994 Rattus no	c 206	18	2.5	5026	5	GGU16848	GGU16848 Gallus gall
134	19	2.7	190243	2	AC102729	AC102729 Mus muscu	c 207	18	2.5	5319	9	AB028953	AB028953 Homo sapi
135	19	2.7	190537	2	AC126156	AC126156 Rattus no	c 208	18	2.5	6349	9	HUMBAT2B4	HUMBAT2B4 Human HLA-B
136	19	2.7	190727	9	AC068724	AC068724 Homo sapi	c 209	18	2.5	6704	9	HUMBAT2A	HUMBAT2A Human HLA-B
137	19	2.7	190981	2	AC108961	AC108961 Rattus no	c 210	18	2.5	6801	10	RNU04998	RNU04998 Rattus norv
138	19	2.7	194246	9	AL627230	AL627230 Human DNA	c 211	18	2.5	6842	10	AF014956	AF014956 Rattus no

212	18	2.5	7851	10	RNU09357	U09357 Rattus norv	18	2.5	96132	2	AC017927	AC017927 Drosophil
c 213	18	2.5	11149	1	AE004587	AE004587 Pseudomon	18	2.5	97218	9	AC092385	AC092385 Homo sapi
c 214	18	2.5	11986	9	U77616	U77616 Human achae	18	2.5	97375	9	AL353898	AL353898 Human DNA
c 215	18	2.5	12931	9	HS358H9	AL023576 Human DNA	18	2.5	97451	2	AC068603	AC068603 Homo sapi
c 216	18	2.5	13161	1	AE000093	AE000093 Rhizobium	18	2.5	98853	2	AL30929	AL30929 Rattus no
c 217	18	2.5	15523	1	AE000705	AE000705 Aquifex a	18	2.5	99103	9	AL805934	AL805934 Human DNA
c 218	18	2.5	25406	9	AL513313	AL513313 Human DNA	18	2.5	100000	2	AP000505	AP000505 Homo sapi
c 219	18	2.5	32140	9	AC073863	AC073863 Homo sapi	18	2.5	100236	2	AC095963	AC095963 Rattus no
c 220	18	2.5	36886	9	AP001238	AP001238 Homo sapi	18	2.5	100436	2	AC087298	AC087298 Homo sapi
c 221	18	2.5	37918	9	AP005232	AP005232 Homo sapi	18	2.5	101445	9	AL133411	AL133411 Human DNA
c 222	18	2.5	39640	1	SCL2	AL137778 Streptomy	18	2.5	103196	9	AL589847	AL589847 Human DNA
c 223	18	2.5	39042	9	AP001224	AP001224 Homo sapi	18	2.5	103822	9	AL353639	AL353639 Human DNA
c 224	18	2.5	41589	9	AC020955	AC020955 Homo sapi	18	2.5	104785	9	AP001465	AP001465 Homo sapi
c 225	18	2.5	41630	3	U97592	U97592 Caenorhabdi	18	2.5	106216	9	AL161908	AL161908 Human DNA
c 226	18	2.5	43470	9	AP001216	AP001216 Homo sapi	18	2.5	107568	2	AF212832	AF212832 Homo sapi
c 227	18	2.5	44235	9	AC005262	AC005262 Homo sapi	18	2.5	107714	2	AL356306	AL356306 Homo sapi
c 228	18	2.5	44985	9	AC110781	AC110781 Homo sapi	18	2.5	110000	2	AC079625	AC079625 2 of
c 229	18	2.5	47625	2	AC1117803	AC1117803 Mus muscu	18	2.5	110000	2	AC091288	AC091288 2 of
c 230	18	2.5	49910	9	AC011689	AC011689 Homo sapi	18	2.5	110000	2	AC098773	AC098773 1 of
c 231	18	2.5	51411	2	AC101008	AC101008 Mus muscu	18	2.5	110000	2	AC108448	AC108448 2 of
c 232	18	2.5	54554	9	AC009500	AC009500 Homo sapi	18	2.5	110000	2	AC108448	AC108448 1 of
c 233	18	2.5	54787	9	AL355803	AL355803 Human DNA	18	2.5	110000	2	AC108448	AC108448 2 of
c 234	18	2.5	55832	2	AC124326	AC124326 Mus muscu	18	2.5	110000	2	HSS171M	HSS171M 0
c 235	18	2.5	56825	2	AC1113044	AC1113044 Mus muscu	18	2.5	110937	2	AC129054	AC129054 Rattus no
c 236	18	2.5	58661	2	AC068509	AC068509 Homo sapi	18	2.5	112293	2	AC129410	AC129410 Rattus no
c 237	18	2.5	57729	9	AL449284	AL449284 Human DNA	18	2.5	112620	2	AC131439	AC131439 Rattus no
c 238	18	2.5	58434	2	AC108446	AC108446 Homo sapi	18	2.5	112295	9	AC084337	AC084337 Homo sapi
c 239	18	2.5	58434	2	AC108446	AC108446 Homo sapi	18	2.5	112361	9	AC027316	AC027316 Homo sapi
c 240	18	2.5	58970	2	AC101231	AC101231 Mus muscu	18	2.5	112365	9	AC027317	AC027317 Homo sapi
c 241	18	2.5	59302	2	AC111339	AC111339 Rattus no	18	2.5	113793	2	AC098438	AC098438 Rattus no
c 242	18	2.5	59352	2	AC061983	AC061983 Homo sapi	18	2.5	114642	9	AL357033	AL357033 Human DNA
c 243	18	2.5	59396	2	AC009799	AC009799 Homo sapi	18	2.5	114835	9	AP001628	AP001628 Homo sapi
c 244	18	2.5	59999	9	AL499627	AL499627 Human DNA	18	2.5	116012	2	AC096210	AC096210 Rattus no
c 245	18	2.5	60269	9	AL5112490	AL5112490 Human DNA	18	2.5	116683	2	AC095543	AC095543 Rattus no
c 246	18	2.5	60612	2	AC079212	AC079212 Homo sapi	18	2.5	116836	2	AC098503	AC098503 Rattus no
c 247	18	2.5	61962	2	AC123616	AC123616 Mus muscu	18	2.5	116857	9	HSDJ655K7	HSDJ655K7
c 248	18	2.5	62197	9	AL589939	AL589939 Human DNA	18	2.5	118280	9	HSDJ753D5	HSDJ753D5
c 249	18	2.5	64244	2	AC101546	AC101546 Mus muscu	18	2.5	119660	2	AC123101	AC123101 Rattus no
c 250	18	2.5	64529	2	AC108449	AC108449 Homo sapi	18	2.5	119707	2	AL773521	AL773521 Sus scrof
c 251	18	2.5	64586	2	AC011279	AC011279 Homo sapi	18	2.5	119842	9	AC108537	AC108537 Rattus no
c 252	18	2.5	64953	2	AC015569	AC015569 Homo sapi	18	2.5	119847	9	AF064866	AF064866 Homo sapi
c 253	18	2.5	65302	2	AC111951	AC111951 Mus muscu	18	2.5	120480	9	AP000806	AP000806 Homo sapi
c 254	18	2.5	66066	2	AC126400	AC126400 Homo sapi	18	2.5	120637	10	CNS07YF1	CNS07YF1 Mus muscu
c 255	18	2.5	66104	2	AC123880	AC123880 Mus muscu	18	2.5	121982	9	HS1107C24	HS1107C24
c 256	18	2.5	66789	2	AC103807	AC103807 Homo sapi	18	2.5	122432	2	AL3390073	AL3390073 Homo sapi
c 257	18	2.5	68567	9	AL389916	AL389916 Human DNA	18	2.5	123219	6	AX195073	AX195073 Sequence
c 258	18	2.5	68875	9	AC096559	AC096559 Homo sapi	18	2.5	123302	2	AC095135	AC095135 Rattus no
c 259	18	2.5	70297	2	AC118615	AC118615 Mus muscu	18	2.5	124687	9	AL592164	AL592164 Human DNA
c 260	18	2.5	70474	9	AC109483	AC109483 Homo sapi	18	2.5	125000	9	AB017602	AB017602 Homo sapi
c 261	18	2.5	70642	2	AC099870	AC099870 Mus muscu	18	2.5	125110	9	AL450267	AL450267 Human DNA
c 262	18	2.5	72229	2	AC101639	AC101639 Mus muscu	18	2.5	125254	2	AC087399	AC087399 Homo sapi
c 263	18	2.5	72245	9	HS93C23	AL008713 Human DNA	18	2.5	125376	9	AP001627	AP001627 Homo sapi
c 264	18	2.5	74188	2	AC021315	AC021315 Homo sapi	18	2.5	125949	9	AC025442	AC025442 Homo sapi
c 265	18	2.5	75192	2	AC009215	AC009215 Drosophil	18	2.5	125959	2	AC122086	AC122086 Rattus no
c 266	18	2.5	76410	2	AC016093	AC016093 Homo sapi	18	2.5	126243	2	AC130997	AC130997 Rattus no
c 267	18	2.5	77175	2	AC105650	AC105650 Rattus no	18	2.5	126895	2	AL773562	AL773562 Sus scrof
c 268	18	2.5	77396	2	AC021779	AC021779 Homo sapi	18	2.5	128495	9	AL356913	AL356913 Human DNA
c 269	18	2.5	77790	9	AC026108	AC026108 Homo sapi	18	2.5	128868	9	HSB211023	HSB211023
c 270	18	2.5	78467	9	AC008078	AC008078 Homo sapi	18	2.5	131002	2	AC024392	AC024392 Homo sapi
c 271	18	2.5	79043	9	HS9J3614	AC009614 Homo sapi	18	2.5	132994	2	AC119046	AC119046 Rattus no
c 272	18	2.5	86131	2	AC108349	AC108349 Rattus no	18	2.5	133135	2	AL713970	AL713970 Homo sapi
c 273	18	2.5	87753	2	AC117852	AC117852 Rattus no	18	2.5	133141	2	AC128876	AC128876 Rattus no
c 274	18	2.5	88111	2	AC105556	AC105556 Rattus no	18	2.5	133730	2	AC104294	AC104294 Rattus no
c 275	18	2.5	90785	2	AC097694	AC097694 Rattus no	18	2.5	134213	9	CNS05TEV	CNS05TEV Human chr
c 276	18	2.5	90788	2	AC005442	AC005442 Drosophil	18	2.5	135784	9	AL662847	AL662847 Human DNA
c 277	18	2.5	91783	9	AL160006	AL160006 Human DNA	18	2.5	136232	2	AC024006	AC024006 Homo sapi
c 278	18	2.5	91842	9	AC008392	AC008392 Homo sapi	18	2.5	136372	9	AL103828	AL103828 Homo sapi
c 279	18	2.5	92347	2	AC103053	AC103053 Rattus no	18	2.5	139111	9	AL158048	AL158048 Human DNA
c 280	18	2.5	93179	9	AL356272	AL356272 Human DNA	18	2.5	139399	9	AL662801	AL662801 Human DNA
c 281	18	2.5	94629	2	AL139806	AL139806 Human DNA	18	2.5	139655	2	AC125152	AC125152 Mus muscu
c 282	18	2.5	94703	2	AC008563	AC008563 Homo sapi	18	2.5	139982	2	AC113500	AC113500 Mus muscu
c 283	18	2.5	95283	9	HS599F21	AL035662 Human DNA	18	2.5	140257	9	HSDJ551D2	HSDJ551D2 Human DNA
c 284	18	2.5	96128	10	AL663077	AL663077 Mouse DNA	18	2.5	141669	2	AC121194	AC121194 Rattus no

358	18	2.5	142121	9	AC078980	AC078980 Homo sapi	431	18	2.5	164008	2	AC024064	AC024064 Homo sapi
359	18	2.5	142155	10	AC092479	Mus muscu	C 432	18	2.5	164028	9	AC004890	AC004890 Homo sapi
360	18	2.5	142326	2	AC024047	AC024047 Homo sapi	C 433	18	2.5	164248	2	AC074248	AC074248 Homo sapi
361	18	2.5	142616	2	AC028646	AC028646 Homo sapi	C 434	18	2.5	164352	2	AC024008	AC024008 Homo sapi
362	18	2.5	143200	9	AC008413	AC008413 Homo sapi	435	18	2.5	164378	2	AC111675	AC111675 Rattus no
363	18	2.5	143620	9	AC0117425	AC0117425 Homo sapi	C 436	18	2.5	164655	9	AC007687	AC007687 Homo sapi
364	18	2.5	145882	2	AL139131	AL139131 Homo sapi	C 437	18	2.5	164790	2	AC068858	AC068858 Homo sapi
365	18	2.5	146001	2	AC112747	AC112747 Rattus no	438	18	2.5	164838	2	AL691479	AL691479 Homo sapi
366	18	2.5	146614	2	AC118967	AC118967 Rattus no	C 439	18	2.5	165007	9	AC019047	AC019047 Homo sapi
367	18	2.5	146715	9	AL355795	AL355795 Human DNA	C 440	18	2.5	165240	2	AC011040	AC011040 Homo sapi
368	18	2.5	147029	2	AC098249	AC098249 Rattus no	C 441	18	2.5	165501	2	AC037468	AC037468 Homo sapi
369	18	2.5	147109	9	AL591043	AL591043 Human DNA	C 442	18	2.5	165509	2	AC009886	AC009886 Homo sapi
370	18	2.5	147780	9	AP001979	AP001979 Homo sapi	C 443	18	2.5	165841	2	AC021409	AC021409 Homo sapi
371	18	2.5	148270	2	AC027579	AC027579 Homo sapi	C 444	18	2.5	165968	2	AC094158	AC094158 Rattus no
372	18	2.5	148663	2	AC120088	AC120088 Rattus no	C 445	18	2.5	166418	2	AC020990	AC020990 Homo sapi
373	18	2.5	148769	2	AC128968	AC128968 Rattus no	446	18	2.5	166600	9	AL391121	AL391121 Human DNA
374	18	2.5	148996	9	AC102953	AC102953 Homo sapi	447	18	2.5	166996	10	AL606470	AL606470 Mouse DNA
375	18	2.5	148996	9	AC102953	AC102953 Homo sapi	C 448	18	2.5	167130	2	AC114229	AC114229 Rattus no
376	18	2.5	149045	2	AC118440	AC118440 Rattus no	449	18	2.5	167348	2	AC027780	AC027780 Homo sapi
377	18	2.5	149363	2	AC109657	AC109657 Rattus no	C 450	18	2.5	167568	2	AC111734	AC111734 Rattus no
378	18	2.5	149437	2	AC027218	AC027218 Homo sapi	C 451	18	2.5	167687	2	AC023476	AC023476 Homo sapi
379	18	2.5	149532	2	AC123515	AC123515 Oryza sat	C 452	18	2.5	167732	9	AC091092	AC091092 Papio cyn
380	18	2.5	150011	2	AC068232	AC068232 Homo sapi	C 453	18	2.5	168182	2	AC068338	AC068338 Homo sapi
381	18	2.5	150145	9	AC069216	AC069216 Homo sapi	454	18	2.5	168310	2	AC010775	AC010775 Homo sapi
382	18	2.5	150494	2	AC078879	AC078879 Homo sapi	C 455	18	2.5	168318	2	AC024042	AC024042 Homo sapi
383	18	2.5	150573	2	AC102252	AC102252 Mus muscu	C 456	18	2.5	168435	2	AC098629	AC098629 Rattus no
384	18	2.5	150599	9	AL591504	AL591504 Human DNA	C 457	18	2.5	168505	2	AC080010	AC080010 Homo sapi
385	18	2.5	150834	9	AC005399	AC005399 Homo sapi	C 458	18	2.5	168614	9	AL357672	AL357672 Human DNA
386	18	2.5	151840	2	AL691446	AL691446 Mus muscu	C 459	18	2.5	168778	2	AC115743	AC115743 Mus muscu
387	18	2.5	152983	2	AC113733	AC113733 Rattus no	C 460	18	2.5	168906	2	AC129800	AC129800 Rattus no
388	18	2.5	153015	2	AC010442	AC010442 Homo sapi	C 461	18	2.5	168949	9	AC046134	AC046134 Homo sapi
389	18	2.5	153327	9	AC096636	AC096636 Homo sapi	C 462	18	2.5	168988	2	AC106979	AC106979 Rattus no
390	18	2.5	153468	9	AC113208	AC113208 Homo sapi	463	18	2.5	169289	2	AC026491	AC026491 Homo sapi
391	18	2.5	153836	8	AP005344	AP005344 Homo sapi	C 464	18	2.5	169341	2	AC017753	AC017753 Mus muscu
392	18	2.5	153865	9	AP002744	AP002744 Oryza sat	C 465	18	2.5	169384	2	AP001854	AP001854 Homo sapi
393	18	2.5	154064	9	AC022394	AC022394 Homo sapi	C 466	18	2.5	169939	2	AC117053	AC117053 Rattus no
394	18	2.5	154176	2	AC118829	AC118829 Rattus no	C 467	18	2.5	170000	2	AC006564	AC006564 Homo sapi
395	18	2.5	154283	2	AC112229	AC112229 Homo sapi	C 468	18	2.5	170255	2	AC120712	AC120712 Rattus no
396	18	2.5	154461	2	AC025711	AC025711 Homo sapi	C 469	18	2.5	170362	3	AC009250	AC009250 Drosophila
397	18	2.5	154737	9	AC078834	AC078834 Homo sapi	C 470	18	2.5	170670	2	AC121758	AC121758 Homo sapi
398	18	2.5	155065	9	HSJ659119	HSJ659119 Human DNA	C 471	18	2.5	170703	2	AC113391	AC113391 Homo sapi
399	18	2.5	155206	2	AC125884	AC125884 Rattus no	C 472	18	2.5	170725	2	AC087675	AC087675 Homo sapi
400	18	2.5	155488	2	AC008373	AC008373 Homo sapi	C 473	18	2.5	170880	2	AC128397	AC128397 Rattus no
401	18	2.5	155711	2	AC048335	AC048335 Homo sapi	C 474	18	2.5	170880	2	AC128397	AC128397 Rattus no
402	18	2.5	155843	2	AC106772	AC106772 Homo sapi	C 475	18	2.5	170928	9	AL356740	AL356740 Human DNA
403	18	2.5	156089	2	AC013750	AC013750 Homo sapi	476	18	2.5	170934	2	AL354684	AL354684 Homo sapi
404	18	2.5	156490	10	AL603709	AL603709 Mouse DNA	477	18	2.5	171142	9	AC069026	AC069026 Homo sapi
405	18	2.5	156814	9	AC006484	AC006484 Homo sapi	C 478	18	2.5	171146	9	AC117933	AC117933 Papio cyn
406	18	2.5	156957	9	AP001977	AP001977 Homo sapi	C 479	18	2.5	171200	9	AP000864	AP000864 Homo sapi
407	18	2.5	157183	9	AC011731	AC011731 Homo sapi	C 480	18	2.5	171261	9	AC129286	AC129286 Rattus no
408	18	2.5	157236	2	AC117068	AC117068 Rattus no	C 481	18	2.5	171539	9	CNS07EFS	AL512362 Human chr
409	18	2.5	157328	2	AC122990	AC122990 Rattus no	482	18	2.5	172238	9	AC090942	AC090942 Homo sapi
410	18	2.5	157566	9	AC022517	AC022517 Homo sapi	483	18	2.5	172261	2	AC111840	AC111840 Rattus no
411	18	2.5	158414	2	AC095422	AC095422 Rattus no	484	18	2.5	172360	2	AC024552	AC024552 Homo sapi
412	18	2.5	158519	9	AL135926	AL135926 Human DNA	485	18	2.5	172452	9	AC106332	AC106332 Rattus no
413	18	2.5	158653	9	AC105217	AC105217 Homo sapi	486	18	2.5	172465	9	AC110080	AC110080 Homo sapi
414	18	2.5	158910	9	AC007607	AC007607 Homo sapi	487	18	2.5	172693	2	AC074246	AC074246 Homo sapi
415	18	2.5	158944	9	AC096746	AC096746 Homo sapi	488	18	2.5	172847	2	AC116211	AC116211 Rattus no
416	18	2.5	159135	9	AC090060	AC090060 Homo sapi	489	18	2.5	172873	2	AC117799	AC117799 Mus muscu
417	18	2.5	159142	2	AC110680	AC110680 Rattus no	490	18	2.5	173277	2	AC120914	AC120914 Rattus no
418	18	2.5	159360	2	AC122607	AC122607 Rattus no	491	18	2.5	173488	2	AC078887	AC078887 Homo sapi
419	18	2.5	159926	9	AC007653	AC007653 Homo sapi	492	18	2.5	173742	2	AC114507	AC114507 Rattus no
420	18	2.5	160040	2	AC105674	AC105674 Rattus no	C 493	18	2.5	173751	2	AL590292	AL590292 Homo sapi
421	18	2.5	160279	2	AC019024	AC019024 Homo sapi	C 494	18	2.5	174253	2	AC068590	AC068590 Homo sapi
422	18	2.5	160800	2	AP002011	AP002011 Homo sapi	495	18	2.5	174303	2	AC099104	AC099104 Rattus no
423	18	2.5	161773	2	AC103491	AC103491 Rattus no	C 496	18	2.5	174535	9	AC106872	AC106872 Homo sapi
424	18	2.5	161988	2	AC009129	AC009129 Homo sapi	497	18	2.5	174547	9	AC006445	AC006445 Homo sapi
425	18	2.5	162367	2	AC095266	AC095266 Rattus no	C 498	18	2.5	174588	9	AC011841	AC011841 Homo sapi
426	18	2.5	163203	2	AC121206	AC121206 Rattus no	499	18	2.5	174659	2	AC128119	AC128119 Rattus no
427	18	2.5	163387	2	AC130912	AC130912 Rattus no	500	18	2.5	174705	2	AC101958	AC101958 Mus muscu
428	18	2.5	163613	9	AC078983	AC078983 Homo sapi	C 501	18	2.5	175026	2	AL512409	AL512409 Homo sapi
429	18	2.5	163871	9	HSJ158E12	HSJ158E12 Human DNA	502	18	2.5	175249	9	AC119038	AC119038 Homo sapi
430	18	2.5	163995	2	AC095112	AC095112 Rattus no	503	18	2.5	175271	2	AC116500	AC116500 Mus muscu

C 504	18	2.5	175776	2	AC112511	Homo sapi	AC112511	Homo sapi	C 577	18	2.5	189747	2	AC087791	Homo sapi	AC087791	Homo sapi
C 505	18	2.5	175916	9	AC007861	Homo sapi	AC007861	Homo sapi	C 578	18	2.5	189927	10	AC116588	Mus muscu	AC116588	Mus muscu
C 506	18	2.5	176123	9	AL390718	Human DNA	AL390718	Human DNA	C 579	18	2.5	190180	2	AC110539	Mus muscu	AC110539	Mus muscu
C 507	18	2.5	176209	9	AC009518	Homo sapi	AC009518	Homo sapi	C 580	18	2.5	190185	2	AC102050	Mus muscu	AC102050	Mus muscu
C 508	18	2.5	176360	2	AC129633	Rattus no	AC129633	Rattus no	C 581	18	2.5	190189	2	AC107477	Rattus no	AC107477	Rattus no
C 509	18	2.5	176644	9	AF002982	Homo sapi	AF002982	Homo sapi	C 582	18	2.5	190357	2	AC012259	Homo sapi	AC012259	Homo sapi
C 510	18	2.5	177034	9	AP002840	Homo sapi	AP002840	Homo sapi	583	18	2.5	190651	9	AL353811	Human DNA	AL353811	Human DNA
C 511	18	2.5	177250	2	AP000778	Homo sapi	AP000778	Homo sapi	584	18	2.5	190832	2	AC098161	Rattus no	AC098161	Rattus no
C 512	18	2.5	177286	9	AC008085	Homo sapi	AC008085	Homo sapi	585	18	2.5	190882	9	AL133355	Human DNA	AL133355	Human DNA
C 513	18	2.5	177300	2	AC102453	Mus muscu	AC102453	Mus muscu	C 586	18	2.5	191020	2	AC111129	Mus muscu	AC111129	Mus muscu
C 514	18	2.5	177447	2	AC104687	Homo sapi	AC104687	Homo sapi	C 587	18	2.5	191410	10	AC083814	Mus muscu	AC083814	Mus muscu
C 515	18	2.5	177521	2	AL161438	Homo sapi	AL161438	Homo sapi	C 588	18	2.5	191525	9	AC103830	Homo sapi	AC103830	Homo sapi
C 516	18	2.5	177541	2	AC129140	Rattus no	AC129140	Rattus no	C 589	18	2.5	192086	2	AC117634	Mus muscu	AC117634	Mus muscu
C 517	18	2.5	177801	2	AC114391	Rattus no	AC114391	Rattus no	C 590	18	2.5	192239	9	AC009796	Homo sapi	AC009796	Homo sapi
C 518	18	2.5	177818	2	AC120701	Rattus no	AC120701	Rattus no	591	18	2.5	192370	2	AC016857	Homo sapi	AC016857	Homo sapi
C 519	18	2.5	177941	9	AL445423	Human DNA	AL445423	Human DNA	592	18	2.5	192383	2	AC129753	Rattus no	AC129753	Rattus no
C 520	18	2.5	177976	2	AC090755	Homo sapi	AC090755	Homo sapi	593	18	2.5	192565	9	AC098935	Homo sapi	AC098935	Homo sapi
C 521	18	2.5	178080	2	AC011919	Homo sapi	AC011919	Homo sapi	594	18	2.5	192724	2	AC073825	Mus muscu	AC073825	Mus muscu
C 522	18	2.5	178168	2	AC024412	Homo sapi	AC024412	Homo sapi	595	18	2.5	193134	2	AC016702	Homo sapi	AC016702	Homo sapi
C 523	18	2.5	178171	2	AC026961	Homo sapi	AC026961	Homo sapi	C 596	18	2.5	193358	9	AL135960	Human DNA	AL135960	Human DNA
C 524	18	2.5	178410	2	AC125148	Mus muscu	AC125148	Mus muscu	C 597	18	2.5	193400	2	AC090669	Homo sapi	AC090669	Homo sapi
C 525	18	2.5	178478	2	AP002834	Homo sapi	AP002834	Homo sapi	C 598	18	2.5	193471	9	HSAL131016	Homo sapi	AJ131016	Homo sapi
C 526	18	2.5	178481	3	AC090872	Drosophil	AC090872	Drosophil	C 599	18	2.5	194630	2	AC128412	Rattus no	AC128412	Rattus no
C 527	18	2.5	178716	2	AC093216	Rattus no	AC093216	Rattus no	C 600	18	2.5	194973	9	AP002008	Homo sapi	AP002008	Homo sapi
C 528	18	2.5	178908	2	AC110206	Mus muscu	AC110206	Mus muscu	C 601	18	2.5	195197	9	AC020911	Homo sapi	AC020911	Homo sapi
C 529	18	2.5	178916	2	AP002874	Homo sapi	AP002874	Homo sapi	602	18	2.5	195270	9	AC096534	Homo sapi	AC096534	Homo sapi
C 530	18	2.5	179357	9	AC074191	Homo sapi	AC074191	Homo sapi	603	18	2.5	195290	2	AC074364	Homo sapi	AC074364	Homo sapi
C 531	18	2.5	179443	2	AC079051	Homo sapi	AC079051	Homo sapi	604	18	2.5	195538	9	AC092733	Homo sapi	AC092733	Homo sapi
C 532	18	2.5	179610	2	AC018445	Homo sapi	AC018445	Homo sapi	605	18	2.5	195792	2	AC118087	Rattus no	AC118087	Rattus no
C 533	18	2.5	179720	2	AC131436	Rattus no	AC131436	Rattus no	C 606	18	2.5	195792	2	AC118087	Rattus no	AC118087	Rattus no
C 534	18	2.5	179756	2	AC130143	Rattus no	AC130143	Rattus no	607	18	2.5	196274	2	AL645797	Mus muscu	AL645797	Mus muscu
C 535	18	2.5	180588	2	AL807398	Mus muscu	AL807398	Mus muscu	C 608	18	2.5	196319	2	AL645797	Mus muscu	AL645797	Mus muscu
C 536	18	2.5	180859	2	AC098994	Rattus no	AC098994	Rattus no	609	18	2.5	196377	2	AL691432	Homo sapi	AL691432	Homo sapi
C 537	18	2.5	181047	2	AC016765	Homo sapi	AC016765	Homo sapi	C 610	18	2.5	196378	2	AC117504	Homo sapi	AC117504	Homo sapi
C 538	18	2.5	181075	10	CNS07PY2	Mus muscu	AL713885	Mus muscu	611	18	2.5	197061	10	AL606914	Mouse DNA	AL606914	Mouse DNA
C 539	18	2.5	181182	2	AC084832	Homo sapi	AC084832	Homo sapi	612	18	2.5	197738	2	AC096146	Rattus no	AC096146	Rattus no
C 540	18	2.5	181254	2	AP000825	Homo sapi	AP000825	Homo sapi	613	18	2.5	197924	2	AC120771	Rattus no	AC120771	Rattus no
C 541	18	2.5	181589	9	AP000868	Homo sapi	AP000868	Homo sapi	614	18	2.5	198079	2	AC044917	Homo sapi	AC044917	Homo sapi
C 542	18	2.5	181648	2	AC027094	Homo sapi	AC027094	Homo sapi	C 615	18	2.5	198464	2	AC022764	Homo sapi	AC022764	Homo sapi
C 543	18	2.5	181672	2	AC119327	Rattus no	AC119327	Rattus no	C 616	18	2.5	198647	2	AL845157	Mus muscu	AL845157	Mus muscu
C 544	18	2.5	181683	2	AC021618	Homo sapi	AC021618	Homo sapi	617	18	2.5	198719	2	AC015716	Homo sapi	AC015716	Homo sapi
C 545	18	2.5	181991	9	AC025882	Homo sapi	AC025882	Homo sapi	618	18	2.5	199254	2	AC021144	Homo sapi	AC021144	Homo sapi
C 546	18	2.5	182202	2	AC067869	Homo sapi	AC067869	Homo sapi	619	18	2.5	199347	2	AL805952	Mus muscu	AL805952	Mus muscu
C 547	18	2.5	182314	9	AC009145	Homo sapi	AC009145	Homo sapi	C 620	18	2.5	199371	2	AC110515	Mus muscu	AC110515	Mus muscu
C 548	18	2.5	182760	2	AC123803	Mus muscu	AC123803	Mus muscu	621	18	2.5	199806	2	AC025580	Homo sapi	AC025580	Homo sapi
C 549	18	2.5	182895	2	AC011043	Homo sapi	AC011043	Homo sapi	C 622	18	2.5	200000	2	AC004689	Homo sapi	AC004689	Homo sapi
C 550	18	2.5	183309	2	AC018968	Homo sapi	AC018968	Homo sapi	C 623	18	2.5	200098	2	AC091161	Homo sapi	AC091161	Homo sapi
C 551	18	2.5	183358	9	AC019041	Homo sapi	AC019041	Homo sapi	C 624	18	2.5	200203	2	AC104890	Mus muscu	AC104890	Mus muscu
C 552	18	2.5	183584	9	AP003126	Homo sapi	AP003126	Homo sapi	C 625	18	2.5	200218	2	AC117248	Mus muscu	AC117248	Mus muscu
C 553	18	2.5	183584	30	AL360171	Human DNA	AL360171	Human DNA	626	18	2.5	200340	9	AC009997	Homo sapi	AC009997	Homo sapi
C 554	18	2.5	183619	2	AC111069	Mus muscu	AC111069	Mus muscu	C 627	18	2.5	200581	2	AC102652	Mus muscu	AC102652	Mus muscu
C 555	18	2.5	183674	2	AC016996	Homo sapi	AC016996	Homo sapi	C 628	18	2.5	200589	2	AC127735	Rattus no	AC127735	Rattus no
C 556	18	2.5	183685	2	AC093199	Rattus no	AC093199	Rattus no	C 629	18	2.5	200627	2	AC192225	Homo sapi	AC192225	Homo sapi
C 557	18	2.5	184007	2	AC120614	Rattus no	AC120614	Rattus no	C 630	18	2.5	200709	9	AC007317	Homo sapi	AC007317	Homo sapi
C 558	18	2.5	184321	2	AC025890	Homo sapi	AC025890	Homo sapi	C 631	18	2.5	200882	2	AC112377	Rattus no	AC112377	Rattus no
C 559	18	2.5	184525	2	AC127614	Rattus no	AC127614	Rattus no	C 632	18	2.5	201157	2	AC079189	Homo sapi	AC079189	Homo sapi
C 560	18	2.5	184598	9	AL139406	Human DNA	AL139406	Human DNA	C 633	18	2.5	201190	2	AC022256	Homo sapi	AC022256	Homo sapi
C 561	18	2.5	184666	9	DJ201G24	Homo sapi	AF129756	Homo sapi	C 634	18	2.5	201412	9	AC096921	Homo sapi	AC096921	Homo sapi
C 562	18	2.5	185147	2	AP002388	Homo sapi	AP002388	Homo sapi	C 635	18	2.5	201477	2	AC102653	Mus muscu	AC102653	Mus muscu
C 563	18	2.5	185967	9	GMS01DVR	Human chr	AL136001	Human chr	C 636	18	2.5	201570	2	AC095868	Rattus no	AC095868	Rattus no
C 564	18	2.5	186048	2	AC074190	Homo sapi	AC074190	Homo sapi	C 637	18	2.5	202086	10	AC080015	Mus muscu	AC080015	Mus muscu
C 565	18	2.5	186076	2	AC127664	Rattus no	AC127664	Rattus no	C 638	18	2.5	202231	2	AC113244	Homo sapi	AC113244	Homo sapi
C 566	18	2.5	186368	9	AP001189	Homo sapi	AP001189	Homo sapi	C 639	18	2.5	202235	2	AC113738	Homo sapi	AC113738	Homo sapi
C 567	18	2.5	186980	2	AC130961	Rattus no	AC130961	Rattus no	C 640	18	2.5	202358	10	AL596187	Mouse DNA	AL596187	Mouse DNA
C 568	18	2.5	187004	9	AC023154	Homo sapi	AC023154	Homo sapi	641	18	2.5	202634	2	AC114771	Homo sapi	AC114771	Homo sapi
C 569	18	2.5	187254	2	AC124649	Homo sapi	AC124649	Homo sapi	642	18	2.5	202686	10	AL589870	Mouse DNA	AL589870	Mouse DNA
C 570	18	2.5	187490	2	AC048378	Homo sapi	AC048378	Homo sapi	C 643	18	2.5	203010	9	AC006530	Homo sapi	AC006530	Homo sapi
C 571	18	2.5	187492	2	AC129260	Rattus no	AC129260	Rattus no	644	18	2.5	203131	2	AL831780	Mus muscu	AL831780	Mus muscu
C 572	18	2.5	188868	9	AC023232	Homo sapi	AC023232	Homo sapi	C 645	18	2.5	203481	30	AC023470	Homo sapi	AC023470	Homo sapi
C 573	18	2.5	188936	2	AC110238	Mus muscu	AC110238	Mus muscu	C 646	18	2.5	204038	2	AC121821	Mus muscu	AC121821	Mus muscu
C 574	18	2.5	189123	2	AC093998	Rattus no	AC093998	Rattus no	647	18	2.5	204045	2	AL805918	Mus muscu	AL805918	Mus muscu
C 575	18	2.5	189339	2	AC123548	Mus muscu	AC123548	Mus muscu	648	18	2.5	204166	2	AL629385	Rattus no	AL629385	Rattus no
C 576	18	2.5	189639	2	AC008246	Homo sapi	AC008246	Homo sapi	C 649	18	2.5	204641	2	AC016056	Homo sapi	AC016056	Homo sapi

c 650	18	2.5	204720	2	AC008052	AC008052 Homo sapi	c 723	18	2.5	340000	9	HS21C083	AL163283 Homo sapi
c 651	18	2.5	205397	2	AC124366	AC124366 Mus muscu	c 724	18	2.5	340000	9	HS21C101	AL163301 Homo sapi
c 652	18	2.5	205673	2	AC073131	AC073131 Homo sapi	c 725	18	2.5	344000	1	TAC1D1	AL445063 Thermopla
c 653	18	2.5	205796	2	AL713891	AL713891 Mus muscu	c 726	18	2.5	347310	2	AC018743	AC018743 Homo sapi
c 654	18	2.5	205873	2	AC073147	AC073147 Homo sapi	c 727	18	2.5	350000	10	AC091453	AC091453 Mus muscu
c 655	18	2.5	206457	9	AC013268	AC013268 Homo sapi	c 728	17	2.4	151	9	HSACEINT3	AF022146 Homo sapi
c 656	18	2.5	206804	2	AC113474	AC113474 Mus muscu	c 729	17	2.4	202	9	HS36D8R	258347 H.sapiens C
c 657	18	2.5	207374	2	CNS07EFU	AL583722 Human chr	c 730	17	2.4	224	9	HSU52699	US2699 Human tenas
c 658	18	2.5	207593	2	AC023474	AC023474 Homo sapi	c 731	17	2.4	232	6	AX310198	AX310198 Sequence
c 659	18	2.5	207706	2	AL163393	AL163393 Mus muscu	c 732	17	2.4	270	9	AB00905514	AB009070 Homo sapi
c 660	18	2.5	208315	1	AF003017	AF003017 Mesorhizo	c 733	17	2.4	278	9	HSAL010550	AFJ010550 Homo sapi
c 661	18	2.5	208817	2	AC094908	AC094908 Rattus no	c 734	17	2.4	290	9	AF485427	AF485427 Homo sapi
c 662	18	2.5	208844	2	AC125070	AC125070 Mus muscu	c 735	17	2.4	290	9	HS33B9F	Z65337 H.sapiens C
c 663	18	2.5	208983	9	AC021124	AC021124 Homo sapi	c 736	17	2.4	291	9	AF482657	Z65337 H.sapiens C
c 664	18	2.5	209512	9	CNS018OV	AL109758 Human chr	c 737	17	2.4	300	9	HS3Q1026	Z65337 H.sapiens C
c 665	18	2.5	209693	2	AL163363	AL163363 Homo sapi	c 738	17	2.4	311	14	AF008009	Z65337 H.sapiens C
c 666	18	2.5	210000	2	AC004599	AC004599 Homo sapi	c 739	17	2.4	350	6	AX246782	AF008009 Hepatitis
c 667	18	2.5	211201	9	AC009958	AC009958 Homo sapi	c 740	17	2.4	364	11	AU026036	AX246782 Sequence
c 668	18	2.5	211463	2	AC016508	AC016508 Homo sapi	c 741	17	2.4	369	6	A40218	AU026036 Rattus no
c 669	18	2.5	211960	2	AC090288	AC090288 Mus muscu	c 742	17	2.4	369	6	CDAL131335	A40218 Sequence 1
c 670	18	2.5	212553	2	AC099581	AC099581 Mus muscu	c 743	17	2.4	369	8	DGL131334	AJ131335 Cynodon d
c 671	18	2.5	212621	2	AL808013	AL808013 Mus muscu	c 744	17	2.4	369	8	HLA131336	AJ131334 Dactylis
c 672	18	2.5	213053	2	AC114611	AC114611 Mus muscu	c 745	17	2.4	369	8	HLA131336	AJ131336 Lolium it
c 673	18	2.5	213946	2	AC102534	AC102534 Mus muscu	c 746	17	2.4	369	8	PPRI131337	AJ131333 Poa prate
c 674	18	2.5	214000	10	AC093317	AC093317 Mus muscu	c 747	17	2.4	369	8	TAE131338	AJ131337 Poa prate
c 675	18	2.5	215524	10	AL603913	AL603913 Mouse DNA	c 748	17	2.4	378	9	S76053	AJ131338 Triticum
c 676	18	2.5	218074	9	HUAC002044	AC002044 Human Chr	c 749	17	2.4	420	6	AR025424	S76053 LW opsin=lo
c 677	18	2.5	218093	2	AC114999	AC114999 Mus muscu	c 750	17	2.4	420	6	AR025424	AR025424 Sequence
c 678	18	2.5	218237	2	AL805924	AL805924 Mus muscu	c 751	17	2.4	421	11	G67698	AR025424 Sequence
c 679	18	2.5	218511	2	AC099420	AC099420 Rattus no	c 752	17	2.4	422	14	AF060831	G67698 MARC3086-30
c 680	18	2.5	218588	2	AC116317	AC116317 Homo sapi	c 753	17	2.4	432	11	G06957	AF060831 Hepatitis
c 681	18	2.5	219381	2	AC125077	AC125077 Mus muscu	c 754	17	2.4	438	10	RATTCRAP	G06957 human STS W
c 682	18	2.5	219522	2	AC091324	AC091324 Mus muscu	c 755	17	2.4	525	8	PPHPLPII	L37971 Rattus norv
c 683	18	2.5	219696	2	AC112960	AC112960 Mus muscu	c 756	17	2.4	539	4	AF163296	X75925 P.pratense
c 684	18	2.5	220684	2	AC095514	AC095514 Rattus no	c 757	17	2.4	539	4	AF163297	AF163297 Equus cab
c 685	18	2.5	220727	2	AL672234	AL672234 Mus muscu	c 758	17	2.4	547	9	HUMPLAP2A	AF163297 Equus cab
c 686	18	2.5	221003	2	AC103294	AC103294 Rattus no	c 759	17	2.4	617	6	AX011652	M19891 Human germ
c 687	18	2.5	221986	9	AC010999	AC010999 Homo sapi	c 760	17	2.4	645	10	MMBABI7AA	AX011652 Sequence
c 688	18	2.5	222722	2	AC125348	AC125348 Mus muscu	c 761	17	2.4	715	9	HS332076	X70804 M.musculus
c 689	18	2.5	223412	2	AC124500	AC124500 Mus muscu	c 762	17	2.4	724	3	AF519414	AJ332076 Homo sapi
c 690	18	2.5	224257	2	AC091248	AC091248 Mus muscu	c 763	17	2.4	724	11	PM6C8G	AF519414 Strongylo
c 691	18	2.5	224790	2	AC127556	AC127556 Mus muscu	c 764	17	2.4	736	3	AF519413	AL684926 Penicill
c 692	18	2.5	225016	2	AC105703	AC105703 Rattus no	c 765	17	2.4	745	11	G67670	AF519413 Strongylo
c 693	18	2.5	226013	2	AC073680	AC073680 Mus muscu	c 766	17	2.4	757	8	PEQ131963	G67670 MARC4001-40
c 694	18	2.5	228220	10	AL603829	AL603829 Mouse DNA	c 767	17	2.4	763	9	HS333930	AJ131963 Doritis p
c 695	18	2.5	228872	2	AC105471	AC105471 Rattus no	c 768	17	2.4	877	10	BC008256	AJ333930 Homo sapi
c 696	18	2.5	228330	2	AC087417	AC087417 Mus muscu	c 769	17	2.4	905	9	HS334267	BC008256 Mus muscu
c 697	18	2.5	229302	2	AC023534	AC023534 Homo sapi	c 770	17	2.4	939	8	AF159386	AJ334267 Homo sapi
c 698	18	2.5	232270	2	AC098445	AC098445 Rattus no	c 771	17	2.4	942	3	AF218885S3	AF159386 Secale ce
c 699	18	2.5	234133	2	AC105610	AC105610 Rattus no	c 772	17	2.4	962	9	HSMB02047	AF218887 Drosophil
c 700	18	2.5	235886	2	AC024173	AC024173 Mus muscu	c 773	17	2.4	984	9	AF211977	AL137360 Homo sapi
c 701	18	2.5	236165	6	A79351	A79351 Sequence 2	c 774	17	2.4	999	6	AX018072	AF211977 Homo sapi
c 702	18	2.5	236165	6	A79351	A79351 Sequence 2	c 775	17	2.4	1025	6	AX018072	AX018072 Sequence
c 703	18	2.5	239289	6	A93003	A93003 Sequence 2	c 776	17	2.4	1030	1	AF115252	AF115252 Homo sapi
c 704	18	2.5	239995	2	AC073154	AC073154 Mus muscu	c 777	17	2.4	1035	1	AF164522	AF115252 Homo sapi
c 705	18	2.5	244254	9	HSAC001228	AC001228 244Kb Con	c 778	17	2.4	1041	5	AF185587	AF164522 Moraxella
c 706	18	2.5	244382	2	AC125044	AC125044 Mus muscu	c 779	17	2.4	1118	8	AF305075	AF185587 Rana pipi
c 707	18	2.5	244978	9	AF241726	AF241726 Homo sapi	c 780	17	2.4	1165	4	AF060515	AF305075 Nicotiana
c 708	18	2.5	245207	2	AL732491	AL732491 Mus muscu	c 781	17	2.4	1307	9	HSPTK6S1	AF060515 Homo sapi
c 709	18	2.5	249469	3	AE003653	AE003653 Drosophil	c 782	17	2.4	1368	9	BC006361	AF091738 Oryctolag
c 710	18	2.5	251202	2	AC091902	AC091902 Homo sapi	c 783	17	2.4	1383	1	AF373208	U61406 Homo sapien
c 711	18	2.5	253108	2	AC104517	AC104517 Mus muscu	c 784	17	2.4	1493	6	AR025393	BC006361 Homo sapi
c 712	18	2.5	259158	2	AL645478	AL645478 Mus muscu	c 785	17	2.4	1493	6	AR025393	AF373208 Bacillus
c 713	18	2.5	259498	2	AC020876	AC020876 Mus muscu	c 786	17	2.4	1640	6	AX018177	AR025393 Sequence
c 714	18	2.5	260310	2	AL645852	AL645852 Mus muscu	c 787	17	2.4	1643	10	MUSEARATFA	AR094203 Sequence
c 715	18	2.5	262432	2	AC127551	AC127551 Mus muscu	c 788	17	2.4	1653	10	BC013170	AX018177 Sequence
c 716	18	2.5	262951	2	AC124848	AC124848 Homo sapi	c 789	17	2.4	1657	3	AF172639	L25674 Mus musculu
c 717	18	2.5	264752	10	AL669856	AL669856 Mouse DNA	c 790	17	2.4	1734	6	AR068185	BC013170 Mus muscu
c 718	18	2.5	266552	2	AC091362	AC091362 Rattus no	c 791	17	2.4	1734	6	AR076937	AF172639 Drosophil
c 719	18	2.5	271789	2	AC098259	AC098259 Rattus no	c 792	17	2.4	1734	6	AR076937	AR068185 Sequence
c 720	18	2.5	272047	2	AC123944	AC123944 Mus muscu	c 793	17	2.4	1734	6	AR078770	AR076937 Sequence
c 721	18	2.5	340000	9	AP001747	AP001747 Homo sapi	c 794	17	2.4	1734	6	AR128037	AR078770 Sequence
c 722	18	2.5	340000	9	HS21C003	AL163203 Homo sapi	c 795	17	2.4	1734	14	NDU37191	AR128037 Sequence

796	17	2.4	1734	14	NDU37193	U37193 Newcastle d	869	17	2.4	3416	6	AR055725	Sequence
797	17	2.4	1737	14	AF222036	AF222036 Influenza	870	17	2.4	3416	6	AR058275	Sequence
798	17	2.4	1757	14	AF222035	AF222035 Influenza	871	17	2.4	3416	6	HSU33284	Human prote
799	17	2.4	1772	14	AF222027	AF222027 Influenza	c 872	17	2.4	3444	10	BC016891	BC016891 Mus muscu
800	17	2.4	1773	14	AF222026	AF222026 Influenza	c 873	17	2.4	3504	6	AR085763	Sequence
801	17	2.4	1775	9	AK057638	AK057638 Homo sapi	c 874	17	2.4	3504	6	I73041	I73041 Sequence 3
802	17	2.4	1797	9	AF058317	AF058317 Homo sapi	c 875	17	2.4	3507	6	AX189651	AX189651 Sequence
803	17	2.4	1797	9	HS269477	AJ269477 Homo sapi	c 876	17	2.4	3594	9	HSU12472	HSU12472 Human gluta
804	17	2.4	1803	4	DOGBNPA	M31777 Dog brain n	877	17	2.4	3617	9	HSU12472	HSU12472 Human gluta
805	17	2.4	1803	6	AX050405	AX050405 Sequence	878	17	2.4	3620	9	HSU12472	HSU12472 Human gluta
806	17	2.4	1804	6	AR073103	AR073103 Sequence	c 879	17	2.4	3620	9	S80542	S80542 Homo sapien
807	17	2.4	1818	3	AF193812	AF193812 Sequence	c 879	17	2.4	3649	1	AF062350	AF062350 Bacillus
808	17	2.4	1824	9	AF096001	AF096001 Homo sapi	880	17	2.4	3671	1	U01158	U01158 Rhodospirill
809	17	2.4	1838	3	AF181624	AF181624 Rhodophil	c 881	17	2.4	3780	1	AB012288	AB012288 Bacillus
810	17	2.4	1867	9	HS269477	AJ269477 Homo sapi	c 882	17	2.4	3802	1	AFACOSYN	AFACOSYN
811	17	2.4	1907	6	AR034177	AJ250807 Homo sapi	883	17	2.4	3905	9	HSU12472	HSU12472 Human gluta
812	17	2.4	1907	6	AR034177	AR034177 Sequence	c 884	17	2.4	3913	1	PTCRYPRTB	PTCRYPRTB
813	17	2.4	1907	6	AR111525	AR111525 Sequence	c 885	17	2.4	3936	1	PTCRYPRTB	PTCRYPRTB
814	17	2.4	1907	6	AR158151	AR158151 Sequence	c 886	17	2.4	3936	1	PTCRYPRTB	PTCRYPRTB
815	17	2.4	1925	9	BC015935	BC015935 Homo sapi	c 887	17	2.4	3956	10	AF366052	AF366052 Mus muscu
816	17	2.4	1935	9	HUMPYPI	D13897 Human DNA f	c 887	17	2.4	3974	10	RNU77971	RNU77971 Rattus norv
817	17	2.4	1959	10	BC008138	BC008138 Mus muscu	c 888	17	2.4	4003	9	HSCU2NSO	HSCU2NSO
818	17	2.4	1962	14	M16573	M16573 Newcastle d	889	17	2.4	4041	9	AB046859	AB046859 Homo sapi
819	17	2.4	1971	10	AF258602	AF258602 Mus muscu	890	17	2.4	4089	9	HUMPAK2R	HUMPAK2R
820	17	2.4	1986	10	AF041788	AF041788 Rattus no	c 891	17	2.4	4127	9	AK074158	AK074158 Homo sapi
821	17	2.4	1989	10	AF031642	AF031642 Rattus no	892	17	2.4	4151	9	HSU43522	HSU43522
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833	17	2.4	2203	6	AX140304	AX140304 Sequence	c 904	17	2.4	4922	9	AF352730	AF352730 Homo sapi
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846	17	2.4	2479	10	BC027297	BC027297 Mus muscu	c 917	17	2.4	6042	1	AF358862	AF358862 Bacillus
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852	17	2.4	2528	6	AX464328	AX464328 Sequence	c 923	17	2.4	7518	9	AF284036	AF284036 Homo sapi
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854	17	2.4	2568	6	AX011636	AX011636 Sequence	c 925	17	2.4	7928	6	AX039412	AX039412 Sequence
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856	17	2.4	2644	6	AX140299	AX140299 Sequence	c 927	17	2.4	8542	2	AC048355	AC048355 Mus muscu
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859	17	2.4	2730	1	AF502245	AF502245 Moorella	c 930	17	2.4	8671	9	HUMITR	HUMITR
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944	17	2.4	9980	6	AX336437	AX336437 Sequence
945	17	2.4	9980	6	AX410706	AX410706 Sequence
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951	17	2.4	11444	1	AE010187	AE010187 Pyrococcu
952	17	2.4	11684	8	AB058924	AB058924 Hordeum v
953	17	2.4	11769	10	AF144095	AF144095 Mus muscu
954	17	2.4	11876	9	AF144094	AF144094 Homo sapi
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956	17	2.4	13469	10	AB013484S1	AB013484 Mus muscu
957	17	2.4	13875	6	AR069851	AR069851 Sequence
958	17	2.4	13875	6	AF309418	AF309418 Human putat
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960	17	2.4	15186	14	AF375823	AF375823 Newcastl
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962	17	2.4	18319	10	AF287911	AF287911 Mus muscu
963	17	2.4	20551	1	AE008713	AE008713 Salmonell
964	17	2.4	21498	2	AC020297	AC020297 Drosophil
965	17	2.4	22673	2	AC012925	AC012925 Drosophil
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981	17	2.4	33903	3	AC012326	AC012326 Leishmani
982	17	2.4	34363	2	AC107872	AC107872 Homo sapi
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984	17	2.4	35487	9	HSA276674	AJ276674 Homo sapi
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## ALIGNMENTS

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 DEFINITION  
 ACCESSION AF123659  
 VERSION AF123659.1 GI:4572475  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5492) Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M. The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999) 99199287 MEDLINE 10097140 PUBMED 2 (bases 1 to 5492) Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M. Direct Submission Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer Institute, 233S 10th street, Philadelphia, PA 19107, USA FEATURES Location/Qualifiers source 1. 5492 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="8" /map="8p22" 1. 5492 /genes="FEZ1" 112..1902 /genes="FEZ1" /codon\_start=1 /product="FEZ1" /protein\_id="AAD23840.1" /db\_xref="GI:4572476" /translations="MGVSSSLISGHSFHSKCRASOVKLRKSHLKKLNYSGLGLRF GFSQDSGHGKSSSKMSGSEDFYIKVSKARGSHHPDYLTALSSDGLGQAGVDFDPT PPKLMPFSQNLGSEKGAVPFAFPVLPKRSAILHSSPESASHQHPAPPKPKSQ ELKPLGCSGALSDFGRNSMESLPTSSSYQLDPLVTPGTSRFGSGAHNTTQGLV LODSNMWSLKALSFSDGSKLHNSKADKSPFCSPISPTDECSIQLEOKLJREGA VLQLOEFKELELASLAYEERRRRDELEGPEPKGNKLGKQASQKSAQVQVHLIQ LKLOQBEKRLQLESLMEQDLLETKLRSYERKTSFGPALEETQWECVQKSGEIS LLKQOLKESQTEVNKASEILGKAOQLTRGLELRTQDLEGALRTKGLGLEVC ENLQKQKNEALLREKVLLEQLELQRAQALARDMGPTPEDVPALQRELERLR AEUREKQHDQMSGFQHERLVWKEKEKVIQYQKQLQSQVYVAMYNORLEKALQ LARGDSAGEPLVDLEGADIPEDIIATIE"

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Query Match 100.0%; Score 715; DB 9; Length 5492;  
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Qy 121 GTGGCTGCCACCCACGGGAGGCGCTGGGGGAGGCTGTGCTCCGCCATGTGTCTCC 180  
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Qy 181 GGTACCTTCCATACACAGAGAGTGACGCTTCTCCATATCTCCATATCTCCATGGCCCTGTCCCAGG 240  
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Qy 301 TGGGCTGCCACCCACGGGAGGCGCTGGGGGAGGCTGTGCTCCGCCATGTGTCTCC 360  
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Qy 361 TGCACCTTGCAACCTCACCTTCTCTGTGGGTGTTCTTTCTCTGCCTGTCTCAAAAGCGCCC 420



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VERSION AF123653.1 GI:4572463  
KEYWORDS  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 9108)  
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,  
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.  
The FEZ1 gene at chromosome 9p22 encodes a leucine-zipper protein,  
and its expression is altered in multiple human tumors  
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
99199287  
10097140  
2 (bases 1 to 9108)  
Ishii.H., Baffa.R., Numata.S.I., Murakumo.Y., Rattan.S., Inoue.H.,  
Mori.M., Fidanza.V., Alder.H. and Croce.C.M.  
Direct Submission  
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
Institute, 233S 10th street, Philadelphia, PA 19107, USA  
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BASE COUNT 2021 a 2628 c 2504 g 1952 t 3 others  
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Query Match 100.0%; Score 715; DB 9; Length 9108;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 7926 CAATCCAGGAAGAGCAGTCCAGTCCAGTCTGCTCAGACGTTTGCCTGAGAAGAA 7985  
Qy 121 GTGGCTGCCACACCCAGGGGAAGCCCTGAGGGGAGGCTGTGTCCGCCATGTGTCCC 180  
Db 7986 GTGGCTGCCACACCCAGGGGAAGCCCTGAGGGGAGGCTGTGTCCGCCATGTGTCCC 8045  
Qy 181 GGTACCTTCCATACACAGAGAGTGCAGCCCTTCCATATCTCCATGGCCCTGTCCCAGG 240  
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Qy 241 CCGGCCCAGATGTGTCCCCAGGCGCTGTGCTTACCTGCAAGGTGGCAGATGTCTCCC 300  
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Qy 301 TGGGCTGCCACACGCGCCCGCCAGAGTGGCCACCGTGGCACTAGAAATGCAAGTATCC 360  
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Db 8286 TCATATTCTTGGACCATGCCAGATCTGCTCTCTGGAAGAGGCTCTGACAGCAGAA 8345  
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DEFINITION Homo sapiens chromosome 8 clone RP11-353K12 map 8, \*\*\* SEQUENCING  
IN PROGRESS \*\*\*, 3 unordered pieces.  
ACCESSION AC025853  
VERSION AC025853.13 GI:21431202  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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ACCESSION  AC107283
VERSION    AC107283.3 GI:21737480
KEYWORDS   HTG; HTGS PHASE1.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 113331)
AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Albrooks,S.L., Amarutunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
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            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstein,G. and Gibbs,R.
            Direct Submission
            Unpublished
            2 (bases 1 to 113331)
            Worley,K.C.
            Direct Submission
            Submitted (18-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 113331)
            Worley,K.C.
            Direct Submission
            Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Jul 12, 2002 this sequence version replaced gi:18702073.
            ----- Genome Center
            Center: Baylor College of Medicine
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ----- Project Information
            -----

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Center project name: GPFI  
Center clone name: CH230-28C24  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 62012 bases at least Q40  
Consensus quality: 5120 bases at least Q30  
Consensus quality: 68175 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 48 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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18708: contig of 1623 bp in length  
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GAGGAAGGGTGGTCCCCCT 39
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LOCUS Homo sapiens BAC clone RP11-512120 from 4, complete sequence.
DEFINITION AC073991
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VERSION AC073991.2 GI:14209802
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 159838)
AUTHORS Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence

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Genome Res. 8 (11), 1097-1108 (1998)

98063792

9847074

2 (bases 1 to 159838)

Harris, A. and Kozlowski, A.

The sequence of Homo sapiens BAC clone RP11-512120

Unpublished

3 (bases 1 to 159838)

Waterston, R.H.

Direct Submission

Submitted (08-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 159838)

Waterston, R.H.

Direct Submission

Submitted (03-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

5 (bases 1 to 159838)

Waterston, R.H.

Direct Submission

Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On May 26, 2001 this sequence version replaced gi:8980014.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)

----- Summary Statistics

-----

Center project name: H\_NH0512120

-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Taten, M., Catanese, J.J. and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-669F3; the clone sequenced to the right is AC006230. Actual start of this clone is at base position 1 of RP11-512120; actual end is at base position 159838 of RP11-512120.

Location/Qualifiers

1..159838

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FEATURES

source



MO 63108, USA

## COMMENT

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc/index.shtml>  
 ----- Project Information -----  
 Center project name: H\_NH0665024  
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 Chemistry: Dye-terminator ET; 0% of reads  
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 Assembly program: Phrap; version 0.990319  
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 Consensus quality: 231845 bases at least Q20  
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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 87 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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DICHRGASISHGKVLNSGERVMCPHGFYDSQGRVITPANGRNTVPENFVKSY

```

Query Match 2.9%; Score 21; DB 1; Length 11215;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 TCITTCCTGCCCTGTCACAAA 414  
|||||  
Db 6347 TCITTCCTGCCCTGTCACAAA 6327

RESULT 8  
AL353695

LOCUS Human DNA sequence from clone RP11-17L7 on chromosome 9, complete  
DEFINITION linear PRI 13-JUL-2001

ACCESSION AL353695  
VERSION AL353695.7 GI:14787448  
KEYWORDS HTG.  
SOURCE Human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 84661)

REFERENCE  
AUTHORS Laird,G.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

COMMENTS  
On Jul 17, 2001 this sequence version replaced gi:14267775.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em., EMBL; Sw.,  
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; information on the WORMPEP



database can be found at  
[http://www.sanger.ac.uk/projects/c\\_elegans/wormpep](http://www.sanger.ac.uk/projects/c_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr9>  
 RP11-17L7 is from the library RP11-11.1 constructed by the group of  
 Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone  
 RP11-17L7 it may be shorter because we sequence overlapping  
 sections only once, except for a 100 base overlap.  
 The true left end of clone RP11-57C19 is at 84562 in this sequence.  
 The true right end of clone RP11-618A20 is at 100 in this sequence.

## FEATURES

Location/Qualifiers

source

1..84661  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP11-17L7"  
 /clone\_lib="RP11-11.1"

repeat\_region 444..747  
 /note="AluY repeat: matches 1..304 of consensus"  
 repeat\_region 908..1002  
 /note="WERSA repeat: matches 97..187 of consensus"  
 repeat\_region 923..1013  
 /note="WERSA repeat: matches 8..91 of consensus"  
 repeat\_region 1301..1443  
 /note="WIR repeat: matches 100..250 of consensus"  
 repeat\_region 1495..1833  
 /note="THEIC repeat: matches 2..371 of consensus"  
 repeat\_region 2114..2346  
 /note="AluYb repeat: matches 1..231 of consensus"  
 repeat\_region 2680..2774  
 /note="L2 repeat: matches 2651..2746 of consensus"  
 repeat\_region 2822..2917  
 /note="L2 repeat: matches 2362..2450 of consensus"  
 repeat\_region 3940..4131  
 /note="WIR repeat: matches 16..218 of consensus"  
 repeat\_region 4255..4278  
 /note="AluYb repeat: matches 114..137 of consensus"  
 repeat\_region 4279..4603  
 /note="AluSx repeat: matches 1..304 of consensus"  
 repeat\_region 4604..4762  
 /note="AluYb repeat: matches 137..294 of consensus"  
 repeat\_region 4773..4846  
 /note="L1MB3 repeat: matches 6104..6180 of consensus"  
 repeat\_region 4992..5290  
 /note="AluSx repeat: matches 1..302 of consensus"  
 repeat\_region 5871..5927  
 /note="WIR repeat: matches 33..91 of consensus"  
 repeat\_region 7528..7582  
 /note="WERSA repeat: matches 47..99 of consensus"  
 repeat\_region 7839..7973  
 /note="L2 repeat: matches 2637..2747 of consensus"  
 repeat\_region 7974..8089  
 /note="WERS33 repeat: matches 1..102 of consensus"  
 repeat\_region 8090..8365  
 /note="AluYb repeat: matches 1..288 of consensus"  
 repeat\_region 8366..8538  
 /note="WERS33 repeat: matches 102..324 of consensus"  
 repeat\_region 8539..8579  
 /note="L2 repeat: matches 2593..2637 of consensus"  
 repeat\_region 8708..8911  
 /note="AluYb repeat: matches 6..210 of consensus"  
 repeat\_region 9015..9117  
 /note="WLR1E repeat: matches 418..521 of consensus"  
 repeat\_region 9226..9358  
 /note="WLR1E repeat: matches 283..426 of consensus"  
 repeat\_region 9440..9743  
 /note="AluSx repeat: matches 3..307 of consensus"  
 repeat\_region 9943..10069

/note="FLAM A repeat: matches 1..126 of consensus"  
 10204..10511  
 /note="AluSx repeat: matches 1..309 of consensus"  
 10618..10843  
 /note="L1MB3 repeat: matches 7497..7728 of consensus"  
 10850..10988  
 /note="FLAM C repeat: matches 3..142 of consensus"  
 11380..11688  
 /note="AluSx repeat: matches 3..311 of consensus"  
 11692..12000  
 /note="AluSx repeat: matches 1..312 of consensus"  
 12132..12348  
 /note="L2 repeat: matches 2079..2302 of consensus"  
 12399..12460  
 /note="L2 repeat: matches 1881..1945 of consensus"  
 13093..13284  
 /note="AluSx repeat: matches 114..293 of consensus"  
 13285..13595  
 /note="AluSx repeat: matches 1..306 of consensus"  
 13596..13698  
 /note="AluSx repeat: matches 9..114 of consensus"  
 14000..14083  
 /note="L2 repeat: matches 2626..2708 of consensus"  
 14312..14374  
 /note="WERS7B repeat: matches 295..376 of consensus"  
 14414..14724  
 /note="AluSx repeat: matches 1..312 of consensus"  
 16091..16187  
 /note="WIR repeat: matches 47..163 of consensus"  
 16306..16547  
 /note="L2 repeat: matches 2182..2461 of consensus"  
 17845..18096  
 /note="AluYb repeat: matches 2..249 of consensus"  
 18104..18146  
 /note="L2 repeat: matches 2704..2745 of consensus"  
 18235..18307  
 /note="L2 repeat: matches 2580..2660 of consensus"  
 18367..18575  
 /note="WIR repeat: matches 12..231 of consensus"  
 18700..19006  
 /note="AluSx repeat: matches 1..307 of consensus"  
 19351..19783  
 /note="AluSg/x repeat: matches 69..303 of consensus"  
 19784..19867  
 /note="42 copies 2 mer ag 65% conserved"  
 20041..20525  
 /note="L2 repeat: matches 2123..2652 of consensus"  
 20526..20834  
 /note="AluSg repeat: matches 1..310 of consensus"  
 20835..20847  
 /note="L2 repeat: matches 2113..2123 of consensus"  
 20875..21010  
 /note="FLAM C repeat: matches 1..133 of consensus"  
 21020..21234  
 /note="WIR repeat: matches 13..228 of consensus"  
 21213..21347  
 /note="L2 repeat: matches 2605..2708 of consensus"  
 21486..21628  
 /note="WIR repeat: matches 7..148 of consensus"  
 21778..21815  
 /note="L2 repeat: matches 2709..2747 of consensus"  
 21970..22101  
 /note="AluYb/FRAM repeat: matches 158..289 of consensus"  
 22321..22360  
 /note="20 copies 2 mer ga 95% conserved"  
 23203..23248  
 /note="23 copies 2 mer gt 100% conserved"  
 23336..23369  
 /note="17 copies 2 mer ag 82% conserved"  
 24137..24260  
 /note="FLAM C repeat: matches 1..124 of consensus"  
 24305..24452  
 /note="L2 repeat: matches 2562..2707 of consensus"

```

repeat_region 24557. .24862
/note="AluSq repeat: matches 1. .306 of consensus"
repeat_region 24857. .25075
/note="MSTC repeat: matches 1. .271 of consensus"
repeat_region 25076. .25238
/note="AluJb repeat: matches 136. .298 of consensus"
repeat_region 25243. .25423
/note="FLAM A repeat: matches 20. .99 of consensus"
repeat_region 25427. .25556
/note="MLR1A1 repeat: matches 226. .365 of consensus"
repeat_region 25606. .25789
/note="AluSg/x repeat: matches 110. .291 of consensus"
repeat_region 25804. .26097
/note="MLR1C repeat: matches 182. .466 of consensus"
repeat_region 26252. .26560
/note="AluSg repeat: matches 1. .306 of consensus"
repeat_region 26976. .27291
/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 27494. .27556
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Query Match 2.9%; Score 21; DB 9; Length 84661;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 CCCCCCACTCCAGGAAGAG 76
Db 5568 CCCCCCACTCCAGGAAGAG 5588

RESULT 9
AC114256/c AC114256 147968 bp DNA linear HTG 13-JUL-2002
LOCUS Rattus norvegicus clone CH230-246M19, *** SEQUENCING IN PROGRESS
DEFINITION *** 34 unordered pieces.
ACCESSION AC114256
VERSION AC114256.2 GI:21738399
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 147968)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amarutunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaxia,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleaveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Huly,J., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsone,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,G., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,Z., Miner,T., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtonson,J., Newtonson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,

```

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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 147968)
Worley,K.C.
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 147968)
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:19224583.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GQZM
Center clone name: CH230-246M19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124266 bases at least Q40
Consensus quality: 127938 bases at least Q30
Consensus quality: 130857 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1691: contig of 1691 bp in length
1791: gap of unknown length
2943: contig of 1152 bp in length
3043: gap of unknown length
4200: contig of 1157 bp in length
4300: gap of unknown length
6408: contig of 2108 bp in length
6508: gap of unknown length
7794: contig of 1286 bp in length
7894: gap of unknown length
9561: contig of 1667 bp in length
9661: gap of unknown length
11448: contig of 1787 bp in length
11549: gap of unknown length
14400: contig of 2852 bp in length
14500: gap of unknown length
16918: contig of 2418 bp in length
16919: gap of unknown length
19566: contig of 2548 bp in length
19567: gap of unknown length

```

```

* 19667 22598: contig of 2933 bp in length
* 22600 22699: gap of unknown length
* 22700 24961: contig of 2262 bp in length
* 24962 25061: gap of unknown length
* 25062 27932: contig of 2871 bp in length
* 27933 28032: gap of unknown length
* 28033 29487: contig of 1455 bp in length
* 29488 33203: gap of unknown length
* 33204 33303: contig of 3616 bp in length
* 33304 35182: gap of unknown length
* 35183 35282: contig of 1879 bp in length
* 35283 38483: contig of 3201 bp in length
* 38484 42241: gap of unknown length
* 42242 42341: contig of 3658 bp in length
* 42342 47019: gap of unknown length
* 47020 51107: contig of 4678 bp in length
* 51108 51207: gap of unknown length
* 51208 55407: contig of 3988 bp in length
* 55408 55507: contig of 4200 bp in length
* 55509 59092: gap of unknown length
* 59093 59192: contig of 3585 bp in length
* 59193 63228: gap of unknown length
* 63229 63728: contig of 4436 bp in length
* 63729 67893: gap of unknown length
* 67894 67993: contig of 4165 bp in length
* 67994 72228: gap of unknown length
* 72229 72328: contig of 4235 bp in length
* 72329 76532: gap of unknown length
* 76533 82430: contig of 4204 bp in length
* 82431 82530: contig of 5798 bp in length
* 82531 86168: gap of unknown length
* 86169 86268: contig of 3638 bp in length
* 86269 93722: gap of unknown length
* 93723 93822: contig of 7454 bp in length
* 93823 101568: contig of 7746 bp in length
* 101569 101668: gap of unknown length
* 101669 110928: contig of 9257 bp in length
* 110929 111028: gap of unknown length
* 111029 119576: contig of 8551 bp in length
* 119577 119676: gap of unknown length
* 119677 128029: contig of 8353 bp in length
* 128030 128129: gap of unknown length
* 128130 147968: contig of 19839 bp in length.

```

# FEATURES

```

source
1. 147968
/organism="Rattus norvegicus"
/db xref="taxon:10116"
/clones="CH230-246M19"
BASE COUNT 43293 a 28625 c 27736 g 42051 t 6263 others
ORIGIN

```

Query Match 2.9%, Score 21; DB 2; Length 147968;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 33 TCCCCCTCCCCAGCTGGAGA 53
|||||
Db 75446 TCCCCCTCCCCAGCTGGAGA 75426
|||||

```

```

RESULT 10
AC011156/c AC011156 155334 bp DNA linear HTG 22-JUL-2000
LOCUS Homo sapiens clone RP11-7M2, WORKING DRAFT SEQUENCE, 22 unordered
pieces.
AC011156
AC011156.5 GI:9369469
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.

```

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 155334)

## AUTHORS

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

## TITLE

Homo sapiens, clone RP11-7M2

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 155334)

## AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baldwin,J., Barna,N., Beckerly,R., Boquslavsky,L., Boukhgalter,B.,  
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A., Doyle,M.,  
 Cooke,P., Deaellano,K., Dewar,K., Domino,M., Donelan,L., Gage,D.,  
 Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,  
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
 Lechoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,  
 McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,  
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

## TITLE

Direct Submission

## JOURNAL

Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

On Jul 22, 2000 this sequence version replaced gi:8781683.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2953

Center clone name: 7\_M2

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 141207 bases at least Q40

Consensus quality: 148637 bases at least Q30

Consensus quality: 151499 bases at least Q20

Insert size: 165000; agarose-fp

Insert size: 153234; sum-of-contigs

Quality coverage: 4.0 in Q20 bases; agarose-fp

Quality coverage: 4.3 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 22 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

* 1 1514: contig of 1514 bp in length
* 1515 1614: gap of 100 bp
* 1615 3445: contig of 1831 bp in length
* 3446 3545: gap of 100 bp
* 3546 5810: contig of 2265 bp in length
* 5811 5910: gap of 100 bp
* 5911 7766: contig of 1856 bp in length
* 7767 7866: gap of 100 bp
* 7867 9524: contig of 1658 bp in length
* 9525 9624: gap of 100 bp
* 9625 12146: contig of 2522 bp in length
* 12147 12246: gap of 100 bp
* 12247 14992: contig of 2746 bp in length
* 14993 15092: gap of 100 bp
* 15093 17783: contig of 2691 bp in length
* 17784 17883: gap of 100 bp

```

```
* 17894 21718: contig of 3835 bp in length
* 21719 21816: gap of 100 bp
* 21819 26832: contig of 5014 bp in length
* 26833 26932: gap of 100 bp
* 26933 31533: contig of 4601 bp in length
* 31534 31633: gap of 100 bp
* 31634 35717: contig of 4084 bp in length
* 35718 35817: gap of 100 bp
* 35818 40501: contig of 4684 bp in length
* 40502 40601: gap of 100 bp
* 40602 44757: contig of 4156 bp in length
* 44758 44857: gap of 100 bp
* 44858 53242: contig of 8385 bp in length
* 53243 53342: gap of 100 bp
* 53343 62709: contig of 9367 bp in length
* 62710 62809: gap of 100 bp
* 62810 73051: contig of 10242 bp in length
* 73052 73151: gap of 100 bp
* 73152 83723: contig of 10572 bp in length
* 83724 83823: gap of 100 bp
* 83824 94188: contig of 10365 bp in length
* 94189 94288: gap of 100 bp
* 94289 105339: contig of 11051 bp in length
* 105340 105439: gap of 100 bp
* 105440 126812: contig of 21373 bp in length
* 126813 126912: gap of 100 bp
* 126913 155334: contig of 28422 bp in length.
```

## FEATURES

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source
1. 155334
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-7M2"
/clone_lib="RPC1-11 Human Male BAC"
1. 1514
/note="assembly_fragment"
1615. 3445
/note="assembly_fragment"
3546. 5810
/note="assembly_fragment"
5911. 7766
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7867. 9524
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9625. 12146
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12247. 14992
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35818. 40501
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40602. 44757
/note="assembly_fragment"
44858. 53242
/note="assembly_fragment"
53343. 62709
/note="assembly_fragment"
62810. 73051
/note="assembly_fragment"
73152. 83723
/note="assembly_fragment"
83824. 94188
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94289. 105339
/note="assembly_fragment"
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clone_end:SP6
vector_side:left"
105440..126812
/note="assembly_fragment"
126913..155334
/note="assembly_fragment"
BASE COUNT 38380 a 38857 c 38853 g 37140 t 2104 others
ORIGIN

Query Match 2.9%; Score 21; DB 2; Length 155334;
Best Local Similarity 100.0%; Pred. NO. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CCCCCCAACTCCAGGAAGAG 76
Db 154464 CCCCCCAACTCCAGGAAGAG 154444

RESULT 11
AC122029/c
LOCUS AC122029 163315 bp DNA linear HTG 27-MAY-2002
DEFINITION Mus musculus chromosome UNK clone RP24-400A11, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
ACCESSION AC122029
VERSION AC122029.2 GI:21217607
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 163315)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 163315)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 163315)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On May 27, 2002 this sequence version replaced gi:21040157.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0400A11
----- Summary Statistics -----
Sequencing vector: M13. 0%
Sequencing vector: plasmid, 100%
Chemistry: Dye-primer ET; 0% of reads
Assembly: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 158150 bases at least Q40
Consensus quality: 159182 bases at least Q30
Consensus quality: 159759 bases at least Q20
Insert size: 206000; agarose-1p
Insert size: 161735; sum-of-contigs
Quality coverage: 9.80 in Q20 bases; agarose-1p
Quality coverage: 8.16 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
```

\* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 1454: contig of 1454 bp in length  
 \* 1455: gap of unknown length  
 \* 1555: contig of 2206 bp in length  
 \* 3760: gap of unknown length  
 \* 3861: contig of 1358 bp in length  
 \* 5219: gap of unknown length  
 \* 5319: contig of 2537 bp in length  
 \* 7856: gap of unknown length  
 \* 7956: contig of 9972 bp in length  
 \* 17928: gap of unknown length  
 \* 18028: contig of 17486 bp in length  
 \* 35514: gap of unknown length  
 \* 56404: contig of 20791 bp in length  
 \* 56405: gap of unknown length  
 \* 56505: contig of 42598 bp in length  
 \* 99103: gap of unknown length  
 \* 99203: contig of 62000 bp in length  
 \* 161203: gap of unknown length  
 \* 161303: contig of 653 bp in length  
 \* 161956: gap of unknown length  
 \* 162056: contig of 1260 bp in length.

## FEATURES

source

1. .163315  
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 /db\_xref="taxon:10090"  
 /chromosome="UNK"  
 /clone="RP24-400A11"  
 1. .1454  
 /note="assembly\_name:Contig13"  
 1555. .3760  
 /note="assembly\_name:Contig14"  
 3861. .5218  
 /note="assembly\_name:Contig15"  
 5319. .7855  
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 7956. .17927  
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 18028. .35513  
 /note="assembly\_name:Contig18"  
 35614. .56404  
 /note="assembly\_name:Contig19"  
 56505. .99102  
 /note="assembly\_name:Contig20"  
 99203. .161202  
 /note="assembly\_name:Contig21"  
 161303. .161955  
 /note="assembly\_name:Contig12"  
 162056. .163315  
 /note="assembly\_name:Contig11"  
 /note="assembly\_name:Contig11"  
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 ORIGIN

Query Match 2.9%; Score 21; DB 2; Length 163315;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 497 CCTGCCCCCAGGCCACACA 517  
 Db 64493 CCTGCCCCCAGGCCACACA 64473

## RESULT 12

AC098966 AC098966 164924 bp DNA linear PRI 06-FEB-2002  
 DEFINITION Homo sapiens chromosome 16 clone RP11-465H19, complete sequence.  
 ACCESSION AC098966  
 VERSION AC098966.2 GI:18542981  
 KEYWORDS HTG.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

## REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 164924)  
 DOE Joint Genome Institute.  
 Sequencing of Human Chromosome 16  
 Unpublished  
 2 (bases 1 to 164924)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (07-NOV-2001) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 3 (bases 1 to 164924)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 On Feb 6, 2002 this sequence version replaced gi:16756239.  
 Sequence Quality Assessment:  
 This entry has been annotated with sequence quality  
 estimates computed by the Phrap assembly program.  
 All manually edited bases have been reduced to quality zero.  
 Quality levels above 40 are expected to have less than  
 1 error in 10,000 bp.  
 Base-by-base quality values are not generally visible from the  
 GenBank flat file format but are available as part  
 of this entry's ASN.1 file.

-----

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

-----

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

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FEATURES

Location/Qualifiers

1. .164924

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="16"

/clone="RP11-465H19"

BASE COUNT 47132 a 40504 c 37718 g 39570 t

ORIGIN

Query Match 2.9%; Score 21; DB 9; Length 164924;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 488 AGCAGAGAGCTGGCCCCAGG 508

Db 47187 AGCAGAGAGCTGGCCCCAGG 47207

-----

RESULT 13

AC068091/c

LOCUS

DEFINITION

AC068091

SEQUENCE, 3 unordered pieces.

ACCESSION

AC068091.5

VERSION

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.

KEYWORDS

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 184835)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 8, clone RP11-387M9

Unpublished

2 (bases 1 to 184835)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

AUTHORS



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8750..8907  
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9881..9915  
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21328..21634  
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24846..25168  
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34890..34916  
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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 GGAAGAGGCTCTGGACAGCA 477
      |||||
DB 168969 GGAAGAGGCTCTGGACAGCA 168949

RESULT 15
AF139185 LOCUS 6975 bp mRNA linear ROD 02-APR-2001
DEFINITION Rattus norvegicus myomegalin mRNA, complete cds.
ACCESSION AF139185
VERSION AF139185.1 GI:4761643
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus.
Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 6975)
AUTHORS Verde, I., Pahlke, G., Salanova, M., Zhang, G., Wang, S., Coletti, D.,
Onuffer, J., Jin, S. L. and Conti, M.
TITLE Myomegalin is a novel protein of the golgi/centrosome that
interacts with a cyclic nucleotide phosphodiesterase
J. Biol. Chem. 276 (14), 11189-11198 (2001)
MEDLINE 21179171
PUBMED 11334006
REFERENCE 2 (bases 1 to 6975)
AUTHORS Pahlke, G., Verde, I., Salanova, M., Jin, S.-L.C., Zhang, G., Onuffer, J.
and Conti, M.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-1999) Gynecology & Obstetrics, Stanford
University Medical Center, 300 Pasteur Drive, Room A344, Stanford,
CA 94305-5317, USA
FEATURES
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location/Qualifiers
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue type="skeletal muscle; heart; testis"
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/db_xref="GI:4761644"
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OKQDTTOSLKMESRETEELYQVTEGQNTMAKPEMLHQSLQOLQSGSIAP
AQOVALDLQALFCSOLEIKLQRLQKORQOLADGRCWQFVEAAAOEREOQKEA
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QELQLQRTDTTDLTDTNEVLEKQRQIDRAVALERVIDEFKSALEKQKELRQ
LRLAVDRDLRLRVLNSAEATMQSMESLLRARGLEVEQLIATCONLQWKEELE
TKFHWQKEQESIIOQLQTLSDNRNKEVEDLSATLLHKLGPQSEVEELCQRLQKE
RVLDLLDRNKQMEHEMVQGLQSGMGTREQERQAVAEKQVAFERNSELQALRQ
VILGKELAAQAFISNOPAGATSVGPHHGEQTOGQSTOMPSSRDDSTSLTAREASIP
RSLGDSVTAGLEKELSNAXEELMAKKERESQIELSALQSMVAQVEELQVQAD
LESITRNQIQEDLQLOMQLVDPDPAMERLUTQEVILLREKVASVEPOQEGSEN
RRQULLLEGLVDRSLRNEALQAEQYLSLVKFAOPETFERDRTLOVELEGAQV
LRSLEEVGLSRLETLAAIGATAGTAGTETDTSTFTDSEIEEAHNSHQQLI
KVSLEKSLTWTETONTCLQPPSPVCGDNRLHQBEMHLRAEIQHLEPKKAEAEK
ELKQIEAGFSVSHIENTWLSLCLNLAELKEQMEAMSDGMEVEDKEKEGVNVT
VYAKGLSEDSLQAEFRKQGLKSKAYNIINLLKEQLVLRSEGNKEMPFLVRLAR
EVDNWMGLPSEKQHQQENWTAPGRPSLKLGTALSVDYQGLENKSAQDSGH
QPEFLSPGKHLRSQACQCRQYQDLQKLLISEATVFAQANLEKRAILSLSLVK
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FLSDDIEACSDMDVASEYTHYEKKEKPSNAAASASQGLKEPRSSISLPTQNPVK
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BASE COUNT 1971 a 1820 c 1947 g 1237 t
ORIGIN

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Query Match      2.8%; Score 20; DB 10; Length 6975;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTGGCCCGCCAGGCCCCAGCA 515
      |||||
DB 3516 GCCTGGCCCGCCAGGCCCCAGCA 3535

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Search completed: June 17, 2003, 04:00:26  
Job time : 1371.49 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:01 ; Search time 126.225 Seconds  
(without alignments)  
12756.396 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_7806\_8520

Perfect score: 715

Sequence: 1 actgcccacgagacagag.....ttccctctagctctccag 715

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq 101002.\*

- 1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*
- 2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
- 3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*
- 4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*
- 5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*
- 6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*
- 7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*
- 8: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*
- 9: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*
- 10: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*
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- 22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715	100.0	5492	21	AAA64508 cDNA sequence of t
2	715	100.0	9048	21	AAA64507 Nucleotide sequenc
3	486	68.0	1855	22	AA181887 Human polynucleoti
4	63	8.8	591	21	AAA64516 F37 probe used to
5	49	6.9	393	16	AAT23583 Human gene signatu
6	20	2.8	9679	21	AAD00768 Rat phosphodiester
7	20	2.8	10437	22	AAS41709 Genomic sequence #
8	20	2.8	12620	22	ABAI6691 Human nervous syst
9	19	2.7	531	24	ABN79134 Human ORF4081 cDNA

Human phosphatidyl	10	19	2.7	2472	24	ABL59550	Human protein enco
Human protein enco	11	19	2.7	2730	22	AAH99704	Human polynucleoti
Human polynucleoti	12	19	2.7	2735	22	AAH99710	Human polynucleoti
Human polynucleoti	13	19	2.7	2735	22	AA159663	Human polynucleoti
Human polynucleoti	14	19	2.7	2735	22	AA159664	Human polynucleoti
Human polynucleoti	15	19	2.7	2739	22	AA157877	Human polynucleoti
Human polynucleoti	16	19	2.7	2916	22	AA157878	Human polynucleoti
Human polynucleoti	17	19	2.7	27082	22	AAK70447	Human polynucleoti
Human polynucleoti	18	18	2.5	485	22	AAK70447	Human polynucleoti
Human polynucleoti	19	18	2.5	583	24	ABN65898	Human polynucleoti
Human polynucleoti	20	18	2.5	628	22	AAJ18393	Human polynucleoti
Human polynucleoti	21	18	2.5	860	22	AAK70648	Human polynucleoti
Human polynucleoti	22	18	2.5	860	22	AAK70649	Human polynucleoti
Human polynucleoti	23	18	2.5	860	22	AAK70650	Human polynucleoti
Human polynucleoti	24	18	2.5	1680	19	AAV39818	Human polynucleoti
Human polynucleoti	25	18	2.5	1680	24	ABK48203	Human polynucleoti
Human polynucleoti	26	18	2.5	2144	24	AAK70648	Human polynucleoti
Human polynucleoti	27	18	2.5	2662	21	AAK70648	Human polynucleoti
Human polynucleoti	28	18	2.5	3031	22	ABAI8518	Human polynucleoti
Human polynucleoti	29	18	2.5	4919	24	ABN59815	Human polynucleoti
Human polynucleoti	30	18	2.5	5643	22	AAK51612	Human polynucleoti
Human polynucleoti	31	18	2.5	6643	22	ABAI6216	Human polynucleoti
Human polynucleoti	32	18	2.5	6704	24	ABK84002	Human polynucleoti
Human polynucleoti	33	18	2.5	11336	22	AAK70648	Human polynucleoti
Human polynucleoti	34	18	2.5	26379	21	AAZ88922	Human polynucleoti
Human polynucleoti	35	18	2.5	67212	21	AAA08954	Human polynucleoti
Human polynucleoti	36	18	2.5	123219	23	AAH88703	Human polynucleoti
Human polynucleoti	37	18	2.5	534720	19	AAV30458	Human polynucleoti
Human polynucleoti	38	18	2.5	536165	19	AAV30459	Human polynucleoti
Human polynucleoti	39	17	2.4	50	22	AAJ33953	Human polynucleoti
Human polynucleoti	40	17	2.4	51	22	AAJ32942	Human polynucleoti
Human polynucleoti	41	17	2.4	232	24	ABN76645	Human polynucleoti
Human polynucleoti	42	17	2.4	300	20	AAZ14903	Human polynucleoti
Human polynucleoti	43	17	2.4	311	22	AAK85132	Human polynucleoti
Human polynucleoti	44	17	2.4	350	22	AAK38654	Human polynucleoti
Human polynucleoti	45	17	2.4	362	22	AAK68500	Human polynucleoti
Human polynucleoti	46	17	2.4	365	23	ABV08368	Human polynucleoti
Human polynucleoti	47	17	2.4	367	22	AAK56639	Human polynucleoti
Human polynucleoti	48	17	2.4	368	20	AAV87083	Human polynucleoti
Human polynucleoti	49	17	2.4	382	23	ABV38275	Human polynucleoti
Human polynucleoti	50	17	2.4	416	22	AAK60046	Human polynucleoti
Human polynucleoti	51	17	2.4	418	21	AAK60586	Human polynucleoti
Human polynucleoti	52	17	2.4	420	19	AAV09992	Human polynucleoti
Human polynucleoti	53	17	2.4	456	22	AAI89467	Human polynucleoti
Human polynucleoti	54	17	2.4	457	23	ABV05112	Human polynucleoti
Human polynucleoti	55	17	2.4	467	22	AAK35563	Human polynucleoti
Human polynucleoti	56	17	2.4	490	22	AAK32396	Human polynucleoti
Human polynucleoti	57	17	2.4	525	15	AAQ77731	Human polynucleoti
Human polynucleoti	58	17	2.4	543	22	AAK11774	Human polynucleoti
Human polynucleoti	59	17	2.4	563	22	AAK78328	Human polynucleoti
Human polynucleoti	60	17	2.4	563	22	AAK78329	Human polynucleoti
Human polynucleoti	61	17	2.4	563	22	AAK78330	Human polynucleoti
Human polynucleoti	62	17	2.4	563	22	AAK78723	Human polynucleoti
Human polynucleoti	63	17	2.4	563	22	AAK78724	Human polynucleoti
Human polynucleoti	64	17	2.4	563	22	AAK78725	Human polynucleoti
Human polynucleoti	65	17	2.4	617	20	AAZ52905	Human polynucleoti
Human polynucleoti	66	17	2.4	660	23	AAK76917	Human polynucleoti
Human polynucleoti	67	17	2.4	690	22	AAI22819	Human polynucleoti
Human polynucleoti	68	17	2.4	691	24	ABQ54423	Human polynucleoti
Human polynucleoti	69	17	2.4	882	23	AAK82232	Human polynucleoti
Human polynucleoti	70	17	2.4	960	23	AAK82232	Human polynucleoti
Human polynucleoti	71	17	2.4	967	21	AAK82232	Human polynucleoti
Human polynucleoti	72	17	2.4	993	22	AAI25098	Human polynucleoti
Human polynucleoti	73	17	2.4	999	20	AAZ33442	Human polynucleoti
Human polynucleoti	74	17	2.4	1066	21	AAZ38135	Human polynucleoti
Human polynucleoti	75	17	2.4	1107	23	AAK80914	Human polynucleoti
Human polynucleoti	76	17	2.4	1128	22	AAI82348	Human polynucleoti
Human polynucleoti	77	17	2.4	1225	24	ABL90131	Human polynucleoti
Human polynucleoti	78	17	2.4	1238	21	AAA09482	Human polynucleoti
Human polynucleoti	79	17	2.4	1254	21	AAA40579	Human polynucleoti
Human polynucleoti	80	17	2.4	1264	20	AAZ06243	Human polynucleoti
Human polynucleoti	81	17	2.4	1275	20	AAZ06258	Human polynucleoti
Human polynucleoti	82	17	2.4	1298	21	AAK74927	Human polynucleoti

83	17	2.4	1345	24	ABN86910	Human NOV1 encodin	156	17	2.4	5454	24	AA38865	Human kinase (PKIN
84	17	2.4	1380	22	ABA09465	Human membrane-ass	c 157	17	2.4	6075	25	AAK79246	Human immune/haema
85	17	2.4	1409	21	AAZ97090	Human secreted pro	158	17	2.4	6100	15	AAQ79728	Human L5/3 tumour
86	17	2.4	1452	23	ABL27531	Drosophila melanog	159	17	2.4	6100	18	AAK62440	Human L5/3 growth
87	17	2.4	1493	19	AAZ09951	cDNA encoding a no	c 160	17	2.4	6232	24	AAK42134	Human Kruppel-like
88	17	2.4	1558	21	AAZ65254	Human secreted pro	c 161	17	2.4	6232	24	AAK42135	Human Kruppel-like
89	17	2.4	1635	13	AAZ18205	Mutant thermotabl	162	17	2.4	6239	24	AAK93553	Human breast speci
90	17	2.4	1734	17	AAAT18010	Newcastle disease	163	17	2.4	6866	22	AAK70762	Human immune/haema
91	17	2.4	1752	23	AAAT18010	DNA encoding novel	164	17	2.4	6866	22	AAK71754	Human immune/haema
92	17	2.4	1803	22	AAK82675	Canine BNP fragmen	165	17	2.4	7487	23	AAK92457	DNA encoding novel
93	17	2.4	1804	11	AAQ02851	cDNA encoding a ca	166	17	2.4	7574	22	AAK74485	Human immune/haema
94	17	2.4	1840	23	ABL02133	Drosophila melanog	167	17	2.4	7574	22	AAK74613	Human immune/haema
95	17	2.4	1867	24	ABA99929	NDV HN DNA fragmen	168	17	2.4	7928	22	AAK62287	cDNA encoding a sp
96	17	2.4	1898	22	AAK91895	Human secreted pro	169	17	2.4	8543	23	ABV22726	Human prostate exp
97	17	2.4	1899	13	AAQ24009	Mutant thermotabl	170	17	2.4	8543	23	ABV22851	Human benign prost
98	17	2.4	1907	14	AAQ46678	NDV Haemagglutinin	c 171	17	2.4	8628	24	ABK64727	Human Jun B proto
99	17	2.4	1937	16	AAQ99633	Newcastle's diseas	c 172	17	2.4	8791	17	AAK37090	Human Jun B proto
100	17	2.4	2037	21	AAQ66421	Human secreted pro	c 173	17	2.4	9110	24	ABK47941	Colon adenocarcino
101	17	2.4	2043	13	AAQ24008	Mutant thermotabl	c 174	17	2.4	9517	24	ABL61755	Lung cancer relate
102	17	2.4	2043	13	AAQ24008	Mutant thermotabl	c 175	17	2.4	9517	24	ABL65220	Lung cancer relate
103	17	2.4	2085	20	AAK01362	Nucleobase permeas	c 176	17	2.4	9517	24	ABL66638	Lung cancer relate
104	17	2.4	2112	22	AAK74448	Human PRO17 nucleo	c 177	17	2.4	9664	22	ABK16496	Human cardiovascular
105	17	2.4	2203	22	AAK89786	Nucleotide sequenc	c 178	17	2.4	9664	22	AAK36626	Human cardiovascular
106	17	2.4	2277	13	AAQ24007	Mutant thermotabl	c 179	17	2.4	9848	21	AAK98272	Mouse IP3 receptor
107	17	2.4	2295	22	AAH23330	Human transferase	c 180	17	2.4	9871	12	AAQ13593	Inositol-3-phospha
108	17	2.4	2367	13	AAQ24006	Mutant thermotabl	181	17	2.4	9980	24	ABN96855	Gene #3353 used to
109	17	2.4	2379	23	AAK89880	DNA encoding novel	182	17	2.4	9980	24	ABN96855	Kidney cancer rela
110	17	2.4	2437	22	AAK89785	Nucleotide sequenc	183	17	2.4	10053	22	AAK73765	Human immune/haema
111	17	2.4	2493	13	AAQ24005	Mutant thermotabl	184	17	2.4	10659	23	ABK12132	Drosophila melanog
112	17	2.4	2507	16	AAQ81189	Breast tumour kina	185	17	2.4	10828	24	ABK12302	Human tyrosine hyd
113	17	2.4	2512	16	AAQ92369	TfII DNA-polymeras	186	17	2.4	12290	22	ABK19042	Human nervous syst
114	17	2.4	2519	22	AAH35022	Human colon cancer	187	17	2.4	13329	24	ABK12301	Human tyrosine hyd
115	17	2.4	2520	22	AAH35035	Human colon cancer	188	17	2.4	13875	13	AAQ20240	Human centromeric
116	17	2.4	2528	21	AAK58375	Human PRO848 nucle	c 189	17	2.4	15987	22	AAK83692	Human immune/haema
117	17	2.4	2528	21	AAZ65079	Membrane-bound pro	c 190	17	2.4	15987	22	ABK42414	Genomic sequence #
118	17	2.4	2528	22	AAK21474	Human cDNA sequenc	c 191	17	2.4	16038	22	AAK89507	Human digestive sy
119	17	2.4	2528	22	AAK44225	Human PRO848 (UNQ5	c 192	17	2.4	16831	22	AAK73455	Human immune/haema
120	17	2.4	2556	23	AAK80084	DNA encoding novel	193	17	2.4	17084	22	AAK70764	Human immune/haema
121	17	2.4	2567	20	AAZ52889	Human prostate tum	194	17	2.4	17084	22	AAK71755	Human immune/haema
122	17	2.4	2644	22	AAK89784	Nucleotide sequenc	c 195	17	2.4	17904	22	ABA07913	Human ovarian and
123	17	2.4	3129	22	ABA16690	Human nervous syst	c 196	17	2.4	17904	22	AAK03730	Human reproductive
124	17	2.4	3133	20	AAK57463	Rat U3 gene trap d	c 197	17	2.4	19199	22	AAK70995	Human immune/haema
125	17	2.4	3225	24	AAK26467	Human kinase PKIN-	c 198	17	2.4	19659	22	AAK64731	Human immune/haema
126	17	2.4	3416	17	AAK30373	Protein tyrosine ki	c 199	17	2.4	19659	22	AAK75600	Human immune/haema
127	17	2.4	3416	17	AAK40859	Human PK-2 protei	c 200	17	2.4	19659	22	AAK91504	Human digestive sy
128	17	2.4	3416	24	AAK84297	Human cDNA differe	c 201	17	2.4	23452	22	AAK42122	Genomic sequence #
129	17	2.4	3504	17	AAK16553	CryIF class toxin	c 202	17	2.4	23457	22	AAK42121	Genomic sequence #
130	17	2.4	3507	22	AAH28241	Nucleotide sequenc	c 203	17	2.4	23458	22	AAK42120	Genomic sequence #
131	17	2.4	3527	23	AAK66986	DNA encoding novel	c 204	17	2.4	26657	24	AAK172317	Human transporter
132	17	2.4	3594	24	ABK84227	Human cDNA differe	c 205	17	2.4	32192	22	ABA17963	Human nervous syst
133	17	2.4	3621	19	AAK17800	Human related adhe	c 206	17	2.4	32192	22	AAK37292	Human musculoskele
134	17	2.4	3628	23	ABL27530	Drosophila melanog	c 207	17	2.4	32192	22	AAK07103	Human reproductive
135	17	2.4	3834	21	AAZ51204	Rat hypoxia regula	c 208	17	2.4	32195	22	AAK36105	Human cardiovascular
136	17	2.4	3957	22	ABA06411	Human cDNA SEQ ID	c 209	17	2.4	32195	22	AAK31532	Human DNA for a no
137	17	2.4	4089	21	AAZ36693	Nucleotide sequenc	c 210	17	2.4	32195	22	AAK31538	Human DNA for a no
138	17	2.4	4151	24	ABK84331	Human cDNA differe	c 211	17	2.4	32195	23	ABK44045	Genomic DNA encodi
139	17	2.4	4175	22	AAK62285	DNA encoding a hu	c 212	17	2.4	32195	24	ABQ66856	Human polynucleoti
140	17	2.4	4177	15	AAQ68943	Sfil fragment cont	c 213	17	2.4	32195	24	ABQ66852	Human polynucleoti
141	17	2.4	4177	15	AAQ70570	Sfil fragment cont	c 214	17	2.4	37925	22	AAK72372	Human immune/haema
142	17	2.4	4177	18	AAK48510	Sfil fragment enco	c 215	17	2.4	42519	22	AAK81318	Human immune/haema
143	17	2.4	4177	20	AAK81147	Seq ID No: 12 of U	c 216	17	2.4	62944	24	ABL66947	Lung cancer relate
144	17	2.4	4177	21	AAK67862	Sfil fragment comp	c 217	17	2.4	62944	24	ABL68262	Kidney cancer rela
145	17	2.4	4177	21	AAZ49295	cDNA encoding NDV	c 218	17	2.4	92638	24	ABQ88096	Human osteoblast d
146	17	2.4	4339	23	ABV23367	Human prostate exp	c 219	17	2.4	100301	24	ABQ88176	Human osteoblast d
147	17	2.4	4420	22	AAK90043	Human resistin gen	c 220	17	2.4	183999	22	AAK92831	Human ABC1 genom
148	17	2.4	4936	22	AAH46904	cDNA encoding huma	c 221	17	2.4	201143	24	ABK83568	Human ABC1 differen
149	17	2.4	4947	16	AAQ68927	Tps17 polymerase	c 222	16	2.2	20	21	AAA07650	HERG gene intron 1
150	17	2.4	5007	22	AAK62286	cDNA encoding a fu	c 223	16	2.2	116	15	AAQ76951	Human genome fragm
151	17	2.4	5190	24	AAK62911	Breast cancer rela	c 224	16	2.2	124	15	AAQ76402	Human genome fragm
152	17	2.4	5207	24	AAK43908	Human kinase prote	c 225	16	2.2	148	22	AAK161577	Soybean 318013 reg
153	17	2.4	5207	24	AAK43909	Human kinase prote	c 226	16	2.2	164	24	ABL81761	Human ovarian can
154	17	2.4	5312	22	AAK40665	DNA encoding huma	c 227	16	2.2	193	22	ABA41047	Probe #19513 for g
155	17	2.4	5312	22	AAK06553	Human reproductive	c 228	16	2.2	193	22	AAK251176	Human brain expres

C 229	16	2.2	193	22	AAK51182	Human bone marrow
C 230	16	2.2	193	22	AAI28191	Probe #18124 for g
C 231	16	2.2	193	22	AAI57234	Probe #25920 used
C 232	16	2.2	212	24	ABSL24712	Human genome-deriv
C 233	16	2.2	212	24	ABL74686	Corn tassell-deriv
C 234	16	2.2	235	22	AAK06580	Mouse microglia an
C 235	16	2.2	244	22	AAK08137	Human breast cance
C 236	16	2.2	266	22	AAH45500	Human REIC related
C 237	16	2.2	287	22	AAK75717	Human immune/haema
C 238	16	2.2	297	21	AAK05431	Human secreted pro
C 239	16	2.2	305	24	ABN18832	Human ORFX polynuc
C 240	16	2.2	314	23	AAK72213	DNA encoding novel
C 241	16	2.2	349	24	ABN78962	Human ORF3909 cDNA
C 242	16	2.2	353	22	AAK64358	Human immune/haema
C 243	16	2.2	356	24	ABN15855	Human ORFX polynuc
C 244	16	2.2	364	24	ABN27002	Human ORFX polynuc
C 245	16	2.2	366	22	AAK59221	Human immune/haema
C 246	16	2.2	366	22	AAH34263	Human colon cancer
C 247	16	2.2	368	21	AAK02351	Human secreted pro
C 248	16	2.2	371	24	ABL83929	Human ovarian can
C 249	16	2.2	379	22	AAI86621	Human polynucleoti
C 250	16	2.2	381	21	AAH30648	Human colon cancer
C 251	16	2.2	383	22	AAI84957	Human polynucleoti
C 252	16	2.2	386	14	AAK02677	Human brain expres
C 253	16	2.2	386	21	AAK27717	Human secreted pro
C 254	16	2.2	388	22	AAI81643	Human polynucleoti
C 255	16	2.2	393	22	ABA44353	Human breast cell
C 256	16	2.2	393	22	ABA54807	Human foetal liver
C 257	16	2.2	393	22	ABA24572	Probe #3038 for ge
C 258	16	2.2	393	22	AAK03083	Human brain expres
C 259	16	2.2	393	22	AAK28535	Human bone marrow
C 260	16	2.2	393	22	AAI13109	Probe #3042 for ge
C 261	16	2.2	393	22	AAI34459	Probe #3145 used t
C 262	16	2.2	393	22	AAI03011	Probe #3002 used t
C 263	16	2.2	393	24	ABN94576	Gene #1074 used to
C 264	16	2.2	393	24	ABN03047	Human genome-deriv
C 265	16	2.2	393	24	ABN23152	Human ORFX polynuc
C 266	16	2.2	409	21	AAK03640	Human secreted pro
C 267	16	2.2	409	22	AAK89184	Human digestive sy
C 268	16	2.2	409	22	AAK89185	Human digestive sy
C 269	16	2.2	425	22	AAK21960	Human collagen gen
C 270	16	2.2	427	22	ABA69666	Human pancreatic c
C 271	16	2.2	427	22	AAK88165	Human digestive sy
C 272	16	2.2	433	22	AAK62405	Human immune/haema
C 273	16	2.2	436	24	ABL81139	Human ovarian can
C 274	16	2.2	438	22	AAK90128	Human prostate can
C 275	16	2.2	440	21	AAK27881	Human secreted pro
C 276	16	2.2	440	22	AAK90121	Human prostate can
C 277	16	2.2	447	14	AAQ59652	Human brain expres
C 278	16	2.2	455	22	AAK90129	Human prostate can
C 279	16	2.2	457	22	AAK45193	cDNA encoding nove
C 280	16	2.2	457	22	AAK90122	Human prostate can
C 281	16	2.2	481	22	AAK55262	Human immune/haema
C 282	16	2.2	481	22	AAK74761	Human immune/haema
C 283	16	2.2	481	23	ABV52441	Human prostate exp
C 284	16	2.2	482	22	ABA08881	Human secreted pro
C 285	16	2.2	499	21	AAK99146	Human pancreatic c
C 286	16	2.2	505	23	AAK84768	Human secreted pro
C 287	16	2.2	511	23	AAK80311	DNA encoding novel
C 288	16	2.2	513	24	ABQ58536	Human colon cancer
C 289	16	2.2	514	23	ABV58429	Human prostate exp
C 290	16	2.2	516	24	ABK09679	Human ovarian tumo
C 291	16	2.2	524	22	ABA62321	Human foetal liver
C 292	16	2.2	524	22	ABA29664	Probe #8130 for ge
C 293	16	2.2	524	22	AAK10657	Human brain expres
C 294	16	2.2	524	22	AAK36542	Human bone marrow
C 295	16	2.2	524	22	AAI17400	Probe #7333 for ge
C 296	16	2.2	524	22	AAI42300	Probe #10986 used
C 297	16	2.2	524	24	ABN83559	Human acyl-CoA deh
C 298	16	2.2	524	24	ABN10538	Human genome-deriv
C 299	16	2.2	545	21	AAH31082	Human colon cancer
C 300	16	2.2	551	22	AAK61554	Human immune/haema
C 301	16	2.2	551	22	AAK69681	Human immune/haema
C 302	16	2.2	551	22	AAK80387	Human immune/haema
C 303	16	2.2	551	22	AAK80388	Human immune/haema
C 304	16	2.2	568	21	AAK09733	Fusarium venenatum
C 305	16	2.2	569	22	ABA310954	Probe #9420 for ge
C 306	16	2.2	569	22	AAK12277	Human brain expres
C 307	16	2.2	569	22	AAK37998	Human bone marrow
C 308	16	2.2	569	22	AAI18768	Probe #8701 for ge
C 309	16	2.2	569	22	AAI43881	Probe #12567 used
C 310	16	2.2	569	24	ABN12001	Human genome-deriv
C 311	16	2.2	573	24	AAK47594	Metridia longa luc
C 312	16	2.2	573	24	AAK46656	Metridia longa luc
C 313	16	2.2	578	24	ABU83163	Human ovarian can
C 314	16	2.2	579	22	AAK65994	C Glutamicum codin
C 315	16	2.2	587	15	AAQ55685	Rabbit CAP18 gene.
C 316	16	2.2	587	20	AAK19928	Lilly male gamete-s
C 317	16	2.2	590	22	ABA62140	Human foetal liver
C 318	16	2.2	590	22	ABA29548	Probe #8014 for ge
C 319	16	2.2	590	22	AAK10459	Human brain expres
C 320	16	2.2	590	22	AAK36360	Human bone marrow
C 321	16	2.2	590	22	AAI17285	Probe #7218 for ge
C 322	16	2.2	590	22	AAI42088	Probe #10774 used
C 323	16	2.2	590	24	ABN10414	Human genome-deriv
C 324	16	2.2	594	22	AAI44533	Probe #13219 used
C 325	16	2.2	617	21	AAK18363	Lung cancer associ
C 326	16	2.2	623	22	AAK69166	Human immune/haema
C 327	16	2.2	623	22	AAK69167	Human immune/haema
C 328	16	2.2	624	24	ABO88907	Human prostate exp
C 329	16	2.2	634	24	ABK73913	Bacillus lichenifo
C 330	16	2.2	635	20	AAK39813	Gastric cancer ass
C 331	16	2.2	637	22	AAK56951	Human immune/haema
C 332	16	2.2	647	22	AAK91659	Human CDNA 5'-end
C 333	16	2.2	647	22	AAK93640	Human CDNA clone (
C 334	16	2.2	661	22	AAH04792	Human CDNA for nov
C 335	16	2.2	668	24	ABK34390	Human polynucleoti
C 336	16	2.2	676	22	AAI81744	Human inflammatory
C 337	16	2.2	700	22	AAH92940	Macaque islet cell
C 338	16	2.2	738	18	AAH95234	Gastric cancer ass
C 339	16	2.2	767	20	AAK39815	Nucleotide sequenc
C 340	16	2.2	771	22	AAI67176	Human neuroblastom
C 341	16	2.2	778	22	AAI96364	Human polynucleoti
C 342	16	2.2	784	22	AAK51974	Human polynucleoti
C 343	16	2.2	791	22	AAI91505	Human CDNA encodin
C 344	16	2.2	793	22	AAK26203	C glutamicum codin
C 345	16	2.2	816	22	AAH65897	Human ATP dependen
C 346	16	2.2	818	24	ABA94145	Human pancreatic c
C 347	16	2.2	821	21	AAK98850	Human polynucleoti
C 348	16	2.2	827	22	AAK52958	Human prostate can
C 349	16	2.2	830	22	AAK90127	Human prostate can
C 350	16	2.2	834	22	AAK90120	Human polynucleoti
C 351	16	2.2	907	22	AAI58762	Arabidopsis thalia
C 352	16	2.2	912	22	AAK06492	Macaque islet cell
C 353	16	2.2	932	18	AAH95235	TA13 CDNA. Nicot
C 354	16	2.2	936	10	AAH92189	Arachidonic acid m
C 355	16	2.2	955	21	AAK57391	Human chicken wing
C 356	16	2.2	982	24	ABA93657	Macaque islet cell
C 357	16	2.2	999	18	AAH95236	Macaque islet cell
C 358	16	2.2	1011	18	AAH95237	Novel human gene.
C 359	16	2.2	1047	24	ABQ86183	Human CIDE-A codin
C 360	16	2.2	1049	21	AAK48763	Human osteoblast d
C 361	16	2.2	1050	24	ABQ88238	Breast cancer rela
C 362	16	2.2	1050	24	ABL63683	DNA encoding novel
C 363	16	2.2	1086	23	AAK84767	Human secreted pro
C 364	16	2.2	1096	20	AAK22275	Human secreted pro
C 365	16	2.2	1100	21	AAK93460	Human secreted pro
C 366	16	2.2	1100	21	AAK75819	Human ORFX ORF1374
C 367	16	2.2	1129	24	ABU90679	Human polynucleoti
C 368	16	2.2	1145	22	AAK87328	Human immune/haema
C 369	16	2.2	1145	22	AAK87329	Human immune/haema
C 370	16	2.2	1225	21	AAK98090	Human colon cancer
C 371	16	2.2	1230	22	AAH68436	C glutamicum codin
C 372	16	2.2	1247	23	AAH59706	Propionibacterium
C 373	16	2.2	1289	21	AAK41140	Arabidopsis thalia
C 374	16	2.2	1290	23	AAK71002	DNA encoding novel

C 375	16	2.2	1292	22	AAH15754	Human cDNA sequenc	C 448	16	2.2	2535	24	ABA90342	Human polynucleoti
C 376	16	2.2	1308	22	AAS42067	Genomic sequence #	C 449	16	2.2	2538	22	AAI58106	Human polynucleoti
C 377	16	2.2	1347	22	AAH64762	Human secreted pro	C 450	16	2.2	2562	22	AAH16160	Human cDNA sequenc
C 378	16	2.2	1347	22	AAKS1783	Human polynucleoti	C 451	16	2.2	2586	20	AAH52255	Protein PRO295 CDN
C 379	16	2.2	1353	22	AAF71965	Corynebacterium gl	C 452	16	2.2	2586	22	AAF92061	Human PRO295 CDNA
C 380	16	2.2	1354	22	ABA09093	Human preproenkeph	C 453	16	2.2	2586	22	AAF72413	Human PRO295 CDNA
C 381	16	2.2	1383	22	AAI06178	Human reproductive	C 454	16	2.2	2586	24	ABL95585	Human angiogenesis
C 382	16	2.2	1383	23	ABL98743	Human testicular a	C 455	16	2.2	2586	24	ABL68096	Human PRO295 CDNA
C 383	16	2.2	1435	24	ABQ73781	Human colon specif	C 456	16	2.2	2589	22	AAI19616	Human DNA polymera
C 384	16	2.2	1495	21	AAKS5201	Human secreted pro	C 457	16	2.2	2608	22	ABL92089	Human Tumour Endot
C 385	16	2.2	1511	24	ABK35819	cDNA sequence #210	C 458	16	2.2	2632	22	AAH45491	Human reduced expr
C 386	16	2.2	1537	21	AACT79967	Human secreted pro	C 459	16	2.2	2660	22	AAH45490	Human reduced expr
C 387	16	2.2	1567	21	AAF16305	Human prostate can	C 460	16	2.2	2694	23	ABV22558	Human prostate exp
C 388	16	2.2	1583	21	AAZ65262	Human secreted pro	C 461	16	2.2	2694	23	ABV28419	Human prostate exp
C 389	16	2.2	1659	20	AAAT39816	Gastric cancer ass	C 462	16	2.2	2715	22	AAI59452	Human polynucleoti
C 390	16	2.2	1734	18	AAAT1745	Paramyxovirus haem	C 463	16	2.2	2785	22	AAI05110	Human reproductive
C 391	16	2.2	1743	21	AAD286927	Netrin coding sequ	C 464	16	2.2	2785	22	AAK75530	Human immune/haema
C 392	16	2.2	1819	22	AAD07351	Human DNA encoding	C 465	16	2.2	2785	23	ABL98002	Human testicular a
C 393	16	2.2	1819	24	ABK84637	Human cDNA differe	C 466	16	2.2	2807	23	AAH84436	DNA encoding novel
C 394	16	2.2	1833	22	AAAS67931	DNA encoding novel	C 467	16	2.2	2840	18	AAK767295	Type I diabetes-as
C 395	16	2.2	1852	22	AAK94173	Human full-length	C 468	16	2.2	2888	24	ABK35818	cDNA sequence #209
C 396	16	2.2	1855	24	ABK35190	Human cDNA encodin	C 469	16	2.2	2935	23	ABL13221	Drosophila melanog
C 397	16	2.2	1882	22	AAH18358	Human cDNA sequenc	C 470	16	2.2	2943	18	AAH88478	Human insulinoma-a
C 398	16	2.2	1897	24	AAD27276	Human transporter	C 471	16	2.2	2943	23	AAH84770	DNA encoding novel
C 399	16	2.2	1898	21	AAF22376	Human secreted pro	C 472	16	2.2	2985	22	ABA06555	Human cDNA SEQ ID
C 400	16	2.2	1906	24	ABL39786	Human NS cDNA sequ	C 473	16	2.2	2990	22	AAI61237	Human polynucleoti
C 401	16	2.2	1916	24	ABL92366	Human secreted pro	C 474	16	2.2	2990	22	AAI61238	Human polynucleoti
C 402	16	2.2	1923	23	AAAT7428	DNA encoding novel	C 475	16	2.2	2994	18	AAH788479	Human insulinoma-a
C 403	16	2.2	1928	23	ABL26971	Drosophila melanog	C 476	16	2.2	3001	24	ABN80332	Human chemically m
C 404	16	2.2	1976	22	ABA46129	Human breast cell	C 477	16	2.2	3032	24	ABL88369	Pain regulated CDN
C 405	16	2.2	1976	22	ABA56675	Human foetal liver	C 478	16	2.2	3046	22	AAK89786	Human digestive sy
C 406	16	2.2	1976	22	ABA6280	Probe #476 for ge	C 479	16	2.2	3090	22	AAI59451	Human polynucleoti
C 407	16	2.2	1976	22	AAK30334	Human bone marrow	C 480	16	2.2	3102	24	ABK31759	DNA encoding novel
C 408	16	2.2	1976	22	AAI14938	Probe #4871 for ge	C 481	16	2.2	3219	23	AAH77606	DNA encoding novel
C 409	16	2.2	1976	22	AAI04715	Probe #4706 used t	C 482	16	2.2	3253	22	AAH17470	Human cDNA sequenc
C 410	16	2.2	1976	24	ABS04921	Human genome-deriv	C 483	16	2.2	3279	14	AAO49397	TMF gene. Homo sa
C 411	16	2.2	1999	22	AAK69415	Human immune/haema	C 484	16	2.2	3282	24	ABK09761	Human ovarian tumo
C 412	16	2.2	2000	19	AAV49651	Human SRCR protein	C 485	16	2.2	3287	18	AAH95220	Macaque islet cell
C 413	16	2.2	2002	24	AAAG2701	cDNA sequence #488	C 486	16	2.2	3310	18	AAH67296	Type I diabetes-as
C 414	16	2.2	2006	20	AAAT20417	Human secreted pro	C 487	16	2.2	3358	20	AAH87773	Human mucin gene M
C 415	16	2.2	2013	24	ABL89702	Human polynucleoti	C 488	16	2.2	3389	23	AAH86290	DNA encoding novel
C 416	16	2.2	2025	22	AAKS2767	Human polynucleoti	C 489	16	2.2	3510	23	AAH666874	DNA encoding novel
C 417	16	2.2	2064	21	AAH65424	Porcine BAC-PIGF2-	C 490	16	2.2	3563	22	AAH18525	Human cDNA sequenc
C 418	16	2.2	2064	21	AAH45648	Human cancer cell	C 491	16	2.2	3628	22	AAH17549	Human cDNA sequenc
C 419	16	2.2	2064	24	AAH45648	Human cancer cell	C 492	16	2.2	3634	22	AAH81730	Human protease and
C 420	16	2.2	2088	24	AAH33852	Human secreted pro	C 493	16	2.2	3698	19	AAH62170	HSV-2 strain SB5 C
C 421	16	2.2	2101	22	AAH24245	Human oxidoreducta	C 494	16	2.2	3711	22	AAH34925	Human colon cancer
C 422	16	2.2	2102	24	AAAG2284	cDNA sequence #71	C 495	16	2.2	3825	8	AAH70261	Sequence of Newcas
C 423	16	2.2	2113	22	AAC91328	Human polynucleoti	C 496	16	2.2	3856	23	AAH87632	DNA encoding novel
C 424	16	2.2	2124	22	AAH81745	Human membrane ass	C 497	16	2.2	4039	19	AAV05886	Human Tbc-1 gene.
C 425	16	2.2	2142	20	AAAT22230	Human secreted pro	C 498	16	2.2	4068	22	AAH86707	Human polynucleoti
C 426	16	2.2	2155	24	ABL90322	Human polynucleoti	C 499	16	2.2	4136	18	AAH95368	Human protein tyro
C 427	16	2.2	2236	23	ABL05697	Drosophila melanog	C 500	16	2.2	4144	22	AAH18648	Human cDNA sequenc
C 428	16	2.2	2238	23	AAAT76384	DNA encoding novel	C 501	16	2.2	4203	22	AAI05112	Human reproductive
C 429	16	2.2	2293	6	AAH50491	Sequence of herpes	C 502	16	2.2	4203	22	AAI05113	Human reproductive
C 430	16	2.2	2297	10	AAH90526	Herpes simplex vir	C 503	16	2.2	4203	22	AAK75531	Human immune/haema
C 431	16	2.2	2301	24	ABA96102	Human membrane tra	C 504	16	2.2	4203	22	AAK75532	Human immune/haema
C 432	16	2.2	2323	23	AAH91161	DNA encoding novel	C 505	16	2.2	4203	23	ABL98004	Human testicular a
C 433	16	2.2	2339	24	AAD33824	Human secreted pro	C 506	16	2.2	4203	23	ABL98005	Human testicular a
C 434	16	2.2	2349	24	ABA90343	Human polynucleoti	C 507	16	2.2	4294	22	AAH86072	Human immune/haema
C 435	16	2.2	2351	23	ABL25332	Drosophila melanog	C 508	16	2.2	4465	20	AAH35142	LTC4 synthase gene
C 436	16	2.2	2370	23	AAH72793	DNA encoding novel	C 509	16	2.2	4465	21	AAH21010	Human low adenosin
C 437	16	2.2	2408	23	ABL27512	Drosophila melanog	C 510	16	2.2	4465	21	AAH34888	Human adenosine re
C 438	16	2.2	2446	22	AAD16281	Human ubiquitin ca	C 511	16	2.2	4465	24	ABL67233	Thyroid cancer rel
C 439	16	2.2	2452	22	AAH84753	Nucleotide sequenc	C 512	16	2.2	4465	24	AAD24654	Human leukotriene
C 440	16	2.2	2459	22	AAKS1822	Human polynucleoti	C 513	16	2.2	4546	23	ABL09809	Drosophila melanog
C 441	16	2.2	2479	19	AAV07906	Human cysteine-ric	C 514	16	2.2	4698	13	AAQ32370	P1A genomic DNA.
C 442	16	2.2	2479	21	AAH75128	cDNA encoding a hu	C 515	16	2.2	4698	15	AAQ72475	Entire P1A genomic
C 443	16	2.2	2479	22	AAH69309	Human DXK-3 DNA.	C 516	16	2.2	4698	16	AAI01176	P815A antigen prec
C 444	16	2.2	2490	19	AAV38798	Homo sapiens cereb	C 517	16	2.2	4698	17	AAI14692	MAGE genomic DNA.
C 445	16	2.2	2495	21	AAAT7555	Human ORFX ORF3110	C 518	16	2.2	4698	20	AAH84111	P1A genomic sequen
C 446	16	2.2	2495	22	AAK94900	Human full-length	C 519	16	2.2	4740	21	AAA95896	Human KLK-L1 gene.
C 447	16	2.2	2522	23	ABL28102	Drosophila melanog	C 520	16	2.2	4844	23	ABL26970	Drosophila melanog

521	16	2.2	4856	23	AAS87633	DNA encoding novel	594	16	2.2	23580	22	AAS28556	Genomic sequence #
522	16	2.2	4888	24	ABO88240	Human osteoblast d	595	16	2.2	23580	22	AAK87248	Human immune/haema
523	16	2.2	4897	23	ABL05696	Drosophila melanog	596	16	2.2	24221	23	ABL09808	Drosophila melanog
524	16	2.2	5034	22	ABA07244	Human pancreatic c	597	16	2.2	24843	24	AAS17764	Human Genomic DNA
525	16	2.2	5034	22	AAK89885	Human digestive sy	598	16	2.2	24843	24	AAS17764	Human Genomic DNA
526	16	2.2	5036	22	ABA07245	Human digestive sy	599	16	2.2	26767	23	ABL08654	Drosophila melanog
527	16	2.2	5036	22	AAK89886	Human digestive sy	600	16	2.2	26960	23	ABL08712	Drosophila melanog
528	16	2.2	5087	21	AAK39482	Human NNT-1 DNA	601	16	2.2	29222	24	ABL39412	Human electron-tra
529	16	2.2	5087	24	ABK11648	Human novel neurot	602	16	2.2	29973	22	AAS29814	Human cytoskeletal
530	16	2.2	5088	19	AAV47511	Human neurotrophic	603	16	2.2	31168	22	ABA07295	Human pancreatic c
531	16	2.2	5088	19	AAV22653	Human genomic DNA	604	16	2.2	31168	22	AAS42115	Genomic sequence #
532	16	2.2	5130	21	AAK21011	Human low adenosin	605	16	2.2	31168	22	AAS27804	DNA encoding novel
533	16	2.2	5130	21	AAK34889	Human adenosine re	606	16	2.2	31168	22	AAK64760	Human immune/haema
534	16	2.2	5306	22	AAS30054	Human lung antigen	607	16	2.2	31168	22	AAK89940	Human digestive sy
535	16	2.2	5333	22	AAK80368	Human immune/haema	608	16	2.2	31348	22	AAS35759	Human cardiovascular
536	16	2.2	5521	22	AAI71603	Human G-protein co	609	16	2.2	31348	22	AAK79227	Human immune/haema
537	16	2.2	5538	22	AAH18660	Human cDNA sequenc	610	16	2.2	32192	22	ABAL5328	Human nervous syst
538	16	2.2	5581	18	AAAT48737	Human leucocyte sp	611	16	2.2	32192	22	ABAL5328	Human nervous syst
539	16	2.2	5581	18	AAAT45451	Human LST-1 (leuko	612	16	2.2	32192	22	AAAL05557	Human reproductive
540	16	2.2	5631	20	AAK98274	Human tumour suppr	613	16	2.2	32192	22	AAAL05532	Human reproductive
541	16	2.2	5652	23	ABL13220	Drosophila melanog	614	16	2.2	32192	23	ABL98141	Human testicular a
542	16	2.2	5788	22	ABAL15481	Human nervous syst	615	16	2.2	32192	23	ABK42529	Genomic sequence #
543	16	2.2	5788	22	ABAL15482	Human nervous syst	616	16	2.2	32195	22	AAS36105	Human cardiovascular
544	16	2.2	5802	19	AAV49652	Human SRCR protein	617	16	2.2	32195	22	AAS31532	Human DNA for a no
545	16	2.2	6095	22	AAS29815	Human cytoskeletal	618	16	2.2	32195	22	AAS31538	Human DNA for a no
546	16	2.2	6120	24	ABN80303	Human chemically m	619	16	2.2	32195	23	ABK44045	Genomic DNA encodi
547	16	2.2	6120	24	ABK28440	DNA transcription	620	16	2.2	32195	23	ABO66856	Human polynucleoti
548	16	2.2	6193	24	ABN95699	Gene #2197 used to	621	16	2.2	32195	24	ABO66862	Human polynucleoti
549	16	2.2	6249	23	AAS79371	DNA encoding novel	622	16	2.2	32249	22	ABAL17555	Human nervous syst
550	16	2.2	6459	22	AAK88336	S. spinosa DNA fra	623	16	2.2	33023	24	ABN96853	Gene #3351 used to
551	16	2.2	6545	23	ABL14373	Drosophila melanog	624	16	2.2	36140	22	AAK91326	Partial sequence o
552	16	2.2	6850	22	AAK81486	Human immune/haema	625	16	2.2	43069	21	AAS26335	Genomic sequence o
553	16	2.2	6850	22	AAK81489	Human immune/haema	626	16	2.2	50000	22	AAK88313	S. spinosa DNA fra
554	16	2.2	7175	22	ABA07728	Human ovarian and	627	16	2.2	50000	22	AAK88316	S. spinosa DNA fra
555	16	2.2	7175	22	AAK02954	Human reproductive	628	16	2.2	51751	22	AAK91327	Genomic sequence o
556	16	2.2	7213	22	AAK85121	Human immune/haema	629	16	2.2	65140	22	ABAL17184	Streptomyces nous
557	16	2.2	7452	16	AAQ85594	Human glycoprotein	630	16	2.2	65608	24	ABAL62910	Streptomyces nous
558	16	2.2	7452	21	AAZ61217	DNA encoding human	631	16	2.2	65608	24	ABAL64414	Breast cancer rela
559	16	2.2	7452	22	AAK90646	Human secreted pro	632	16	2.2	65608	24	ABAL64414	Stomach cancer rel
560	16	2.2	7452	24	ABK48275	DNA encoding human	633	16	2.2	66685	22	AAK07380	Oesophagus cancer
561	16	2.2	7702	21	AAK88739	Human protein tyro	634	16	2.2	80161	20	AAZ21501	Human genomic DNA
562	16	2.2	7702	21	AAZ91908	Human protein tyro	635	16	2.2	81800	24	ABK84756	DNA fragment of Sa
563	16	2.2	7702	21	AAZ59133	LAR tyrosine phosph	636	16	2.2	86080	24	ABQ88164	Human cDNA differe
564	16	2.2	7705	22	AAH98405	Human EST-derived	637	16	2.2	86080	24	ABK83561	Human osteoblast d
565	16	2.2	7705	22	AAK22684	Human cDNA encodin	638	16	2.2	110096	24	ABN95044	Human cDNA differe
566	16	2.2	7741	22	AAS22448	Human cDNA encodin	639	16	2.2	117213	19	AAV62176	Gene #1542 used to
567	16	2.2	7945	23	ABV27897	Human prostate exp	640	16	2.2	125401	22	AAK17186	HSV-2 strain SB5 C
568	16	2.2	9457	23	ABU18290	Drosophila melanog	641	16	2.2	143899	24	AAK38336	Streptomyces nous
569	16	2.2	9618	24	AAK25946	Human protease inh	642	16	2.2	148834	24	ABK83570	Genomic sequence e
570	16	2.2	9618	24	AAK26033	Human protease inh	643	16	2.2	154746	24	AAK25519	Human cDNA differe
571	16	2.2	10210	24	AAS18100	Human angiotensin	644	16	2.2	155074	24	ABN85735	Human herpessvirs
572	16	2.2	10211	19	AAV62152	HSV-2 strain SB5 C	645	16	2.2	220895	24	ABK84798	Human cDNA differe
573	16	2.2	10438	23	ABU14372	Drosophila melanog	646	16	2.2	249487	24	ABN85733	Mouse genomic regi
574	16	2.2	10552	22	ABAL19272	Human nervous syst	647	16	2.2	349980	22	AAH41224	Pyrococcus abyssi
575	16	2.2	10552	22	ABAL19272	Human nervous syst	648	16	2.2	349980	22	AAH68526	C glutamicum codin
576	16	2.2	10557	24	AAS18240	Reference sequence	649	16	2.2	349980	22	AAH68527	C glutamicum codin
577	16	2.2	11853	22	AAS32785	Human genomic DNA	650	16	2.2	349980	22	AAH68529	C glutamicum codin
578	16	2.2	13102	22	ABAL19342	Human nervous syst	651	16	2.2	513445	22	AAI61373	Soybean 318013 reg
579	16	2.2	13206	11	AAQ05243	Rat acyl peptide h	652	16	2.2	4403765	22	AAI99683	Mycobacterium tube
580	16	2.2	13634	23	ABLO2686	Drosophila melanog	653	16	2.2	4403765	22	AAI99683	Mycobacterium tube
581	16	2.2	14212	22	AAK79592	Human immune/haema	654	16	2.2	4411529	22	AAI99682	Mycobacterium tube
582	16	2.2	14212	22	AAK80024	Human immune/haema	655	16	2.2	4411529	22	AAI99682	Mycobacterium tube
583	16	2.2	14212	22	AAK85921	Human immune/haema	656	15	2.1	24	17	AAI99682	Primer P53-5XAMP f
584	16	2.2	14637	22	AAS32620	Human genomic DNA	657	15	2.1	24	18	AAI99682	Primer for exon 4
585	16	2.2	15186	21	AAZ44617	Newcastle disease	658	15	2.1	24	18	AAI99682	Primer for exon 4
586	16	2.2	17679	22	AAI67271	Human FK506-bindin	659	15	2.1	24	18	AAI99682	MBV-specific PCR p
587	16	2.2	17679	22	AAI67272	Human FK506-bindin	660	15	2.1	24	22	AAI99682	Mammalian ZAP-70 P
588	16	2.2	18544	22	AAK80364	Human immune/haema	661	15	2.1	27	20	AAV73863	Human MUC1 derivat
589	16	2.2	20084	22	AAS21773	Human gene for col	662	15	2.1	30	20	AAK32237	Primer for amplifi
590	16	2.2	20084	22	AAK32237	Nucleotide sequenc	663	15	2.1	30	20	AAK32237	Human p53 gene PCR
591	16	2.2	20693	23	ABU16740	Drosophila melanog	664	15	2.1	33	20	AAZ29926	PCR primer CBPI us
592	16	2.2	21535	22	AAS29834	Human cytoskeletal	665	15	2.1	34	15	AAQ77966	Primer for amplifi
593	16	2.2	21535	22	AAS35081	DNA #31 encoding h	666	15	2.1	51	22	AAK31757	Human SNP oligonuc

c 667	15	2.1	60	24	ABN37991	Human spliced tran	c 740	15	2.1	285	21	AA000387	Human Mucin 1 (MUC
c 668	15	2.1	60	24	ABN49231	Human spliced tran	c 741	15	2.1	285	24	ABN76494	Human ORF1441 cDNA
c 669	15	2.1	90	20	ABL87016	Human single nucle	c 742	15	2.1	284	21	ABC01582	Human prostate exp
c 670	15	2.1	92	23	ABL51695	Human GFRA1pha4 ex	c 743	15	2.1	295	23	ABV60596	Human ovarian can
c 671	15	2.1	22	22	ABA35288	Probe #13754 for g	c 744	15	2.1	239	20	ABL80579	Human gene express
c 672	15	2.1	96	22	AAK42422	Human bone marrow	c 745	15	2.1	300	20	AA214894	Human gene express
c 673	15	2.1	112	18	AAV77186	Staphylococcus aur	c 746	15	2.1	300	20	AA213648	Human secreted pro
c 674	15	2.1	116	21	AAC31372	Human secreted pro	c 747	15	2.1	300	21	AA09756	Human colon cancer
c 675	15	2.1	133	22	AAH36493	Human colon cancer	c 748	15	2.1	300	21	AAA00497	Human colon cancer
c 676	15	2.1	139	24	ABL69210	Prostate cancer re	c 749	15	2.1	300	21	AAA00975	Human bone marrow
c 677	15	2.1	139	24	ABL69863	Prostate cancer re	c 750	15	2.1	303	22	AAK40168	Human bone marrow
c 678	15	2.1	147	24	ABK30456	Human G-protein-co	c 751	15	2.1	303	22	AAI46185	M. capsulatus gene
c 679	15	2.1	156	22	ABA69904	Human foetal liver	c 752	15	2.1	306	24	ABO91342	Probe #14871 used
c 680	15	2.1	158	22	ABA36757	Probe #15223 for g	c 753	15	2.1	311	21	AAZ51940	Human sperm anti
c 681	15	2.1	156	22	AAK18105	Human brain expres	c 754	15	2.1	311	21	AAZ51940	Human ovarian can
c 682	15	2.1	156	22	AAK33994	Human bone marrow	c 755	15	2.1	315	21	AA000964	Human secreted pro
c 683	15	2.1	156	22	AAI24679	Human bone marrow	c 756	15	2.1	315	24	ABN75463	Human ORF410 cDNA,
c 684	15	2.1	156	22	AAI50004	Probe #14612 for g	c 757	15	2.1	316	22	AAK86654	Human immune/haema
c 685	15	2.1	156	24	ABS18227	Human genome-deriv	c 758	15	2.1	317	22	AAK74571	Human immune/haema
c 686	15	2.1	160	16	ABT24242	Human gene signatu	c 759	15	2.1	321	24	AAI46139	Human ALADIN gene
c 687	15	2.1	167	22	ABA41172	Probe #19638 for g	c 760	15	2.1	321	24	AAZ62566	CNA sequence #353
c 688	15	2.1	167	22	AAK25300	Human brain expres	c 761	15	2.1	325	22	AAK58397	Human immune/haema
c 689	15	2.1	167	22	AAK51307	Human bone marrow	c 762	15	2.1	325	24	AAI46140	Human ALADIN gene
c 690	15	2.1	167	22	AAI28318	Probe #18251 for g	c 763	15	2.1	327	22	AAK59128	Human immune/haema
c 691	15	2.1	167	24	ABS24850	Human genome-deriv	c 764	15	2.1	327	24	ABL80486	Human ovarian can
c 692	15	2.1	183	21	AAC10175	Human secreted pro	c 765	15	2.1	331	22	AAK72671	Human immune/haema
c 693	15	2.1	184	21	AAC14003	Human secreted pro	c 766	15	2.1	331	22	AAK72672	Human immune/haema
c 694	15	2.1	203	22	AAK57755	Human immune/haema	c 767	15	2.1	331	22	AAK72673	Human immune/haema
c 695	15	2.1	207	24	ABN22940	Human ORFX polynuc	c 768	15	2.1	331	24	ABK11573	Rat obesity relate
c 696	15	2.1	209	20	AAK40902	Human secreted pro	c 769	15	2.1	332	24	ABQ57656	Human colon cancer
c 697	15	2.1	211	21	AAC13886	Human secreted pro	c 770	15	2.1	333	21	AAC02284	Human secreted pro
c 698	15	2.1	211	21	AAC10404	Human secreted pro	c 771	15	2.1	333	23	AAZ84796	DNA encoding novel
c 699	15	2.1	216	24	ABK38903	CNA encoding lung	c 772	15	2.1	334	22	AAH23043	Stem cell growth f
c 700	15	2.1	216	24	ABK39172	CNA encoding lung	c 773	15	2.1	338	24	ABN78870	Human ORF3817 cDNA
c 701	15	2.1	219	24	ABK80415	Bacillus clausii g	c 774	15	2.1	338	24	ABN24031	Human ORFX polynuc
c 702	15	2.1	223	22	AAK65926	Novel human polyn	c 775	15	2.1	339	22	AAI24345	Human breast can
c 703	15	2.1	225	22	AAI12822	Human breast can	c 776	15	2.1	340	22	AAH83877	Human ovarian tumo
c 704	15	2.1	226	22	AAZ52530	Human ovarian PCR-	c 777	15	2.1	340	24	ABL50494	Human nPCR-Seg107
c 705	15	2.1	226	22	AAZ54513	Human ovarian PCR-	c 778	15	2.1	340	24	ABN61007	Human cancer relat
c 706	15	2.1	227	21	AAA57515	Trabecular meshwor	c 779	15	2.1	341	22	AAO101900	Human reproductive
c 707	15	2.1	229	22	ABA75649	Human foetal liver	c 780	15	2.1	341	23	ABL97193	Human testicular a
c 708	15	2.1	229	22	AAK24257	Human brain expres	c 781	15	2.1	342	20	AAH87233	Human single nucle
c 709	15	2.1	229	22	AAI56251	Probe #24937 used	c 782	15	2.1	342	22	AAO66443	Mouse microglia an
c 710	15	2.1	231	14	AAQ60959	Human brain Expres	c 783	15	2.1	343	21	ABO62971	Mycobacterium tube
c 711	15	2.1	231	24	ABN25707	Human ORFX polynuc	c 784	15	2.1	343	22	AAI44150	Human breast can
c 712	15	2.1	234	24	ABN18013	Human ORFX polynuc	c 785	15	2.1	343	22	AAI44150	Human breast can
c 713	15	2.1	247	22	AAH36651	Human colon cancer	c 786	15	2.1	344	24	ABL70735	Novel human polyn
c 714	15	2.1	251	19	AAI11282	Human biallelic po	c 787	15	2.1	349	22	AAK64995	Novel human polyn
c 715	15	2.1	251	19	AAI11281	Human biallelic po	c 788	15	2.1	351	22	AAK60364	Human immune/haema
c 716	15	2.1	255	22	AAH82197	Rat differential t	c 789	15	2.1	355	20	AAV87068	EST clone BH316
c 717	15	2.1	260	22	ABA49402	Human breast cell	c 790	15	2.1	356	22	AAO60577	Mouse microglia an
c 718	15	2.1	260	22	ABA67312	Human foetal liver	c 791	15	2.1	359	22	AAI80858	Human polynucleoti
c 719	15	2.1	260	22	ABA34404	Probe #12870 for g	c 792	15	2.1	361	22	AAH02307	Human lipoprotein
c 720	15	2.1	260	22	AAK15748	Human brain expres	c 793	15	2.1	362	22	AAK75795	Human immune/haema
c 721	15	2.1	260	22	AAK14186	Human bone marrow	c 794	15	2.1	363	21	AAO23356	Human secreted pro
c 722	15	2.1	260	22	AAI22233	Probe #12166 for g	c 795	15	2.1	363	22	AAK64313	Novel human polyn
c 723	15	2.1	260	22	AAI47528	Probe #16214 used	c 796	15	2.1	365	20	AAK20819	Polynucleotide seq
c 724	15	2.1	260	22	AAI07932	Probe #7923 used t	c 797	15	2.1	366	22	AAI85545	Human polynucleoti
c 725	15	2.1	260	24	ABS15491	Human genome-deriv	c 798	15	2.1	366	22	AAH23042	Stem cell growth f
c 726	15	2.1	261	22	AAK64088	Human immune/haema	c 799	15	2.1	367	22	AAI23012	Human breast can
c 727	15	2.1	261	22	ABL53208	Nucleotide sequenc	c 800	15	2.1	371	21	AAI31351	Human secreted pro
c 728	15	2.1	269	21	AAK28262	Human secreted pro	c 801	15	2.1	371	22	ABA51966	Human foetal liver
c 729	15	2.1	270	22	AAK28208	Novel cDNA encodin	c 802	15	2.1	371	22	ABA21784	Probe #250 for gen
c 730	15	2.1	270	22	AAH33015	Human colon cancer	c 803	15	2.1	371	22	AAK00252	Human brain expres
c 731	15	2.1	273	22	AAK28484	Genomic sequence #	c 804	15	2.1	371	22	AAK25693	Human bone marrow
c 732	15	2.1	273	22	AAK28485	Genomic sequence #	c 805	15	2.1	371	22	AAI10321	Probe #254 for gen
c 733	15	2.1	277	24	ABN19823	Human ORFX polynuc	c 806	15	2.1	371	22	AAI31574	Probe #260 used to
c 734	15	2.1	278	22	AAH97915	Murine 7-transmemb	c 807	15	2.1	371	22	AAI00257	Probe #248 used to
c 735	15	2.1	279	24	ABN77037	Human ORF1984 cDNA	c 808	15	2.1	371	24	ABS00272	Human genome-deriv
c 736	15	2.1	283	21	AAAS7514	Trabecular meshwor	c 809	15	2.1	371	22	ABA44248	Human foetal liver
c 737	15	2.1	284	20	AAV89382	EST clone CL399	c 810	15	2.1	379	22	ABA54696	Human foetal liver
c 738	15	2.1	284	22	AAK75717	Human immune/haema	c 811	15	2.1	379	22	ABA24477	Probe #2943 for ge
c 739	15	2.1	284	24	ABN23278	Human ORFX polynuc	c 812	15	2.1	379	22	AAK02982	Human brain expres

813	15	2.1	379	22	AAK28428	Human bone marrow	c 886	15	2.1	442	22	AAI04656	Probe #4647 used t
814	15	2.1	379	22	AAI12995	Probe #2928 used t	c 887	15	2.1	442	24	ABSO4852	Human genome-deriv
815	15	2.1	379	22	AAI13452	Probe #3038 used t	c 888	15	2.1	442	24	ABL61846	Colon adenocarcino
816	15	2.1	379	22	AAI02913	Probe #2904 used t	c 889	15	2.1	443	22	AAI15353	Human breast cance
817	15	2.1	379	22	ABS02936	Human genome-deriv	c 890	15	2.1	443	22	ABN96087	Gene #2585 used to
818	15	2.1	381	21	AAH30934	Human colon cancer	c 891	15	2.1	445	24	ABK64586	Human benign prost
819	15	2.1	381	22	AAI87309	Human polynucleoti	c 892	15	2.1	447	15	AAQ62530	Allinase clone pAI
820	15	2.1	382	22	AAF65213	Novel human polynu	c 893	15	2.1	447	22	ABA52420	Human foetal liver
821	15	2.1	385	21	AAK57701	Arachidonic acid m	c 894	15	2.1	447	22	ABA22215	Probe #681 for gen
822	15	2.1	385	22	AAK57020	Human immune/haema	c 895	15	2.1	447	22	AAK00689	Human brain expres
823	15	2.1	385	24	ABN25901	Human ORFX polynuc	c 896	15	2.1	447	22	AAK26140	Human bone marrow
824	15	2.1	385	24	ABN26541	Human ORFX polynuc	c 897	15	2.1	447	22	AAI10770	Probe #703 for gen
825	15	2.1	388	22	AAI82264	Human polynucleoti	c 898	15	2.1	447	22	AAI32028	Probe #714 used to
826	15	2.1	393	22	AAI91201	Human polynucleoti	c 899	15	2.1	447	22	AAI00696	Probe #687 used to
827	15	2.1	395	22	AAK79670	Human immune/haema	c 900	15	2.1	447	24	ABS00725	Human genome-deriv
828	15	2.1	395	22	AAK93764	Human immune/haema	c 901	15	2.1	449	22	ABA59098	Human foetal liver
829	15	2.1	395	22	AAK95310	Human immune/haema	c 902	15	2.1	449	22	AAK07276	Human brain expres
830	15	2.1	396	22	AAI91264	Human polynucleoti	c 903	15	2.1	449	22	AAK33035	Human bone marrow
831	15	2.1	397	22	ABA09379	Human p53 homology	c 904	15	2.1	449	22	AAI38838	Probe #7524 used t
832	15	2.1	397	22	AAK29367	CDNA encoding nove	c 905	15	2.1	449	24	ABS07849	Human genome-deriv
833	15	2.1	397	24	ABN17460	Human ORFX polynuc	c 906	15	2.1	449	24	ABQ60783	Human defensin 5 D
834	15	2.1	400	22	AAK23267	DNA encoding novel	c 907	15	2.1	450	22	AAK65088	Human immune/haema
835	15	2.1	400	23	AAK64408	DNA encoding novel	c 908	15	2.1	450	22	AAK65089	Human immune/haema
836	15	2.1	400	23	AAK76908	DNA encoding novel	c 909	15	2.1	450	23	AAK89759	DNA encoding novel
837	15	2.1	400	23	AAK91226	DNA encoding novel	c 910	15	2.1	450	23	AAK76455	DNA encoding novel
838	15	2.1	402	23	AAK92406	DNA encoding novel	c 911	15	2.1	450	23	AAK83763	DNA encoding novel
839	15	2.1	401	22	AAK96118	Human neuregulin g	c 912	15	2.1	451	22	AAI81766	Human polynucleoti
840	15	2.1	401	22	AAK97611	Human neuregulin g	c 913	15	2.1	451	24	ABK15916	Human lung tumour
841	15	2.1	401	22	AAK67113	Novel human polynu	c 914	15	2.1	452	16	AAK20964	Human gene signatu
842	15	2.1	402	22	AAK66385	C glutamic codin	c 915	15	2.1	453	21	ABQ63054	Mycobacterium tube
843	15	2.1	402	22	AAK66246	Novel human polynu	c 916	15	2.1	453	21	AAZ42758	Human 5' EST isola
844	15	2.1	402	23	ABV05128	Human prostate exp	c 917	15	2.1	453	22	AAK31105	Human musculoskele
845	15	2.1	405	22	AAI88744	Human polynucleoti	c 918	15	2.1	453	23	ABL24873	Drosophila melanog
846	15	2.1	407	21	AAK17911	Human secreted pro	c 919	15	2.1	455	22	ABA57465	Human foetal liver
847	15	2.1	409	22	AAI89479	Human polynucleoti	c 920	15	2.1	455	22	ABA26960	Probe #5426 for ge
848	15	2.1	409	24	ABL78169	Human ovarian canc	c 921	15	2.1	455	22	AAK05504	Human brain expres
849	15	2.1	410	22	AAK75147	Human immune/haema	c 922	15	2.1	455	22	AAK27138	Human bone marrow
850	15	2.1	410	24	ABL82338	Human ovarian canc	c 923	15	2.1	455	22	AAK31105	Human bone marrow
851	15	2.1	411	22	AAK09623	Human breast cance	c 924	15	2.1	455	22	AAI15548	Probe #5481 for ge
852	15	2.1	411	24	ABQ60009	Human colon cancer	c 925	15	2.1	455	22	AAI33035	Probe #1721 used t
853	15	2.1	412	22	AAK15501	Human breast cance	c 926	15	2.1	455	22	AAI37014	Probe #5700 used t
854	15	2.1	412	24	ABK39009	CDNA encoding lung	c 927	15	2.1	455	24	ABSO5856	Human genome-deriv
855	15	2.1	416	22	AAH35488	Human colon cancer	c 928	15	2.1	458	22	ABA52086	Human foetal liver
856	15	2.1	419	20	AAK51878	Human secreted pro	c 929	15	2.1	458	22	ABA21898	Probe #364 for gen
857	15	2.1	424	14	AAQ53216	Sequence encoding	c 930	15	2.1	458	22	AAK00368	Human brain expres
858	15	2.1	426	22	AAK27960	Novel cDNA encoding	c 931	15	2.1	458	22	AAK25811	Human bone marrow
859	15	2.1	426	24	ABK62372	Rat sequence diffe	c 932	15	2.1	458	22	AAI10440	Probe #373 for gen
860	15	2.1	427	22	ABA57273	Human foetal liver	c 933	15	2.1	458	22	AAI31693	Probe #379 used to
861	15	2.1	427	22	ABA26836	Probe #5302 for ge	c 934	15	2.1	458	22	AAI00376	Probe #367 used to
862	15	2.1	427	22	AAK05300	Human brain expres	c 935	15	2.1	458	24	ABS00392	Human genome-deriv
863	15	2.1	427	22	AAK30892	Human bone marrow	c 936	15	2.1	461	20	AAK39539	Human secreted pro
864	15	2.1	427	22	AAI15450	Probe #5383 for ge	c 937	15	2.1	461	24	ABN60707	Human cancer relat
865	15	2.1	427	22	AAI36805	Probe #4991 used t	c 938	15	2.1	463	22	AAH72149	Human cervical can
866	15	2.1	427	24	ABSO5640	Human genome-deriv	c 939	15	2.1	463	24	ABS08205	Human genome-deriv
867	15	2.1	429	21	AAK48145	Zea mays DNA fragm	c 940	15	2.1	466	21	AAK01377	Human secreted pro
868	15	2.1	430	22	AAH23056	Stem cell growth f	c 941	15	2.1	467	24	ABN73004	CDNA sequence 1043
869	15	2.1	431	24	ABN21098	Human ORFX polynuc	c 942	15	2.1	468	21	AAK79292	Pinus radiata cell
870	15	2.1	432	22	AAI56352	Probe #25038 used	c 943	15	2.1	468	24	ABN73035	CDNA sequence PB r
871	15	2.1	433	22	AAK24618	Human ovarian PCR-	c 944	15	2.1	470	20	AAK40578	Human secreted pro
872	15	2.1	433	22	AAH83241	Human ovarian tumo	c 945	15	2.1	470	22	ABA58932	Human foetal liver
873	15	2.1	437	22	AAK59365	Human immune/haema	c 946	15	2.1	470	22	ABA59267	Human foetal liver
874	15	2.1	439	22	AAH11434	Human cDNA clone (	c 947	15	2.1	470	22	ABA27798	Probe #6264 for ge
875	15	2.1	439	23	AAK58724	CDNA #1400 encodin	c 948	15	2.1	470	22	ABA28002	Probe #6468 for ge
876	15	2.1	440	24	ABL89689	Human polynucleoti	c 949	15	2.1	470	22	AAK07095	Human brain expres
877	15	2.1	441	21	AAK69703	Human ovarian carc	c 950	15	2.1	470	22	AAK07479	Human brain expres
878	15	2.1	441	22	AAK64882	Human immune/haema	c 951	15	2.1	470	22	AAK32835	Human bone marrow
879	15	2.1	441	24	ABN72597	Ovarian carcinoma	c 952	15	2.1	470	22	AAK33264	Human bone marrow
880	15	2.1	442	22	ABA46064	Human breast cell	c 953	15	2.1	470	22	AAI16226	Probe #6159 for ge
881	15	2.1	442	22	ABA56602	Human foetal liver	c 954	15	2.1	470	22	AAI16389	Probe #6322 for ge
882	15	2.1	442	22	ABA26215	Probe #4681 for ge	c 955	15	2.1	470	22	AAI38650	Probe #7336 used t
883	15	2.1	442	22	AAK30274	Human bone marrow	c 956	15	2.1	470	22	AAI39058	Probe #7744 used t
884	15	2.1	442	22	AAI14868	Probe #4801 for ge	c 957	15	2.1	470	24	ABS07639	Human genome-deriv
885	15	2.1	442	22	AAI36225	Probe #4911 used t	c 958	15	2.1	470	24	ABS08096	Human genome-deriv



959 15 2.1 470 24 ABN73003  
 960 15 2.1 475 21 AAX79633  
 961 15 2.1 476 22 ABA96249  
 962 15 2.1 477 22 ABA52332  
 963 15 2.1 477 22 ABA22127  
 964 15 2.1 477 22 AAK00604  
 965 15 2.1 477 22 AAK26054  
 966 15 2.1 477 22 AAI10682  
 967 15 2.1 477 22 AAI13938  
 968 15 2.1 477 22 ABS00637  
 969 15 2.1 477 22 ABS02184  
 970 15 2.1 478 22 ABA21990  
 971 15 2.1 478 22 AAK00460  
 972 15 2.1 478 22 AAK25907  
 973 15 2.1 478 22 AAI10537  
 974 15 2.1 478 22 AAI131790  
 975 15 2.1 478 22 AAI00470  
 976 15 2.1 478 24 ABS00490  
 977 15 2.1 480 23 ABV12653  
 978 15 2.1 481 20 AAX1874  
 979 15 2.1 482 22 AAD10355  
 980 15 2.1 484 22 AAS29085  
 981 15 2.1 484 22 AAS29956  
 982 15 2.1 484 22 AAS29958  
 983 15 2.1 484 22 AAI99995  
 984 15 2.1 485 24 ABN73022  
 985 15 2.1 487 22 ABA44799  
 986 15 2.1 487 22 ABA52254  
 987 15 2.1 487 22 ABA24999  
 988 15 2.1 487 22 AAK03509  
 989 15 2.1 487 22 AAI13550  
 990 15 2.1 487 22 AAI34913  
 991 15 2.1 487 22 AAI03439  
 992 15 2.1 487 24 ABS03498  
 993 15 2.1 489 24 AAK54931  
 994 15 2.1 491 24 AAB94901  
 995 15 2.1 493 20 AAV88064  
 996 15 2.1 494 22 AAH71087  
 997 15 2.1 496 24 ABL80151  
 998 15 2.1 498 22 AAH35626  
 999 15 2.1 498 22 AAF90635  
 1000 15 2.1 498 22 AAF90668

## ALIGNMENTS

RESULT 1  
 ID AAA64508 standard; cDNA; 5492 BP.  
 XX  
 AC AAA64508;  
 XX  
 DT 02-JAN-2001 (first entry)  
 XX  
 DE .cDNA sequence of the wild type human FEZ1 gene.  
 XX

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
 KW tumour proliferation; tubulin; microtubule; protein Efr1-gamma;  
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
 KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

XX WO200050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX

(UVJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human  
 FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
 cancer -

Example 2; Fig 5B; 255pp; English.

XX The present sequence represents the cDNA sequence of the human FEZ1 gene.  
 FEZ1 is a tumour suppressor gene, located at chromosome location 8p22.  
 Decreased or no expression of FEZ1 is detected in a variety of cancer  
 cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
 also interacts with tubulin, with microtubules, and with protein  
 Efr1-gamma. Post-translational phosphorylation and dephosphorylation  
 modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
 expression are useful for inducing cells to proliferate. Compounds  
 which modulate FEZ1 association with tubulin are useful for alleviating  
 tubulin hyper- or hypo- polymerisation disorders, such as those  
 associated with aberrant initiation of mitosis, modulation of the  
 initiation and rate of cell proliferation and cell growth, modulation of  
 cell shape, cell rigidity, cell motility, rate and stage of cellular  
 DNA replication, intracellular distribution of organelles, metastatic  
 potential of cell and cellular transformation from a non-cancerous to  
 cancerous phenotype. Compounds which modulate FEZ1 binding and  
 phosphorylation are also useful for alleviating a disorder, such as  
 tumorigenesis, tumour survival, growth and metastasis.

XX Sequence 5492 BP; 1137 A; 1704 C; 1565 G; 1086 T; 0 other;

Query Match 100.0%; Score 715; DB 21; Length 5492;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTGCCCCCGGACAGAGAGAGGCTGGCTCCCTCCCGAGGTGGAGACCCCCCC 60

Db 4215 ACTGCCCCCGGACAGAGAGAGGCTGGCTCCCTCCCGAGGTGGAGACCCCCCC 4274

Qy 61 CAATCCAGGAAAGAGCAGTCCAGTGTCTGCCTCAGACGTTGGCTGAGAAGAA 120

Db 4275 CAATCCAGGAAAGAGCAGTCCAGTGTCTGCCTCAGACGTTGGCTGAGAAGAA 4334

Qy 121 GTGCTGCCACCCAGGGGAAGCCCTGAGGGGAGGCTGTGCTCCGCCATGTGTGCC 180

Db 4335 GTGCTGCCACCCAGGGGAAGCCCTGAGGGGAGGCTGTGCTCCGCCATGTGTGCC 4394

Qy 181 GGTACCTTCCATACACAGAGAGTGCAGCCTTCTCCATATCTCCATGCGCCTGTCC 240

Db 4395 GGTACCTTCCATACACAGAGAGTGCAGCCTTCTCCATATCTCCATGCGCCTGTCC 4454

Qy 241 CCGGCCCCAGATGTGTCCCGCCCGAGGCTTGTCTTACGTCCAAAGTGGCAGATGCTTCCC 300

Db 4455 CCGGCCCCAGATGTGTCCCGCCCGAGGCTTGTCTTACGTCCAAAGTGGCAGATGCTTCCC 4514

Qy 301 TGGGCTGCCACAGCCCGCCCGCCAGAGTGCCACCGTGGCAGTGAATGCAAGTATCC 360

Db 4515 TGGGCTGCCACAGCCCGCCCGCCAGAGTGCCACCGTGGCAGTGAATGCAAGTATCC 4574

Qy 361 TGGGACCTTCAACCTCACCTTCTGTGGGTGTCTTTCTGCTCCCTGTCCAAAAGCGCCC 420

Db 4575 TGGGACCTTCAACCTCACCTTCTGTGGGTGTCTTTCTGCTCCCTGTCCAAAAGCGCCC 4634

Qy 421 TCATATTCTTGGACCATGCCAGATTCTGCCTCTCTGGAAGAGGCTCTGGACAGAGAA 480

Db 4635 TCATATTCTTGGACCATGCCAGATTCTGCCTCTCTGGAAGAGGCTCTGGACAGAGAA 4694

Qy 481 GCCTCCAGACAGAGCCTGGCCCCCAGGCCCGCCAGAGGTGGGCTTCTGCTCCCTTCCCT 540

Db 4695 GCCTCCAGACAGAGCCTGGCCCCCAGGCCCGCCAGAGGTGGGCTTCTGCTCCCTTCCCT 4754





PF 26-FEB-2001; 2001WO-US04927.  
XX  
PR 28-FEB-2000; 2000US-0515126.  
PR 18-MAY-2000; 2000US-0577409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
XX WPI; 2001-514838/56.  
DR P-PSDB; AAO01956.  
XX  
XX Isolated nucleic acids and polypeptides, useful for preventing  
PT diagnosing and treating e.g. leukaemia, inflammation and immune  
PT disorders -  
XX  
XX Claim 1; SEQ ID NO 1947; 1399pp + Sequence Listing; English.  
XX  
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1855 BP; 423 A; 480 C; 588 G; 364 T; 0 other;  
Query Match 68.0%; Score 486; DB 22; Length 1855;  
Best Local Similarity 100.0%; Pred. No. 3.7e-23; Indels 0; Gaps 0;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 230 CCGTGTCCAGCGCGCCAGATGTGTCCCGCCAGCGCTTGTCTTACCTCAAGGTGCA 289  
DB 1025 CCGTGTCCAGCGCGCCAGATGTGTCCCGCCAGCGCTTGTCTTACCTCAAGGTGCA 966  
QY 290 GATGTCTTCCCTGGGCTGCCAGACGCGCCCGCCAGAGTGCGCCACCGTGGCACTAGAA 349  
DB 965 GATGTCTTCCCTGGGCTGCCAGACGCGCCCGCCAGAGTGCGCCACCGTGGCACTAGAA 906  
QY 350 TGCAAGTATCTCGCACTTGCACCTTGCCTTCTGTGGGTGTCTTCTTCTGCTCTCTC 409  
DB 905 TGCAAGTATCTCGCACTTGCACCTTGCCTTCTGTGGGTGTCTTCTTCTGCTCTCTC 846  
QY 410 CAAAGCGCCCTTCACTATTCTTGGACCAATGCCAGATTTGCTCTCTGTGAAGAGGCTCT 469  
DB 845 CAAAGCGCCCTTCACTATTCTTGGACCAATGCCAGATTTGCTCTCTGTGAAGAGGCTCT 786  
QY 470 GACAGCAGACGCTCCAGCAGACAGCTGCGCCCGCCAGCGCCCGCCAGCGGTGGCTTCC 529  
DB 785 GGACAGCAGACGCTCCAGCAGACAGCTGCGCCCGCCAGCGCCCGCCAGCGGTGGCTTCC 726  
QY 530 TGCCCTTCTCTTGGGCGCGCTGTGCGCGGACCGCACTGACCCACTCGGATGGACCAACC 589  
DB 725 TGCCCTTCTCTTGGGCGCGCTGTGCGCGGACCGCACTGACCCACTCGGATGGACCAACC 666  
QY 590 TGCTCTGTGCTCCCAAGGACGCTTGACAGGAGAGAGAGAGCACTCCGATCACTCACAAGG 649  
DB 665 TGCTCTGTGCTCCCAAGGACGCTTGACAGGAGAGAGAGAGCACTCCGATCACTCACAAGG 606  
QY 650 ATCGGACTTGCGCTTGGACCTGGGACGACCTGGGACTGTACGGGGTTCCTCTAGTCTC 709  
DB 605 ATCGGACTTGCGCTTGGACCTGGGACGACCTGGGACTGTACGGGGTTCCTCTAGTCTC 546  
QY 710 TCCAG 715  
|||||

DB 545 TCCAG 540  
RESULT 4  
ID AAA64516 standard; DNA; 591 BP.  
XX  
AC AAA64516;  
XX  
DT 02-JAN-2001 (first entry)  
XX  
DE F37 probe used to isolate a human FEZ1 gene.  
XX  
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein EFL-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2000050565-A2.  
XX  
PD 31-AUG-2000.  
XX  
PF 25-FEB-2000; 2000WO-US04950.  
XX  
PR 25-FEB-1999; 99US-0121537.  
XX  
PA (UXJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Croce CM, Ishii H;  
XX  
XX WPI; 2000-558396/51.  
XX  
PT New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -  
XX  
XX Example 1; Fig 5Q; 255pp; English.  
XX  
XX The present sequence represents a probe which is used for isolating a  
CC human FEZ1 gene. The encoding mRNA is transcribed by tumour cells. FEZ1  
CC is a tumour suppressor gene, located at chromosome location 8p22.  
CC Decreased or no expression of FEZ1 is detected in a variety of cancer  
CC cells. Expression of FEZ1 inhibits tumour growth and proliferation. FEZ1  
CC also interacts with tubulin, with microtubules, and with protein  
CC EFL-gamma. Post-translational phosphorylation and dephosphorylation  
CC modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene  
CC expression are useful for inducing cells to proliferate. Compounds  
CC which modulate FEZ1 association with tubulin are useful for alleviating  
CC tubulin hyper- or hypo- polymerisation disorders, such as those  
CC associated with aberrant initiation of mitosis, modulation of the  
CC initiation and rate of cell proliferation and cell growth, modulation of  
CC cell shape, cell rigidity, cell motility, rate and stage of cellular  
CC DNA replication, intracellular distribution of organelles, metastatic  
CC potential of cell and cellular transformation from a non-cancerous to  
CC cancerous phenotype. Compounds which modulate FEZ1 binding and  
CC phosphorylation are also useful for alleviating a disorder, such as  
CC tumorigenesis, tumour survival, growth and metastasis.  
XX  
SQ Sequence 591 BP; 111 A; 160 C; 163 G; 157 T; 0 other;  
Query Match 8.8%; Score 63; DB 21; Length 591;  
Best Local Similarity 100.0%; Pred. No. 3.3e-20;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 653 GGACTCTCCCTGGACCTGGGACGACTGTGTACGGGGTTCCTCTAGTCTCTCC 712  
DB 1 GGACTCTCCCTGGACCTGGGACGACTGTGTACGGGGTTCCTCTAGTCTCTCC 60  
QY 713 CAG 715  
|||||

Db 61 CAG 63

RESULT 5  
 AAT23583  
 ID AAT23583 standard; cDNA to mRNA; 393 BP.  
 XX AC AAT23583;  
 XX DT 02-SEP-1996 (first entry)  
 XX DE Human gene signature HUMGS05436.  
 XX KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 XX OS Homo sapiens.  
 XX PN W09514772-A1.  
 XX PD 01-JUN-1995.  
 XX PF 11-NOV-1994; 94WO-JP01916.  
 XX PR 12-NOV-1993; 93JP-0355504.  
 XX PA (MATS//) MATSUBARA K.  
 XX PA (OKUB//) OKUBO K.  
 XX PI Matsubara K, Okubo K;  
 XX WPI; 1995-206931/27.  
 XX DR Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues  
 XX Claim 1; Page 1404; 2245pp; Japanese.  
 XX PS A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in AAT19001-T26837 and which is able to hybridise to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 XX Sequence 393 BP; 73 A; 117 C; 121 G; 78 T; 4 other;  
 SQ

Query Match 6.9%; Score 49; DB 16; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 649 GATCGACTGTGCCCTGGACCTGGAGCACTGGACTGTGTCACGGGTT 697  
 |||  
 1 GATCGACTGTGCCCTGGACCTGGAGCACTGGACTGTGTCACGGGTT 49

Db

RESULT 6  
 AAD00768  
 ID AAD00768 standard; cDNA; 9679 BP.  
 XX AC AAD00768;  
 XX DT 08-SEP-2000 (first entry)  
 XX DE Rat phosphodiesterase interacting protein, myomegalin cDNA.  
 XX KW Rat; phosphodiesterase interacting protein; myomegalin; PDE; CAMP-PDE;  
 KW cyclic adenosine monophosphate phosphodiesterase; antiasthmatic; asthma;  
 KW antiinflammatory; antipruritic; dermatological; antibacterial; shock;  
 KW analgesic; immunosuppressive; antitumor; vasotropic; antiarthritic;  
 KW antidiabetic; urticaria; antiallergic; antiarteriosclerotic; diagnosis;  
 KW antirheumatic; treatment; inflammatory disease; psoriasis; arthritis;  
 KW atherosclerosis; Crohn's disease; cystic fibrosis; chronic bronchitis;  
 KW eosinophilic granuloma; proliferative skin disease; ulcerative colitis;  
 KW reperfusion injury; atopic dermatitis; diabetes insipidus;  
 KW conjunctivitis; adult respiratory distress syndrome; allergic rhinitis;  
 KW arterial restenosis; ankylosing spondylitis; transplant rejection;  
 KW graft versus host disease; ss.  
 XX OS Rattus sp.  
 XX PN W0200027861-A1.  
 XX PD 18-MAY-2000.  
 XX PF 12-NOV-1999; 99WO-US26860.  
 XX PR 12-NOV-1998; 98US-0108255.  
 XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX PI Conti M, Pahlke G;  
 XX WPI; 2000-376479/32.  
 XX P-PSDB; AAY71158.  
 XX PT Polynucleotide encoding a phosphodiesterase (PDE) interacting  
 PT polypeptide, useful for diagnosis and treatment of asthma, cystic  
 PT fibrosis, Crohn's disease, and rheumatoid arthritis -  
 XX Disclosure; Fig 2; 77pp; English.  
 XX The present sequence is a cDNA encoding a phosphodiesterase (PDE)  
 CC interacting protein, myomegalin from rat skeletal muscle cDNA library.  
 CC The protein modulates the functions and properties of PDEs, specifically  
 CC CAMP-PDEs, and also targets them to specific subcellular compartments.  
 CC Rat myomegalin has at least four differently sized transcripts, two of  
 CC which are expressed in heart (7.5 and 5.9 kb), two in skeletal muscle  
 CC (7.5 and 4.3 kb) and one in testis (2.5 kb). The present sequence  
 CC can be used in the diagnosis and treatment of disease conditions  
 CC associated with PDE activity. The diseases include asthma, cystic  
 CC fibrosis, inflammatory airway disease, chronic bronchitis, eosinophilic  
 CC granuloma, psoriasis, proliferative skin diseases, endotoxin shock,  
 CC septic shock, ulcerative colitis, Crohn's disease, reperfusion injury,  
 CC inflammatory arthritis, atopic dermatitis, urticaria, adult respiratory  
 CC distress syndrome, diabetes insipidus, allergic rhinitis, allergic  
 CC conjunctivitis, vernal conjunctivitis, arterial restenosis,  
 CC atherosclerosis, inflammatory diseases associated with irritation and  
 CC pain, rheumatoid arthritis, ankylosing spondylitis, transplant  
 CC rejection and graft versus host disease, disease conditions associated  
 CC with hypersecretion of gastric acid, and disease conditions in which  
 CC cytokines are mediators.  
 XX Sequence 9679 BP; 2549 A; 2626 C; 2636 G; 1867 T; 1 other;  
 SQ

Query Match 2.8%; Score 20; DB 21; Length 9679;  
 Best Local Similarity 100.0%; Pred. No. 13;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 496 GCCTGGCCCCAGGCCCCAGA 515
Db 5267 GCCTGGCCCCAGGCCCCAGA 5286
RESULT 7
AAS41709
ID AAS41709 standard; DNA; 10437 BP.
XX
AC AAS41709;
XX
DT 17-DEC-2001 (first entry)
XX
DE Genomic sequence #25 encoding novel human enzyme polypeptide.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251986.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251889.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 PR  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX  
 XX WPI; 2001-465566/50.  
 DR  
 XX  
 XX Novel polypeptides and polynucleotides useful for diagnosing,  
 XX preventing, treating neural, immune system, muscular, reproductive,  
 PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous  
 PT diseases -  
 PT  
 XX  
 XX Disclosure; SEQ ID No 1835; 1180pp; English.  
 PS  
 XX  
 XX The present invention relates to the isolation of novel human enzyme  
 CC polypeptides (AAU2915-AAU23814), and the cDNA and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders  
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),  
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders  
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),  
 CC blood-related disorders (e.g. haemophilia), reproductive disorders  
 CC (e.g. infertility) and infectious disorders (e.g. Influenza). The  
 CC polynucleotides of the invention can also be used in gene therapy.  
 CC AA541685-AAS42192 represent DNA sequences encoding for the novel human  
 CC enzyme polypeptides of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences..  
 XX  
 SQ Sequence 10437 BP; 2265 A; 3267 C; 2795 G; 2110 T; 0 other;  
 Query Match 2.8%; Score 20; DB 22; Length 10437;  
 Best\_Local\_Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 223 CCATGGCCCTGTCCAGGCC 242  
 |||||  
 Db 2240 CCATGGCCCTGTCCAGGCC 2259  
 |||||  
 RESULT 8  
 ID ABA16691/c  
 ID ABA16691 standard; DNA; 12620 BP.  
 XX  
 XX  
 AC ABA16691;  
 XX

DT 23-JAN-2002 (first entry)  
 XX Human nervous system related polynucleotide SEQ ID NO 9022.  
 DE  
 XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnucide;  
 KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;  
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200159063-A2.  
 PN  
 XX  
 XX 16-AUG-2001.  
 PD  
 XX  
 XX 17-JAN-2001; 2001WO-US01334.  
 PF  
 XX  
 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.

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PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 14-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0242221.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 05-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 03-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
XX Disclosure; SEQ ID NO 9022; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 12620 BP; 2244 A; 3902 C; 3765 G; 2709 T; 0 other;

Query Match 2.8%; Score 20; DB 22; Length 12620;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 223 CCATGGCCCTGTCCAGGCC 242
Db 4030 CCATGGCCCTGTCCAGGCC 4011
|||||
|||||

RESULT 9
ABN79134
ID ABN79134 standard; cDNA; 531 BP.
XX
XX AC ABN79134;
XX
XX DT 08-JUL-2002 (first entry)
XX
XX DE Human ORF4081 cDNA, SEQ ID NO:8161.
XX
XX Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibitor; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotrophic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
```

KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;  
KW cardiatic; hypotensive; antithyroid; antiinflammatory; immunomodulator;  
KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.  
XX Homo sapiens.  
XX WO200190366-A2.  
XX 29-NOV-2001.  
XX 24-MAY-2001; 2001WO-US17076.  
XX 24-MAY-2000; 2000US-206690P.  
XX (CURA-) CURAGEN CORP.  
XX Leach MD, Shimkets RA;  
XX WPI; 2002-106200/14.  
XX P-PSDB; ABP35108.

XX Novel human polypeptides and polynucleotides useful for diagnosing,  
XX preventing and treating cardiovascular disease, neurodegenerative,  
XX hyperproliferative disorders and disorders related to organ  
XX transplantation -  
XX Claim 1; Page 2286; 2508pp; English.  
XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins  
XX designated ORF (open reading frame) 1-4534, and sequences ABN75054-  
XX ABN79587 represent cDNAs encoding them. The invention also encompasses  
XX polypeptides at least 80% identical to the ORF1-ORF4534 (collectively  
XX referred to as ORFX) proteins, polynucleotides at least 85% identical to  
XX the ORFX nucleic acid sequences, vectors and host cells comprising ORFX  
XX polynucleotides, the recombinant production of ORFX proteins, antibodies  
XX specific for ORFX proteins, methods of detecting ORFX polynucleotides and  
XX polypeptides, methods of screening for modulators of ORFX expression or  
XX activity, and methods of screening individuals for a predisposition to an  
XX ORFX-associated disorder. The ORFX proteins of the invention have a wide  
XX range of biological activities, such as cytokine, cell proliferation,  
XX cell differentiation, immune modulation, haematopoiesis regulation,  
XX tissue growth, angiogenesis, activin or inhibin activity, chemotactic/  
XX chemokinetic activity, haemostatic activity, thrombolytic activity,  
XX receptor/ligand, antiinflammatory activity, tumour inhibition activity,  
XX and antiinfective activity, and may also be involved in the determination  
XX of bodily characteristics, fertility and behaviour. ORFX proteins,  
XX nucleic acids and antibodies may be used in the treatment of cancers,  
XX other proliferative disorders such as psoriasis and benign tumours,  
XX neurological disorders such as epilepsy and Alzheimer's disease,  
XX cardiovascular diseases, immune system disorders, disorders related to  
XX organ transplantation, disorders of tissue growth and regeneration,  
XX diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester  
XX storage disease, and infectious diseases caused by viral, bacterial,  
XX fungal and other pathogens. ORFX nucleic acids may also be used as a  
XX source of primers and probes, in the detection of ORFX genomic sequences  
XX or transcripts, in the identification and cloning of homologous  
XX sequences, in genetic diagnosis, and in forensic biology. The ORFX  
XX nucleic acids may additionally be used to produce transgenic animals  
XX which may be useful for studying the function and/or activity of ORFX  
XX protein, and in drug screening. The ORFX proteins may also be used as  
XX immunogens to generate specific antibodies, which are useful in the  
XX diagnosis, treatment and monitoring of ORFX-associated diseases.

XX Sequence 531 BP; 169 A; 138 C; 140 G; 84 T; 0 other;  
XX Query Match 2.7%; Score 19; DB 24; Length 531;  
XX Best Local Similarity 100.0%; Pred. No. 42;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Qy 473 CAGCAGAGCCTCCACGA 491  
XX ||||||||||||||||  
XX Db 382 CAGCAGAAGCCTCCACGA 400

## RESULT 10

ABL59550  
ID ABL59550 standard; cDNA; 2472 BP.

XX ABL59550;  
XX 16-JUL-2002 (first entry)  
XX Human phosphatidylserine decarboxylase cDNA SEQ ID NO:50.

XX Human; phosphatidylserine decarboxylase; tumour; lipid associated gene;  
XX lipid metabolism; lipid synthesis; enzyme; gene; ss.  
XX Homo sapiens.

XX WO200227028-A1.

XX 04-APR-2002.

XX 27-SEP-2001; 2001WO-US30366.

XX 28-SEP-2000; 2000US-0676052.

XX (ATAI-) ATAIRGIN TECHNOLOGIES INC.

XX Skinner MK, Patton JL, Chaudhary J;

XX WPI; 2002-402054/43.

XX Identifying tumor characteristics in a tissue sample taken from a  
XX patient, involves determining the copy number or expression level of  
XX genes associated with lipid metabolism, synthesis or action -  
XX Example 1; Page 107-108; 113pp; English.  
XX The present invention describes a method for identifying tumour  
XX characteristics, comprising measuring a copy number or expression level  
XX of at least two genes associated with lipid metabolism, synthesis, or  
XX action in cells from a patient tissue sample, and comparing the results  
XX with a copy number or expression level of the genes in a normal cell.  
XX Also described is an array of nucleic acid polymers immobilised on a  
XX solid support, comprising a solid support, at least two different nucleic  
XX acid polymers which are each specific for a different gene associated  
XX with lipid metabolism, synthesis or action, where each nucleic acid  
XX polymer is located at a predetermined position on the solid support, and  
XX the array comprises nucleic acid polymers which are specific for less  
XX than 100 genes other than the selected genes. The method is useful for  
XX determining tumour characteristics in a tissue sample taken from a  
XX patient. The present sequence represents a human lipid-associated gene  
XX related cDNA sequence, which is used in the exemplification of the  
XX present invention.

XX Sequence 2472 BP; 537 A; 711 C; 684 G; 540 T; 0 other;

XX Query Match 2.7%; Score 19; DB 24; Length 2472;

XX Best Local Similarity 100.0%; Pred. No. 41;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 143 GGCCCTGAGCGGAGGCTG 161

XX ||||||||||||||||

XX Db 295 GGCCCTGAGCGGAGGCTG 313

## RESULT 11

AAH99704/c

ID AAH99704 standard; cDNA; 2730 BP.

XX AAH99704;

XX 16-OCT-2001 (first entry)

XX Human protein encoding cDNA sequence SEQ ID NO:539.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiaggregant; haemostatic; vulnary; antiulcer; osteopathic; eczema;  
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.  
 XX Homo sapiens.  
 XX WO200153455-A2.  
 XX 26-JUL-2001.  
 XX 22-DEC-2000; 2000WO-US35017.  
 XX 23-DEC-1999; 99US-0471275.  
 XX 21-JAN-2000; 2000US-0488725.  
 XX 25-APR-2000; 2000US-0552317.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT;  
 XX WPI: 2001-457603/49.  
 XX P-PSDB; AAM25763.  
 XX Isolated human polynucleotides encoding polypeptides, useful for the  
 XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
 XX Claim 1; Page 592; 1217pp; English.  
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 XX AAM25963. The proteins can have activities based on the tissues and  
 XX cells they are expressed in, such as: antiinflammatory; antirheumatic;  
 XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnary;  
 XX antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;  
 XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 XX encoding them can be used in gene therapy, antisense therapy and vaccine  
 XX production. The proteins and polynucleotides are useful for screening for  
 XX agonists or antagonists of a protein and for the treatment and diagnosis  
 XX of disorders associated with the activity of a protein e.g. inflammation,  
 XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 XX osteoporosis, severe combined immunodeficiency, eczema, allergic  
 XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 XX Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 XX neurological disorders.  
 XX Sequence 2730 BP; 589 A; 764 C; 795 G; 582 T; 0 other;  
 XX Query Match 2.7%; Score 19; DB 22; Length 2730;  
 XX Best Local Similarity 100.0%; Pred. No. 40;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 143 GCCTCTAGGCGGAGGCTG 161  
 DB 2204 GCCTCTAGGCGGAGGCTG 2186

RESULT 12  
 AAH99710/c  
 ID AAH99710 standard; CDNA; 2735 BP.  
 XX AC AAH99710;  
 XX DT 16-OCT-2001 (first entry)  
 XX DE Human protein encoding cDNA sequence SEQ ID NO:545.  
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiaggregant; haemostatic; vulnary; antiulcer; osteopathic; eczema;  
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.  
 XX Homo sapiens.  
 XX WO200153455-A2.  
 XX 26-JUL-2001.  
 XX 22-DEC-2000; 2000WO-US35017.  
 XX 23-DEC-1999; 99US-0471275.  
 XX 21-JAN-2000; 2000US-0488725.  
 XX 25-APR-2000; 2000US-0552317.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT;  
 XX WPI: 2001-457603/49.  
 XX P-PSDB; AAM25769.  
 XX Isolated human polynucleotides encoding polypeptides, useful for the  
 XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
 XX Claim 1; Page 597-598; 1217pp; English.  
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 XX AAM25963. The proteins can have activities based on the tissues and  
 XX cells they are expressed in, such as: antiinflammatory; antirheumatic;  
 XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnary;  
 XX antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;  
 XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 XX encoding them can be used in gene therapy, antisense therapy and vaccine  
 XX production. The proteins and polynucleotides are useful for screening for  
 XX agonists or antagonists of a protein and for the treatment and diagnosis  
 XX of disorders associated with the activity of a protein e.g. inflammation,  
 XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 XX osteoporosis, severe combined immunodeficiency, eczema, allergic  
 XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 XX Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 XX neurological disorders.



SQ Sequence 2735 BP; 592 A; 767 C; 794 G; 582 T; 0 other;  
Query Match 2.7%; Score 19; DB 22; Length 2735;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 143 GGCCCTGAGCGGAGGCTG 161  
Db 2209 GGCCCTGAGCGGAGGCTG 2191

RESULT 13  
AAI59663/c  
ID AAI59663 standard; cDNA; 2735 BP.  
XX  
AC AAI59663;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 3652.  
XX  
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US34263.  
XX  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI; 2001-442253/47.  
DR P-PSDB; AAM40507.  
XX  
XX Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
XX Claim 1; SEQ ID NO 3652; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
SQ Sequence 2735 BP; 592 A; 767 C; 794 G; 582 T; 0 other;  
Query Match 2.7%; Score 19; DB 22; Length 2735;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 143 GGCCCTGAGCGGAGGCTG 161  
Db 2209 GGCCCTGAGCGGAGGCTG 2191

RESULT 14  
AAI59664/c  
ID AAI59664 standard; cDNA; 2735 BP.  
XX  
AC AAI59664;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 3653.  
XX  
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US34263.  
XX  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI; 2001-442253/47.  
DR P-PSDB; AAM40508.  
XX  
XX Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
XX Claim 1; SEQ ID NO 3653; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
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Best Local Similarity 100.0%; Pred. No. 40;  
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AC AAI57877;  
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KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia; ss.  
XX  
OS Homo sapiens.  
XX  
WO200153312-A1.  
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PD 26-JUL-2001.  
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PF 26-DEC-2000; 2000WO-US34263.  
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PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0596042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0691036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Dmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR P-PSDB; AAM38721.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
PS Claim 1; SEQ ID NO 80; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX

SQ Sequence 2739 BP; 574 A; 801 C; 772 G; 592 T; 0 other;

Query Match 2.7%; Score 19; DB 22; Length 2739;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 153.225 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0

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C 8	17	2.4	1734	2	US-08-663-566A-10
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c 105	15	2.1	422	2	US-08-967-101-18	Sequence 18, Appl	c 178	15	2.1	2144	4	US-08-984-709A-20	Sequence 20, Appl
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c 117	15	2.1	703	4	US-09-392-184-6	Sequence 6, Appl	c 190	15	2.1	2255	4	US-08-871-572B-3	Sequence 3, Appl
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c 119	15	2.1	739	4	US-09-369-364A-10	Sequence 10, Appl	c 192	15	2.1	2256	1	US-08-001-711-1	Sequence 1, Appl
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c 137	15	2.1	1217	4	US-09-372-422A-11	Sequence 11, Appl	c 210	15	2.1	3023	4	US-09-308-022-4	Sequence 4, Appl
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c 146	15	2.1	1896	4	US-09-232-197-30	Sequence 30, Appl	c 219	15	2.1	3393	1	US-08-040-741-5	Sequence 5, Appl
c 147	15	2.1	1896	4	US-09-232-201-30	Sequence 30, Appl	c 220	15	2.1	3393	1	US-08-295-502-1	Sequence 1, Appl
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c 149	15	2.1	1915	2	US-08-466-589-11	Sequence 11, Appl	c 222	15	2.1	3506	3	US-09-091-899-9	Sequence 9, Appl
c 150	15	2.1	1915	2	US-08-700-636-11	Sequence 11, Appl	c 223	15	2.1	3624	4	US-09-231-017B-398	Sequence 398, App
c 151	15	2.1	1915	3	US-08-467-574-11	Sequence 11, Appl	c 224	15	2.1	3624	4	US-09-056-105-17	Sequence 17, Appl
c 152	15	2.1	1915	4	US-09-217-345-11	Sequence 11, Appl	c 225	15	2.1	3814	4	US-09-302-812-5	Sequence 5, Appl
c 153	15	2.1	1915	4	US-08-487-596-17	Sequence 17, Appl	c 226	15	2.1	3814	4	US-09-511-477-5	Sequence 5, Appl
c 154	15	2.1	1933	3	US-08-974-380-1	Sequence 1, Appl	c 227	15	2.1	3814	4	US-09-511-507-5	Sequence 5, Appl
c 155	15	2.1	1960	3	US-09-165-240-4	Sequence 4, Appl	c 228	15	2.1	3879	4	US-09-221-017B-1053	Sequence 1053, Ap
c 156	15	2.1	1960	4	US-09-568-059-4	Sequence 4, Appl	c 229	15	2.1	4011	1	US-08-121-057-3	Sequence 3, Appl
c 157	15	2.1	1968	1	US-08-321-071A-17	Sequence 17, Appl	c 230	15	2.1	4011	2	US-08-509-187D-3	Sequence 3, Appl
c 158	15	2.1	2000	1	US-08-622-353-1	Sequence 1, Appl	c 231	15	2.1	4011	2	US-09-121-396-3	Sequence 3, Appl
c 159	15	2.1	2000	1	US-08-622-352A-1	Sequence 1, Appl	c 232	15	2.1	4011	5	PCT-US93-03704A-3	Sequence 3, Appl
c 160	15	2.1	2000	3	US-08-826-390-1	Sequence 1, Appl	c 233	15	2.1	4079	1	US-08-121-057-2	Sequence 2, Appl
c 161	15	2.1	2004	1	US-08-233-015-1	Sequence 1, Appl	c 234	15	2.1	4079	2	US-08-509-187D-2	Sequence 2, Appl
c 162	15	2.1	2012	2	US-08-555-568B-16	Sequence 16, Appl	c 235	15	2.1	4079	2	US-09-121-396-2	Sequence 2, Appl
c 163	15	2.1	2012	4	US-09-513-223-16	Sequence 231, App	c 236	15	2.1	4079	5	PCT-US93-03704A-2	Sequence 2, Appl
c 164	15	2.1	2043	4	US-09-149-476-231	Sequence 231, App	c 237	15	2.1	4122	4	US-09-321-831-1	Sequence 1, Appl
c 165	15	2.1	2064	1	US-08-164-839-30	Sequence 30, Appl	c 238	15	2.1	4185	3	US-08-964-268-1	Sequence 1, Appl
c 166	15	2.1	2064	1	US-08-164-839-32	Sequence 32, Appl	c 239	15	2.1	4430	2	US-08-918-914-2	Sequence 2, Appl
c 167	15	2.1	2064	1	US-08-583-799-30	Sequence 30, Appl	c 240	15	2.1	4441	4	US-09-641-999-2	Sequence 2, Appl
c 168	15	2.1	2064	1	US-08-583-799-32	Sequence 32, Appl	c 241	15	2.1	4471	2	US-08-615-942A-1	Sequence 1, Appl
c 169	15	2.1	2094	1	US-08-471-058-6	Sequence 6, Appl	c 242	15	2.1	4543	2	US-08-519-547A-5	Sequence 5, Appl
c 170	15	2.1	2094	2	US-08-944-050-1	Sequence 1, Appl	c 243	15	2.1	4736	4	US-09-056-105-12	Sequence 12, Appl
c 171	15	2.1	2094	3	US-08-471-057-6	Sequence 6, Appl	c 244	15	2.1	4741	4	US-09-056-105-11	Sequence 11, Appl
c 172	15	2.1	2094	4	US-09-381-488-1	Sequence 1, Appl	c 245	15	2.1	4780	2	US-08-365-486A-20	Sequence 20, Appl
c 173	15	2.1	2094	4	US-09-381-488-3	Sequence 3, Appl	c 246	15	2.1	4780	3	US-09-123-708-3	Sequence 3, Appl

247	15	2.1	4780	3	US-09-123-624-3	Sequence 3, Appli	320	14	2.0	38	4	US-09-306-998-35	Sequence 35, Appl
248	15	2.1	4780	4	US-08-880-342-20	Sequence 20, Appl	321	14	2.0	42	1	US-08-233-009-53	Sequence 53, Appl
249	15	2.1	4877	2	US-08-404-531B-7	Sequence 7, Appli	C 322	14	2.0	42	1	US-08-233-009-54	Sequence 54, Appl
250	15	2.1	4877	3	US-08-404-531B-8	Sequence 8, Appli	C 323	14	2.0	44	3	US-08-660-645A-35	Sequence 35, Appl
251	15	2.1	4877	3	US-08-476-900A-7	Sequence 7, Appli	C 324	14	2.0	44	3	US-09-298-718-35	Sequence 35, Appl
252	15	2.1	4877	3	US-08-476-900A-8	Sequence 8, Appli	C 325	14	2.0	44	4	US-09-546-569-35	Sequence 35, Appl
253	15	2.1	4877	3	US-08-488-546A-7	Sequence 8, Appli	C 326	14	2.0	44	4	US-08-980-832-14	Sequence 14, Appl
254	15	2.1	4877	3	US-08-488-546A-8	Sequence 8, Appli	C 327	14	2.0	45	2	US-08-353-476-26	Sequence 26, Appl
255	15	2.1	5197	1	US-08-131-365B-53	Sequence 53, Appl	C 328	14	2.0	47	4	US-09-641-638-874	Sequence 874, App
256	15	2.1	5197	2	US-08-668-123-53	Sequence 53, Appl	C 329	14	2.0	50	1	US-08-171-389-331	Sequence 331, App
257	15	2.1	5300	4	US-08-938-669A-1	Sequence 1, Appli	C 330	14	2.0	50	1	US-08-123-936-331	Sequence 331, App
258	15	2.1	5304	4	US-08-938-669A-2	Sequence 2, Appli	C 331	14	2.0	50	2	US-08-475-228A-331	Sequence 331, App
259	15	2.1	5408	1	US-08-471-058-20	Sequence 20, Appl	C 332	14	2.0	50	3	US-08-482-080A-331	Sequence 331, App
260	15	2.1	5408	3	US-08-471-057-20	Sequence 20, Appl	C 333	14	2.0	50	4	US-09-354-947-331	Sequence 331, App
261	15	2.1	5538	2	US-08-231-193A-55	Sequence 55, Appl	C 334	14	2.0	50	5	PCT-US93-12388-331	Sequence 331, App
262	15	2.1	5538	3	US-08-486-273A-55	Sequence 55, Appl	335	14	2.0	54	2	US-08-585-684B-2473	Sequence 2473, Ap
263	15	2.1	5538	3	US-08-940-086A-55	Sequence 55, Appl	336	14	2.0	54	4	US-09-038-073-2473	Sequence 2473, Ap
264	15	2.1	5538	4	US-08-940-035A-55	Sequence 55, Appl	337	14	2.0	63	3	US-08-660-645A-33	Sequence 33, Appl
265	15	2.1	5538	4	US-08-935-105A-55	Sequence 55, Appl	338	14	2.0	63	3	US-09-298-718-33	Sequence 33, Appl
266	15	2.1	5538	4	US-08-648-797-55	Sequence 55, Appl	339	14	2.0	63	4	US-09-546-969-33	Sequence 33, Appl
267	15	2.1	5983	4	US-08-264-578-1	Sequence 1, Appli	340	14	2.0	63	4	US-08-980-832-12	Sequence 12, Appl
268	15	2.1	6169	4	US-08-938-669A-3	Sequence 3, Appli	341	14	2.0	99	1	US-08-472-255A-27	Sequence 27, Appl
269	15	2.1	6192	2	US-08-479-537A-1	Sequence 1, Appli	342	14	2.0	99	1	US-08-479-724B-27	Sequence 27, Appl
270	15	2.1	6192	4	US-08-083-116-1	Sequence 1, Appli	343	14	2.0	99	3	US-08-472-256B-27	Sequence 27, Appl
C 271	15	2.1	6192	4	US-08-134-916A-1	Sequence 1, Appli	344	14	2.0	99	4	US-08-952-793-27	Sequence 27, Appl
272	15	2.1	6550	4	US-08-669-656A-1	Sequence 1, Appli	345	14	2.0	99	5	PCT-US96-09455A-27	Sequence 27, Appl
273	15	2.1	7286	5	US-09-097-319A-1	Sequence 1, Appli	346	14	2.0	103	3	US-08-952-664-12	Sequence 12, Appl
274	15	2.1	7286	5	PCT-US95-11684-1	Sequence 1, Appli	347	14	2.0	103	4	US-09-487-874-12	Sequence 12, Appl
275	15	2.1	7785	2	US-08-276-967-1	Sequence 1, Appli	348	14	2.0	106	4	US-09-506-729-63	Sequence 63, Appl
276	15	2.1	7812	4	US-08-368-590-1	Sequence 1, Appli	C 349	14	2.0	141	4	US-08-943-731-8	Sequence 8, Appli
C 277	15	2.1	8625	4	US-08-980-832-1	Sequence 1, Appli	350	14	2.0	149	4	US-08-943-731-8	Sequence 8, Appli
278	15	2.1	9299	4	US-08-097-319A-15	Sequence 15, Appl	351	14	2.0	192	6	US-09-511-625B-30	Sequence 30, Appl
279	15	2.1	9335	4	US-08-097-319A-19	Sequence 19, Appl	C 352	14	2.0	218	4	US-09-506-729-61	Sequence 61, Appl
280	15	2.1	9408	4	US-09-097-319A-16	Sequence 16, Appl	C 353	14	2.0	228	3	US-08-946-914-32	Sequence 32, Appl
C 281	15	2.1	10627	1	US-08-060-925A-12	Sequence 12, Appl	354	14	2.0	228	4	US-09-122-171D-2	Sequence 2, Appli
C 282	15	2.1	11233	1	US-08-980-832-27	Sequence 27, Appl	C 355	14	2.0	228	4	US-09-656-450-32	Sequence 32, Appl
C 283	15	2.1	11613	1	US-08-484-044-10	Sequence 10, Appl	356	14	2.0	231	4	US-08-930-285-20	Sequence 20, Appl
284	15	2.1	11673	4	US-09-334-220-3	Sequence 3, Appli	C 357	14	2.0	231	4	US-08-697-826A-18	Sequence 18, Appl
285	15	2.1	11784	4	US-09-097-319A-9	Sequence 9, Appli	C 358	14	2.0	285	4	US-09-812-484-5	Sequence 5, Appli
286	15	2.1	11991	4	US-09-097-319A-10	Sequence 10, Appl	C 359	14	2.0	301	4	US-09-643-597-304	Sequence 304, App
C 287	15	2.1	13011	2	US-08-791-849A-14	Sequence 14, Appl	360	14	2.0	322	2	US-08-691-814B-112	Sequence 112, App
288	15	2.1	16595	4	US-08-146-053-7	Sequence 7, Appli	361	14	2.0	326	1	US-08-700-575-3	Sequence 3, Appli
289	15	2.1	16836	4	US-09-147-236-1	Sequence 1, Appli	C 362	14	2.0	330	4	US-09-199-637A-24	Sequence 24, Appl
290	15	2.1	16836	4	US-09-147-236-10	Sequence 10, Appl	C 363	14	2.0	330	4	US-09-712-016-75	Sequence 75, Appl
291	15	2.1	19932	2	US-08-477-451-25	Sequence 25, Appl	C 364	14	2.0	336	6	5494663-13	Patent No. 5494663
292	15	2.1	29598	4	US-09-341-587-6	Sequence 6, Appli	365	14	2.0	339	2	US-08-619-542B-30	Sequence 30, Appl
C 293	15	2.1	35828	4	US-09-449-218D-17	Sequence 17, Appl	366	14	2.0	348	1	US-08-466-390-6	Sequence 6, Appli
294	15	2.1	37948	4	US-08-251-645-11	Sequence 11, Appl	367	14	2.0	348	1	US-08-470-950-6	Sequence 6, Appli
295	15	2.1	44453	4	US-08-146-053-5	Sequence 5, Appli	368	14	2.0	348	1	US-08-467-781-6	Sequence 6, Appli
296	15	2.1	45716	4	US-08-965-048-5	Sequence 5, Appli	369	14	2.0	348	1	US-08-195-487-6	Sequence 6, Appli
297	15	2.1	45989	4	US-08-965-048-6	Sequence 6, Appli	370	14	2.0	348	2	US-08-483-924-6	Sequence 6, Appli
C 298	15	2.1	70000	4	US-09-851-896-3	Sequence 3, Appli	371	14	2.0	348	5	PCT-US93-06160-6	Sequence 6, Appli
299	15	2.1	90050	4	US-08-245-041-5	Sequence 5, Appli	C 372	14	2.0	370	3	US-09-188-930-103	Sequence 103, App
C 300	15	2.1	111282	4	US-08-754-250-3	Sequence 3, Appli	373	14	2.0	373	1	US-08-592-126-131	Sequence 131, App
C 301	14	2.0	18	4	US-09-723-535-40	Sequence 40, Appl	374	14	2.0	388	4	US-09-325-932A-108	Sequence 108, App
302	14	2.0	21	4	US-09-338-907-175	Sequence 175, App	C 375	14	2.0	405	2	US-08-116-778B-4	Sequence 4, Appli
303	14	2.0	21	4	US-08-218-207-175	Sequence 175, App	C 376	14	2.0	405	2	US-08-438-562-4	Sequence 4, Appli
C 304	14	2.0	24	2	US-08-521-053-4	Sequence 4, Appli	C 377	14	2.0	405	2	US-08-483-528B-4	Sequence 4, Appli
305	14	2.0	24	2	US-08-521-053-5	Sequence 5, Appli	C 378	14	2.0	405	3	US-08-673-799C-4	Sequence 4, Appli
C 306	14	2.0	26	1	US-08-429-121B-42	Sequence 42, Appl	C 379	14	2.0	405	4	US-09-393-385B-4	Sequence 4, Appli
C 307	14	2.0	26	2	US-08-353-476-13	Sequence 13, Appl	C 380	14	2.0	411	4	US-08-651-155B-206	Sequence 206, App
C 308	14	2.0	26	2	US-09-003-067-42	Sequence 42, Appl	381	14	2.0	412	1	US-07-872-644-22	Sequence 22, Appl
309	14	2.0	26	4	US-09-309-317-10	Sequence 10, Appl	382	14	2.0	412	1	US-08-297-494-22	Sequence 22, Appl
C 310	14	2.0	29	1	US-08-436-464-3	Sequence 3, Appli	383	14	2.0	412	1	US-08-297-510-22	Sequence 22, Appl
311	14	2.0	31	1	US-08-530-492-87	Sequence 87, Appl	384	14	2.0	412	1	US-08-479-532-22	Sequence 22, Appl
312	14	2.0	31	4	US-08-906-517-87	Sequence 87, Appl	385	14	2.0	412	1	US-08-455-526-22	Sequence 22, Appl
C 313	14	2.0	32	1	US-08-436-464-5	Sequence 5, Appli	386	14	2.0	412	1	US-08-455-525-22	Sequence 22, Appl
314	14	2.0	36	3	US-08-957-302A-4	Sequence 4, Appli	387	14	2.0	412	3	US-09-139-491-22	Sequence 22, Appl
C 315	14	2.0	36	3	US-08-957-302A-14	Sequence 14, Appl	388	14	2.0	418	5	PCT-US92-03222-22	Sequence 22, Appl
316	14	2.0	36	3	US-08-957-302A-15	Sequence 15, Appl	389	14	2.0	418	2	US-08-927-307-7	Sequence 7, Appli
317	14	2.0	36	4	US-09-542-403-4	Sequence 4, Appli	390	14	2.0	418	3	US-09-385-947-7	Sequence 7, Appli
C 318	14	2.0	36	4	US-09-542-403-14	Sequence 14, Appl	391	14	2.0	423	1	US-08-470-179-109	Sequence 109, App
319	14	2.0	36	4	US-09-542-403-15	Sequence 15, Appl	C 392	14	2.0	441	1	US-07-998-003A-90	Sequence 90, Appl

C 393	14	2.0	441	1	US-08-453-274B-90	Sequence 90, Appl	466	14	2.0	1022	4	US-09-222-575-67	Sequence 67, Appl
C 394	14	2.0	441	1	US-08-453-695A-90	Sequence 90, Appl	467	14	2.0	1061	3	US-09-286-805-3	Sequence 3, Appl
C 395	14	2.0	441	1	US-08-288-161A-90	Sequence 90, Appl	C 468	14	2.0	1068	4	US-09-403-768-5	Sequence 5, Appl
C 396	14	2.0	441	2	US-08-453-702A-90	Sequence 90, Appl	C 469	14	2.0	1100	4	US-09-372-422A-47	Sequence 47, Appl
C 397	14	2.0	441	4	US-09-099-639-90	Sequence 90, Appl	C 470	14	2.0	1100	4	US-09-222-938A-32	Sequence 32, Appl
C 398	14	2.0	441	5	PCT-US93-12588-90	Sequence 90, Appl	471	14	2.0	1110	2	US-08-693-174-4	Sequence 4, Appl
C 399	14	2.0	441	5	PCT-US95-08071-90	Sequence 90, Appl	472	14	2.0	1110	4	US-09-253-738-4	Sequence 4, Appl
C 400	14	2.0	445	2	US-08-691-814B-124	Sequence 124, App	C 473	14	2.0	1110	4	US-09-336-536-27	Sequence 27, Appl
C 401	14	2.0	461	4	US-08-812-484-26	Sequence 26, Appl	474	14	2.0	1120	4	US-09-214-631-1	Sequence 1, Appl
C 402	14	2.0	471	4	US-09-643-597-328	Sequence 328, App	475	14	2.0	1129	1	US-08-470-261-1	Sequence 1, Appl
C 403	14	2.0	512	4	US-09-221-298-88	Sequence 88, Appl	476	14	2.0	1129	3	US-08-916-989B-1	Sequence 1, Appl
C 404	14	2.0	540	4	US-09-280-116-13	Sequence 13, Appl	477	14	2.0	1129	4	US-09-432-253-1	Sequence 1, Appl
C 405	14	2.0	569	3	US-09-109-204-15	Sequence 15, Appl	478	14	2.0	1129	5	PCT-US94-13187-1	Sequence 1, Appl
C 406	14	2.0	587	4	US-09-385-982-497	Sequence 139, App	C 479	14	2.0	1131	1	US-07-648-796A-14	Sequence 14, Appl
C 407	14	2.0	592	4	US-09-328-111-139	Sequence 139, App	480	14	2.0	1166	4	US-09-149-476-209	Sequence 209, App
C 408	14	2.0	596	4	US-09-328-111-153	Sequence 153, App	C 481	14	2.0	1168	2	US-08-530-569B-11	Sequence 11, Appl
C 409	14	2.0	597	4	US-09-134-001C-2771	Sequence 2771, Ap	C 482	14	2.0	1182	4	US-09-469-242-1	Sequence 1, Appl
C 410	14	2.0	607	4	US-09-385-982-412	Sequence 412, App	C 483	14	2.0	1215	2	US-08-370-156-26	Sequence 26, Appl
C 411	14	2.0	612	2	US-08-308-952-9	Sequence 9, Appl	C 484	14	2.0	1222	1	US-08-328-322-1	Sequence 1, Appl
C 412	14	2.0	612	4	US-08-124-141-12	Sequence 12, Appl	C 485	14	2.0	1222	4	US-09-484-970B-3	Sequence 3, Appl
C 413	14	2.0	642	2	US-08-480-753-5	Sequence 5, Appl	C 486	14	2.0	1225	1	US-08-494-577-11	Sequence 11, Appl
C 414	14	2.0	642	3	US-09-041-889-10	Sequence 10, Appl	487	14	2.0	1235	1	US-08-696-770-1	Sequence 1, Appl
C 415	14	2.0	642	3	US-08-837-058-10	Sequence 10, Appl	488	14	2.0	1235	2	US-09-015-557-1	Sequence 1, Appl
C 416	14	2.0	642	4	US-09-139-637A-26	Sequence 26, Appl	C 489	14	2.0	1235	2	US-08-530-569B-12	Sequence 12, Appl
C 417	14	2.0	658	4	US-09-328-111-816	Sequence 816, App	C 490	14	2.0	1238	2	US-08-795-868-11	Sequence 11, Appl
C 418	14	2.0	670	4	US-09-335-948-3	Sequence 3, Appl	C 491	14	2.0	1238	4	US-09-313-300-10	Sequence 10, Appl
C 419	14	2.0	670	4	US-07-806-932B-4	Sequence 4, Appl	C 492	14	2.0	1238	4	US-09-303-069-11	Sequence 11, Appl
C 420	14	2.0	683	4	US-09-149-476-25	Sequence 25, Appl	C 493	14	2.0	1238	4	US-09-134-250-11	Sequence 11, Appl
C 421	14	2.0	687	3	US-09-143-776-1	Sequence 1, Appl	C 494	14	2.0	1243	4	US-09-191-136-15	Sequence 15, Appl
C 422	14	2.0	696	4	US-08-998-416-954	Sequence 954, App	C 495	14	2.0	1248	4	US-09-545-944-1	Sequence 1, Appl
C 423	14	2.0	696	4	US-09-740-235-16	Sequence 16, Appl	C 496	14	2.0	1253	4	US-08-978-289-9	Sequence 9, Appl
C 424	14	2.0	720	4	US-09-274-825-1	Sequence 1, Appl	C 497	14	2.0	1255	4	US-09-149-476-75	Sequence 75, Appl
C 425	14	2.0	720	4	US-09-627-769-1	Sequence 1, Appl	498	14	2.0	1260	1	US-08-385-186-1	Sequence 1, Appl
C 426	14	2.0	736	1	US-08-846-012A-1	Sequence 1, Appl	C 499	14	2.0	1272	4	US-09-191-136-13	Sequence 13, Appl
C 427	14	2.0	736	2	US-09-100-297-1	Sequence 1, Appl	500	14	2.0	1272	4	US-09-227-357-46	Sequence 46, Appl
C 428	14	2.0	744	1	US-07-648-796A-10	Sequence 10, Appl	C 501	14	2.0	1281	4	US-09-327-487A-3	Sequence 3, Appl
C 429	14	2.0	792	1	US-08-578-709-10	Sequence 10, Appl	C 502	14	2.0	1284	4	US-09-327-487A-4	Sequence 4, Appl
C 430	14	2.0	806	6	5494663-4	Patent No. 5494663	503	14	2.0	1298	3	US-08-911-894-73	Sequence 73, Appl
C 431	14	2.0	810	4	US-09-221-017B-732	Sequence 732, App	504	14	2.0	1300	2	US-09-166-203-41	Sequence 41, Appl
C 432	14	2.0	814	4	US-08-858-207A-238	Sequence 238, App	505	14	2.0	1300	4	US-09-377-309-41	Sequence 41, Appl
C 433	14	2.0	822	1	US-07-936-267A-8	Sequence 8, Appl	C 506	14	2.0	1311	2	US-08-530-569B-1	Sequence 1, Appl
C 434	14	2.0	829	2	US-08-294-143-3	Sequence 3, Appl	507	14	2.0	1317	1	US-08-370-975B-2	Sequence 2, Appl
C 435	14	2.0	829	3	US-09-256-331-3	Sequence 3, Appl	C 508	14	2.0	1341	3	US-09-032-372-9	Sequence 9, Appl
C 436	14	2.0	829	4	US-09-593-483-3	Sequence 3, Appl	C 509	14	2.0	1379	2	US-08-437-607A-1	Sequence 1, Appl
C 437	14	2.0	833	2	US-08-837-029-1	Sequence 1, Appl	C 510	14	2.0	1380	2	US-08-437-607A-4	Sequence 4, Appl
C 438	14	2.0	835	3	US-08-957-302A-9	Sequence 9, Appl	511	14	2.0	1384	1	US-07-607-538C-1	Sequence 1, Appl
C 439	14	2.0	835	4	US-09-542-403A-9	Sequence 9, Appl	512	14	2.0	1384	2	US-08-162-402B-1	Sequence 1, Appl
C 440	14	2.0	840	4	US-08-998-416-341	Sequence 341, App	C 513	14	2.0	1387	2	US-08-979-424-2	Sequence 2, Appl
C 441	14	2.0	842	4	US-08-998-416-517	Sequence 517, App	C 514	14	2.0	1394	1	US-07-730-953-1	Sequence 1, Appl
C 442	14	2.0	844	4	US-09-812-484-5	Sequence 6, Appl	515	14	2.0	1395	3	US-08-957-302A-3	Sequence 3, Appl
C 443	14	2.0	851	3	US-09-126-646-3	Sequence 3, Appl	516	14	2.0	1395	4	US-09-542-403-3	Sequence 3, Appl
C 444	14	2.0	851	4	US-09-421-491-3	Sequence 3, Appl	517	14	2.0	1419	2	US-08-619-542B-29	Sequence 29, Appl
C 445	14	2.0	861	3	US-09-187-050-4	Sequence 4, Appl	C 518	14	2.0	1449	3	US-08-103-170-5	Sequence 5, Appl
C 446	14	2.0	900	4	US-09-149-476-161	Sequence 161, App	C 519	14	2.0	1444	3	US-08-988-876-4	Sequence 4, Appl
C 447	14	2.0	903	4	US-09-934-551-1	Sequence 1, Appl	C 520	14	2.0	1452	2	US-08-807-044-4	Sequence 1, Appl
C 448	14	2.0	918	1	US-08-328-322-3	Sequence 3, Appl	C 521	14	2.0	1452	5	PCT-US91-04986-1	Sequence 1, Appl
C 449	14	2.0	941	2	US-08-203-532F-3	Sequence 3, Appl	C 522	14	2.0	1461	3	US-08-722-126A-4	Sequence 4, Appl
C 450	14	2.0	941	4	US-09-078-465-3	Sequence 3, Appl	523	14	2.0	1461	5	PCT-US95-04258-4	Sequence 4, Appl
C 451	14	2.0	941	5	PCT-US95-01882A-3	Sequence 3, Appl	524	14	2.0	1467	1	US-08-176-620A-3	Sequence 3, Appl
C 452	14	2.0	957	4	US-09-102-344-1	Sequence 1, Appl	525	14	2.0	1467	2	US-08-461-985-3	Sequence 3, Appl
C 453	14	2.0	957	4	US-09-193-637A-22	Sequence 22, Appl	526	14	2.0	1467	2	US-08-461-985-3	Sequence 3, Appl
C 454	14	2.0	958	2	US-08-632-514C-9	Sequence 9, Appl	527	14	2.0	1467	2	US-08-458-887-3	Sequence 3, Appl
C 455	14	2.0	958	3	US-09-188-177-9	Sequence 9, Appl	528	14	2.0	1467	4	US-08-932-787B-3	Sequence 3, Appl
C 456	14	2.0	1001	4	US-09-641-638-220	Sequence 220, App	529	14	2.0	1467	4	US-08-932-012C-3	Sequence 3, Appl
C 457	14	2.0	1001	4	US-09-641-638-221	Sequence 221, App	530	14	2.0	1467	4	US-08-888-818C-3	Sequence 3, Appl
C 458	14	2.0	1001	4	US-09-641-638-285	Sequence 285, App	531	14	2.0	1497	2	US-08-820-170A-41	Sequence 41, Appl
C 459	14	2.0	1001	4	US-09-641-638-555	Sequence 555, App	532	14	2.0	1497	3	US-09-055-699-41	Sequence 41, Appl
C 460	14	2.0	1001	4	US-09-641-638-563	Sequence 563, App	533	14	2.0	1497	4	US-09-273-565-41	Sequence 41, Appl
C 461	14	2.0	1001	4	US-09-641-638-564	Sequence 564, App	534	14	2.0	1497	4	US-09-565-538-41	Sequence 41, Appl
C 462	14	2.0	1006	1	US-08-076-091C-11	Sequence 11, Appl	535	14	2.0	1497	4	US-09-661-468-41	Sequence 41, Appl
C 463	14	2.0	1006	1	US-08-285-641-11	Sequence 11, Appl	536	14	2.0	1498	2	US-08-818-024-2	Sequence 2, Appl
C 464	14	2.0	1017	4	US-08-849-751-1	Sequence 1, Appl	537	14	2.0	1498	4	US-09-334-775A-2	Sequence 2, Appl
C 465	14	2.0	1017	4	US-09-478-816-1	Sequence 1, Appl	C 538	14	2.0	1508	4	US-09-039-046-1	Sequence 1, Appl

c 539	14	2.0	1517	4	US-09-149-476-295	Sequence 295, App	612	14	2.0	1758	3	US-09-191-171-6	Sequence 6, Appl
c 540	14	2.0	1537	4	US-09-556-877-57	Sequence 57, Appl	c 614	14	2.0	1758	4	US-09-385-707-6	Sequence 6, Appl
c 541	14	2.0	1537	4	US-09-620-412C-57	Sequence 57, Appl	c 614	14	2.0	1767	1	US-07-668-648-1	Sequence 1, Appl
542	14	2.0	1540	1	US-07-932-915-1	Sequence 1, Appl	c 615	14	2.0	1767	1	US-07-668-648-5	Sequence 5, Appl
543	14	2.0	1540	5	PCT-US91-05826-1	Sequence 1, Appl	c 616	14	2.0	1767	2	US-08-429-998-1	Sequence 1, Appl
c 544	14	2.0	1544	4	US-09-149-476-103	Sequence 103, App	c 617	14	2.0	1767	2	US-08-429-998-5	Sequence 5, Appl
545	14	2.0	1546	4	US-09-383-18A-1	Sequence 1, Appl	c 618	14	2.0	1767	2	US-08-431-333-1	Sequence 1, Appl
546	14	2.0	1547	2	US-08-902-853-2	Sequence 2, Appl	c 618	14	2.0	1767	2	US-08-431-333-5	Sequence 5, Appl
547	14	2.0	1548	3	US-08-665-259-28	Sequence 28, Appl	c 620	14	2.0	1767	5	PCT-US91-02321-1	Sequence 1, Appl
548	14	2.0	1548	3	US-08-762-500-28	Sequence 28, Appl	c 621	14	2.0	1767	5	PCT-US91-02321-5	Sequence 5, Appl
549	14	2.0	1556	2	US-08-881-857-1	Sequence 1, Appl	c 622	14	2.0	1782	2	US-08-308-952-6	Sequence 6, Appl
550	14	2.0	1556	4	US-09-233-342A-1	Sequence 1, Appl	c 623	14	2.0	1782	4	US-09-124-141-6	Sequence 6, Appl
551	14	2.0	1571	5	PCT-US94-12912-2	Sequence 2, Appl	c 624	14	2.0	1810	1	US-07-755-573C-7	Sequence 7, Appl
552	14	2.0	1575	3	US-08-957-302A-1	Sequence 1, Appl	c 625	14	2.0	1831	4	US-09-484-970B-84	Sequence 84, Appl
553	14	2.0	1575	4	US-09-542-403-1	Sequence 1, Appl	c 626	14	2.0	1831	3	US-09-120-365-6	Sequence 6, Appl
c 554	14	2.0	1590	4	US-09-323-195A-7	Sequence 7, Appl	c 627	14	2.0	1833	4	US-09-515-039-6	Sequence 6, Appl
555	14	2.0	1600	1	US-08-073-384C-12	Sequence 12, Appl	c 628	14	2.0	1844	1	US-07-872-644-26	Sequence 26, Appl
556	14	2.0	1600	1	US-08-254-359A-12	Sequence 12, Appl	c 629	14	2.0	1844	1	US-08-297-494-26	Sequence 26, Appl
557	14	2.0	1600	1	US-08-483-043-12	Sequence 12, Appl	c 630	14	2.0	1844	1	US-08-297-510-26	Sequence 26, Appl
558	14	2.0	1600	1	US-08-481-238-12	Sequence 12, Appl	c 631	14	2.0	1844	1	US-08-479-532-26	Sequence 26, Appl
559	14	2.0	1600	2	US-08-471-066B-12	Sequence 12, Appl	c 632	14	2.0	1844	1	US-08-455-526-26	Sequence 26, Appl
560	14	2.0	1600	2	US-08-484-956-12	Sequence 12, Appl	c 633	14	2.0	1844	1	US-08-455-525-26	Sequence 26, Appl
561	14	2.0	1600	2	US-08-757-653-12	Sequence 12, Appl	c 634	14	2.0	1844	3	US-09-139-491-26	Sequence 26, Appl
562	14	2.0	1600	2	US-08-599-491-12	Sequence 12, Appl	c 635	14	2.0	1844	5	PCT-US92-03222-26	Sequence 26, Appl
563	14	2.0	1600	2	US-08-756-386-12	Sequence 12, Appl	c 636	14	2.0	1858	4	US-09-336-536-56	Sequence 56, Appl
564	14	2.0	1600	2	US-08-823-516-12	Sequence 12, Appl	c 637	14	2.0	1863	3	US-09-126-646-1	Sequence 1, Appl
565	14	2.0	1600	3	US-08-682-853A-12	Sequence 12, Appl	c 638	14	2.0	1863	4	US-09-421-491-1	Sequence 1, Appl
566	14	2.0	1600	3	US-08-759-038-12	Sequence 12, Appl	c 639	14	2.0	1863	4	US-09-637-118B-1	Sequence 1, Appl
567	14	2.0	1600	3	US-08-758-314-12	Sequence 12, Appl	c 640	14	2.0	1869	4	US-09-336-536-26	Sequence 26, Appl
568	14	2.0	1600	4	US-09-350-309-12	Sequence 12, Appl	c 641	14	2.0	1889	3	US-09-187-050-1	Sequence 1, Appl
569	14	2.0	1600	4	US-08-520-946-12	Sequence 12, Appl	c 642	14	2.0	1894	4	US-07-912-122-3	Sequence 3, Appl
c 570	14	2.0	1602	4	US-09-153-804-9	Sequence 9, Appl	c 643	14	2.0	1894	5	PCT-US93-06404-3	Sequence 3, Appl
c 571	14	2.0	1603	4	US-08-065-844A-1	Sequence 1, Appl	c 644	14	2.0	1901	1	US-08-153-848-43	Sequence 43, Appl
c 572	14	2.0	1611	2	US-08-551-211-4	Sequence 4, Appl	c 645	14	2.0	1901	3	US-09-299-843A-43	Sequence 43, Appl
573	14	2.0	1622	1	US-07-996-772A-3	Sequence 3, Appl	c 646	14	2.0	1901	4	US-09-088-337B-43	Sequence 43, Appl
574	14	2.0	1622	1	US-08-446-822-3	Sequence 3, Appl	c 647	14	2.0	1901	5	PCT-US93-11537-43	Sequence 43, Appl
575	14	2.0	1622	4	US-09-328-314-3	Sequence 3, Appl	c 648	14	2.0	1905	1	US-08-164-614A-2	Sequence 2, Appl
576	14	2.0	1622	5	PCT-US93-12586-3	Sequence 3, Appl	c 649	14	2.0	1905	2	US-08-456-489B-2	Sequence 2, Appl
577	14	2.0	1641	4	US-09-178-252-9	Sequence 9, Appl	c 650	14	2.0	1905	5	PCT-US93-01720-2	Sequence 2, Appl
578	14	2.0	1642	1	US-07-996-772A-1	Sequence 1, Appl	c 651	14	2.0	1929	4	US-09-146-950-1	Sequence 1, Appl
c 579	14	2.0	1642	1	US-08-354-456A-3	Sequence 3, Appl	c 652	14	2.0	1934	2	US-08-162-402B-7	Sequence 7, Appl
c 580	14	2.0	1642	1	US-07-999-280A-3	Sequence 3, Appl	c 653	14	2.0	1950	1	US-08-592-126-93	Sequence 93, Appl
c 581	14	2.0	1642	1	US-08-426-279-3	Sequence 3, Appl	c 654	14	2.0	1953	1	US-08-436-044-3	Sequence 3, Appl
c 582	14	2.0	1642	1	US-08-426-279-3	Sequence 3, Appl	c 655	14	2.0	1953	2	US-08-436-054-3	Sequence 3, Appl
c 583	14	2.0	1642	1	US-08-401-632-3	Sequence 3, Appl	c 656	14	2.0	1953	5	PCT-US95-08812-3	Sequence 3, Appl
584	14	2.0	1642	1	US-08-446-822-1	Sequence 1, Appl	c 657	14	2.0	1960	3	US-09-177-431-9	Sequence 9, Appl
c 585	14	2.0	1642	3	US-08-436-570-3	Sequence 3, Appl	c 658	14	2.0	1977	1	US-08-578-709-14	Sequence 14, Appl
c 586	14	2.0	1642	3	US-08-425-876-3	Sequence 3, Appl	c 659	14	2.0	1984	4	US-08-337-067-5	Sequence 5, Appl
c 587	14	2.0	1642	3	US-08-426-243-3	Sequence 3, Appl	c 660	14	2.0	1990	4	US-09-149-476-281	Sequence 281, App
c 588	14	2.0	1642	4	US-08-401-632-3	Sequence 3, Appl	c 661	14	2.0	2010	4	US-09-240-410-1	Sequence 1, Appl
589	14	2.0	1642	4	US-09-328-314-1	Sequence 1, Appl	c 662	14	2.0	2018	2	US-08-557-973-1	Sequence 1, Appl
590	14	2.0	1642	5	PCT-US93-12586-1	Sequence 1, Appl	c 663	14	2.0	2038	2	US-08-631-097-7	Sequence 7, Appl
591	14	2.0	1659	2	US-08-943-087-47	Sequence 47, Appl	c 664	14	2.0	2038	4	US-08-810-712-11	Sequence 11, Appl
592	14	2.0	1660	4	US-09-637-367-21	Sequence 21, Appl	c 665	14	2.0	2041	4	US-09-149-476-131	Sequence 131, App
593	14	2.0	1662	4	US-09-370-398-1	Sequence 1, Appl	c 666	14	2.0	2051	2	US-08-530-569B-13	Sequence 13, Appl
c 595	14	2.0	1677	4	US-09-153-804-10	Sequence 10, Appl	c 667	14	2.0	2055	4	US-09-232-160-9	Sequence 9, Appl
c 596	14	2.0	1679	4	US-09-271-437-3	Sequence 3, Appl	c 668	14	2.0	2055	4	US-09-812-484-3	Sequence 3, Appl
597	14	2.0	1680	1	US-08-234-783-3	Sequence 3, Appl	c 669	14	2.0	2057	2	US-08-820-170A-42	Sequence 42, Appl
598	14	2.0	1680	5	PCT-US95-05523-3	Sequence 3, Appl	c 670	14	2.0	2057	3	US-09-055-699-42	Sequence 42, Appl
599	14	2.0	1682	3	US-09-096-399-1	Sequence 3, Appl	c 671	14	2.0	2057	4	US-09-273-565-42	Sequence 42, Appl
600	14	2.0	1686	2	US-08-648-657-1	Sequence 1, Appl	c 672	14	2.0	2057	4	US-09-565-538-42	Sequence 42, Appl
601	14	2.0	1689	2	US-08-648-657-2	Sequence 2, Appl	c 673	14	2.0	2057	4	US-09-661-468-42	Sequence 42, Appl
602	14	2.0	1689	4	US-09-276-531-101	Sequence 101, App	c 674	14	2.0	2067	2	US-08-713-928B-8	Sequence 8, Appl
603	14	2.0	1696	3	US-09-096-399-3	Sequence 3, Appl	c 675	14	2.0	2070	3	US-08-394-326-1	Sequence 1, Appl
c 604	14	2.0	1721	3	US-09-173-581-16	Sequence 16, Appl	c 676	14	2.0	2070	3	US-09-082-306-1	Sequence 1, Appl
c 605	14	2.0	1721	4	US-09-420-165-16	Sequence 16, Appl	c 677	14	2.0	2073	2	US-08-691-814B-5	Sequence 5, Appl
c 606	14	2.0	1726	4	US-09-232-160-14	Sequence 14, Appl	c 678	14	2.0	2080	2	US-08-878-563A-2	Sequence 2, Appl
c 607	14	2.0	1726	4	US-09-812-484-11	Sequence 11, Appl	c 680	14	2.0	2080	4	US-09-270-117-2	Sequence 2, Appl
c 608	14	2.0	1734	4	US-09-182-145-17	Sequence 17, Appl	c 681	14	2.0	2089	1	US-08-441-139-13	Sequence 13, Appl
609	14	2.0	1734	4	US-09-182-145-18	Sequence 18, Appl	c 682	14	2.0	2093	5	PCT-US95-09941-1	Sequence 1, Appl
c 610	14	2.0	1752	4	US-09-360-779-1	Sequence 1, Appl	c 683	14	2.0	2112	4	US-09-232-160-12	Sequence 12, Appl
c 611	14	2.0	1752	4	US-09-435-335-1	Sequence 1, Appl	c 684	14	2.0	2125	3	US-09-109-204-5	Sequence 5, Appl

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686	14	2.0	2126	3	US-09-110-937-1	Sequence 1, Appli	759	14	2.0	2499	4	US-09-777-537-1	Sequence 1, Appli
687	14	2.0	2126	3	US-09-058-725B-1	Sequence 1, Appli	760	14	2.0	2499	4	US-09-777-538-1	Sequence 1, Appli
688	14	2.0	2126	3	US-09-232-857-1	Sequence 1, Appli	761	14	2.0	2499	5	PCT-US91-07035-1	Sequence 21, Appli
689	14	2.0	2129	2	US-08-836-791-10	Sequence 10, Appli	762	14	2.0	2502	1	US-08-073-384C-21	Sequence 21, Appli
690	14	2.0	2137	4	US-08-991-862-1	Sequence 1, Appli	763	14	2.0	2502	1	US-08-254-359A-21	Sequence 21, Appli
691	14	2.0	2148	5	PCT-US92-00731-12	Sequence 12, Appli	764	14	2.0	2502	1	US-08-483-043-21	Sequence 21, Appli
692	14	2.0	2153	4	US-09-367-206-6	Sequence 6, Appli	765	14	2.0	2502	1	US-08-481-238-21	Sequence 21, Appli
693	14	2.0	2155	3	US-09-191-171-4	Sequence 4, Appli	766	14	2.0	2502	2	US-08-471-066B-21	Sequence 21, Appli
694	14	2.0	2155	4	US-09-385-707-4	Sequence 4, Appli	767	14	2.0	2502	2	US-08-484-956-21	Sequence 21, Appli
695	14	2.0	2159	4	US-09-039-046-4	Sequence 4, Appli	768	14	2.0	2502	2	US-08-757-653-21	Sequence 21, Appli
696	14	2.0	2200	1	US-08-592-126-102	Sequence 102, App	769	14	2.0	2502	2	US-08-599-491-21	Sequence 21, Appli
697	14	2.0	2202	2	US-08-551-211-5	Sequence 5, Appli	770	14	2.0	2502	2	US-08-756-386-21	Sequence 21, Appli
698	14	2.0	2207	4	US-08-956-322-3	Sequence 3, Appli	771	14	2.0	2502	2	US-08-823-516-21	Sequence 21, Appli
699	14	2.0	2232	1	US-08-450-933A-1	Sequence 1, Appli	772	14	2.0	2502	3	US-08-682-853A-21	Sequence 21, Appli
700	14	2.0	2232	3	US-08-446-669-1	Sequence 1, Appli	773	14	2.0	2502	3	US-08-759-038-21	Sequence 21, Appli
701	14	2.0	2232	5	PCT-US91-01360-1	Sequence 1, Appli	774	14	2.0	2502	3	US-08-758-314-21	Sequence 21, Appli
702	14	2.0	2232	5	PCT-US95-00476-1	Sequence 1, Appli	775	14	2.0	2502	4	US-09-350-309-21	Sequence 21, Appli
703	14	2.0	2235	4	US-09-334-601-3	Sequence 3, Appli	776	14	2.0	2502	4	US-08-520-946-21	Sequence 21, Appli
704	14	2.0	2235	4	US-09-484-970B-28	Sequence 28, Appli	777	14	2.0	2505	2	US-08-757-653-167	Sequence 167, App
705	14	2.0	2238	1	US-08-742-011-1	Sequence 1, Appli	778	14	2.0	2505	2	US-08-757-653-187	Sequence 187, App
706	14	2.0	2265	2	US-08-940-332-1	Sequence 1, Appli	779	14	2.0	2505	2	US-08-757-653-189	Sequence 189, App
707	14	2.0	2268	4	US-08-675-773B-4	Sequence 4, Appli	780	14	2.0	2505	2	US-08-823-516-65	Sequence 65, Appli
708	14	2.0	2285	1	US-08-477-674-9	Sequence 9, Appli	781	14	2.0	2505	2	US-08-823-516-68	Sequence 68, Appli
709	14	2.0	2285	1	US-08-473-791-9	Sequence 9, Appli	782	14	2.0	2505	2	US-08-823-516-70	Sequence 70, Appli
710	14	2.0	2285	2	US-08-316-714-9	Sequence 9, Appli	783	14	2.0	2505	3	US-08-759-038-106	Sequence 106, App
711	14	2.0	2285	2	US-08-473-673-9	Sequence 9, Appli	784	14	2.0	2505	3	US-08-759-038-129	Sequence 129, App
712	14	2.0	2290	2	US-08-933-821-1	Sequence 1, Appli	785	14	2.0	2505	3	US-08-759-038-131	Sequence 131, App
713	14	2.0	2290	3	US-08-960-507-1	Sequence 1, Appli	786	14	2.0	2505	3	US-08-758-314-106	Sequence 106, App
714	14	2.0	2290	4	US-09-136-828-1	Sequence 1, Appli	787	14	2.0	2505	3	US-08-758-314-129	Sequence 129, App
715	14	2.0	2290	4	US-09-332-928A-1	Sequence 1, Appli	788	14	2.0	2505	3	US-08-758-314-131	Sequence 131, App
716	14	2.0	2290	4	US-09-136-801-1	Sequence 1, Appli	789	14	2.0	2506	1	US-08-073-384C-1	Sequence 1, Appli
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C 977 14 2.0 4526 3 US-08-881-094-4  
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## ALIGNMENTS

RESULT 1  
US-08-759-581B-3/c  
; Sequence 3, Application US/08759581B  
; Patent No. 5876945

; GENERAL INFORMATION:

; APPLICANT: CHISHOLM, DEXTER A.

; APPLICANT: DINER, BRUCE A.

; APPLICANT: DONALDSON, GAIL K.

; APPLICANT: HERSHEY, HOWARD P.

; APPLICANT: JORDAN, DOUGLAS B.

; APPLICANT: TANG, XIAO-SONG

; APPLICANT: TROST, JEFFREY T.

; APPLICANT: WANG, SHAOJIE

; APPLICANT: WARREN, PATRICK V.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING HERBICIDAL AGENTS THAT INHIBIT D1 PROTEIN

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: U.S.A.

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1

; SOFTWARE: MICROSOFT WORD 2.0C

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/759,581B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: FLOYD, LINDA AXAMETHY

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: CR-9964

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-892-8112

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1680 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

Sequence 4, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 823, Appl  
Sequence 18, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Patent No. 5206352  
Sequence 34, Appl  
Sequence 33, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
GENERAL INFORMAT  
Sequence 702, App

; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; STRAIN: SCENEDESMUS GENE  
US-08-759-581B-3

Query Match 2.5%; Score 18; DB 2; Length 1680;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 CTGAGCGGAGGCTGTGC 164  
Db 1124 CTGAGCGGAGGCTGTGC 1107

## RESULT 2

US-09-304-711-3/c

; Sequence 3, Application US/09304711

; Patent No. 6350573

; GENERAL INFORMATION:

; APPLICANT: DINER, BRUCE A.

; APPLICANT: CHISHOLM, DEXTER A.

; APPLICANT: DONALDSON, GAIL K.

; APPLICANT: HERSHEY, HOWARD P.

; APPLICANT: JORDAN, DOUG B.

; APPLICANT: TANG, XIAO SONG

; APPLICANT: WANG, SHAOJIE

; APPLICANT: TROST, JEFFREY T.

; APPLICANT: WARREN, PATRICK V.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING HERBICIDAL AGENTS THAT

; FILE REFERENCE: CR-9964-C

; CURRENT APPLICATION NUMBER: US/09/304,711

; CURRENT FILING DATE: 1999-05-04

; EARLIER APPLICATION NUMBER: 08/759,581

; EARLIER FILING DATE: DECEMBER 5, 1996

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: MICROSOFT OFFICE 97

; SEQ ID NO 3

; LENGTH: 1680

; TYPE: DNA

; ORGANISM: SCENEDESMUS

US-09-304-711-3

Query Match 2.5%; Score 18; DB 4; Length 1680;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 CTGAGCGGAGGCTGTGC 164  
Db 1124 CTGAGCGGAGGCTGTGC 1107

## RESULT 3

US-09-173-281-3/c

; Sequence 3, Application US/09173281

; Patent No. 644457

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: METHODS FOR IDENTIFYING HERBICIDAL AGENTS THAT INHIBIT D1 PROTEIN

; NUMBER OF SEQUENCES: 29

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD VERSION 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/173,281

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/759,581

; FILING DATE: DECEMBER 5, 1996

ATTORNEY/AGENT INFORMATION:  
NAME: FLOYD, LINDA AXAMETHY  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: CR-9964-A  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1680 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: SCENEDESMUS GENE  
US-09-173-281-3

Query Match 2.4%; Score 18; DB 4; Length 1680;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 CTGAGCGGAGGCTGTGC 164  
|||||  
Db 1124 CTGAGCGGAGGCTGTGC 1107

RESULT 4  
US-08-650-275-35/c  
; Sequence 35, Application US/08650275  
; Patent No. 5798249  
; GENERAL INFORMATION:  
; APPLICANT: Braxton, Scott Michael  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181.318  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/650,275  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0067 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 420 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: GI 1149007  
US-09-181-318-35

Query Match 2.4%; Score 17; DB 3; Length 420;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AGGAAAGGCTGGCTCC 35  
|||||  
Db 58 AGGAAAGGCTGGCTCC 42

RESULT 6  
US-08-650-275-1/c  
; Sequence 1, Application US/08650275  
; Patent No. 5798249  
; GENERAL INFORMATION:  
; APPLICANT: Braxton, Scott Michael  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,275  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0067 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1493 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT04  
CLONE: 890200

US-08-650-275-1

Query Match 2.4%; Score 17; DB 1; Length 1493;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AGGAAAGGCTGGCTCC 35  
Db 58 AGGAAAGGCTGGCTCC 42

## RESULT 7

US-09-181-318-1/c  
Sequence 1, Application US/09181318  
Patent No. 6001632  
GENERAL INFORMATION:  
APPLICANT: Braxton, Scott Michael  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/181,318  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/650,275  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0067 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1493 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT04  
CLONE: 890200

US-09-181-318-1

Query Match 2.4%; Score 17; DB 3; Length 1493;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AGGAAAGGCTGGCTCC 35  
Db 58 AGGAAAGGCTGGCTCC 42

## RESULT 8

US-08-663-566A-10  
Sequence 10, Application US/08663566A  
Patent No. 5853733  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Macdonald, Richard D  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,566A  
FILING DATE: June 13, 1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0400  
TELEFAX: (212)391-0526  
TELEX: 422523

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1734 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1734

US-08-663-566A-10

Query Match 2.4%; Score 17; DB 2; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CCACGGACACAGAGAA 23  
Db 761 CCACGGACACAGAGAA 777

RESULT 9  
US-08-023-610-10  
; Sequence 10, Application US/08023610  
; Patent No. 5928648  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Richard D  
; APPLICANT: Macdonald Ph.D., Richard D  
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys  
; TITLE OF INVENTION: and Uses Thereof  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/023,610  
; FILING DATE: February 26, 1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1734 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1734  
US-08-023-610-10

Query Match 2.4%; Score 17; DB 2; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23  
Db 761 CCACGGAGACAGAGAA 777

RESULT 10  
US-08-065A-10  
; Sequence 10, Application US/08288065A  
; Patent No. 5961982  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Macdonald, Richard D  
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-  
; TITLE OF INVENTION: HVT-050 and Uses Thereof  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA

; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/288,065A  
; FILING DATE: Aug-09-94  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)278-0400  
; TELEFAX: (212)391-0526  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1734 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1734  
US-08-288-065A-10

Query Match 2.4%; Score 17; DB 2; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23  
Db 761 CCACGGAGACAGAGAA 777

RESULT 11  
US-08-362-240A-10  
; Sequence 10, Application US/08362240A  
; Patent No. 5965138  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D  
; APPLICANT: Junker, David  
; APPLICANT: Wild, Martha A  
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,240A  
; FILING DATE: Dec-22-94  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)278-0400  
; TELEFAX: (212)391-0526  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 10:

;; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1734 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1734  
US-08-362-240A-10

Query Match 2.4%; Score 17; DB 2; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23  
|||  
Db 761 CCACGGAGACAGAGAA 777

RESULT 12  
; Sequence 8, Application US/08804372A  
; Patent No. 6183753  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Wild, Martha A.  
; APPLICANT: Winslow, Barbara J.  
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,372A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 2552/39115E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1734 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1734  
US-08-804-372A-8

Query Match 2.4%; Score 17; DB 4; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23  
|||  
Db 761 CCACGGAGACAGAGAA 777

RESULT 13  
PCT-US95-10245-10  
; Sequence 10, Application PC/TUS9510245  
; GENERAL INFORMATION:  
; APPLICANT: SYNTRO CORPORATION  
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/10245  
; FILING DATE: 09-AUG-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0526  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1734 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1734  
PCT-US95-10245-10

Query Match 2.4%; Score 17; DB 5; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGAA 23  
|||  
Db 761 CCACGGAGACAGAGAA 777

RESULT 14  
US-08-850-910A-42  
; Sequence 42, Application US/08850910A  
; Patent No. 5948761  
; GENERAL INFORMATION:  
; APPLICANT: SEILHAMER, J.J.  
; APPLICANT: LEWICKI, J.  
; APPLICANT: SCARBOROUGH, R.M.  
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER, LLP  
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500

CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,910A  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/477,226  
FILING DATE: 08-FEB-1990  
APPLICATION NUMBER: 07/299,880  
FILING DATE: 19-JAN-1989  
APPLICATION NUMBER: 07/206,470  
FILING DATE: 14-JUN-1988  
APPLICATION NUMBER: 07/200,383  
FILING DATE: 31-MAY-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 219002025212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1804 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 365...490  
OTHER INFORMATION:  
NAME/KEY: CDS  
LOCATION: 740...791  
OTHER INFORMATION:  
NAME/KEY: CDS  
LOCATION: 1558...1569  
OTHER INFORMATION:  
US-08-850-910A-42

Query Match 2.4%; Score 17; DB 2; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 TGGCTCCCCCTCCCCAG 45  
|||||  
Db 1015 TGGCTCCCCCTCCCCAG 1031

## RESULT 15

US-07-820-154A-29  
Sequence 29, Application US/07820154A  
Patent No. 5382425  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D., Mark D  
APPLICANT: Junker M.S., David E  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/820,154A  
FILING DATE: 19920113  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1907 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Newcastle disease virus  
STRAIN: B1  
IMMEDIATE SOURCE:  
CLONE: 137-23.803 (PSY1142)  
POSITION IN GENOME:  
MAP POSITION: -50%  
UNITS: %G  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 92...1822 /codon\_start= 92  
OTHER INFORMATION: /product= "NDV heamagglutinin-Neuraminidase"  
OTHER INFORMATION: /gene= "HN"  
OTHER INFORMATION: /number= 1  
US-07-820-154A-29

Query Match 2.4%; Score 17; DB 1; Length 1907;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACGGAGACAGAGGAA 23  
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Db 852 CCACGGAGACAGAGGAA 868

Search completed: June 17, 2003, 06:30:00  
Job time : 58.9887 secs





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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 20:04:56 ; Search time 75.5878 Seconds  
(without alignments)  
13697.491 Million cell updates/sec

Title: US-09-513-888c-1\_COPY\_7806\_8520

Perfect score: 715

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1029858 seqs, 72403093 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications\_NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	19	2.7	2916	US-10-098-841-81	Sequence 81, Appl
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6	18	2.5	492	US-09-783-590-10224	Sequence 10224, A
7	18	2.5	898	US-10-198-846-10677	Sequence 10677, A
8	18	2.5	893	US-10-198-846-1071	Sequence 1071, Ap
9	18	2.5	2144	US-09-822-830A-8	Sequence 8, Appli
10	18	2.5	2662	US-09-925-301-2	Sequence 2, Appli
11	18	2.5	11336	US-09-764-868-1440	Sequence 1440, Ap
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160	17	2.4	2528	9	US-10-128-686A-461	Sequence 461, App	233	17	2.4	4339	9	US-10-198-846-12659	Sequence 12659, A
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241	17	2.4	7893	9	US-10-077-130-3	Sequence 3, Appli	314	16	2.2	738	10	US-09-876-527-24	Sequence 24, Appl
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c 243	17	2.4	9517	10	US-09-954-456-530	Sequence 530, App	c 316	16	2.2	810	9	US-10-271-887-23	Sequence 23, Appli
c 244	17	2.4	9517	10	US-09-954-456-1948	Sequence 1948, Ap	c 317	16	2.2	816	9	US-09-738-626-932	Sequence 932, App
c 245	17	2.4	9664	9	US-10-091-504-2126	Sequence 2126, Ap	c 318	16	2.2	821	10	US-09-925-297-78	Sequence 78, Appl
c 246	17	2.4	9664	9	US-09-764-869-2126	Sequence 2126, Ap	c 319	16	2.2	907	9	US-10-037-270-652	Sequence 652, App
c 247	17	2.4	9848	9	US-10-227-338-3	Sequence 3, Appli	320	16	2.2	912	9	US-10-278-173-1	Sequence 1, Appli
248	17	2.4	9880	10	US-09-880-107-3352	Sequence 3352, Ap	321	16	2.2	932	10	US-09-876-527-25	Sequence 25, Appl
249	17	2.4	10828	10	US-09-942-325A-2	Sequence 2, Appli	322	16	2.2	999	10	US-09-876-527-26	Sequence 26, Appl
250	17	2.4	13229	10	US-09-942-325A-1	Sequence 1, Appli	323	16	2.2	1011	10	US-09-876-527-27	Sequence 27, Appl
251	17	2.4	15987	9	US-10-092-154-1301	Sequence 1301, Ap	324	16	2.2	1050	9	US-09-954-531-953	Sequence 953, App
c 252	17	2.4	17904	9	US-09-764-847-1301	Sequence 1301, Ap	325	16	2.2	1096	9	US-09-776-724A-75	Sequence 75, Appl
c 253	17	2.4	17904	9	US-09-764-847-1301	Sequence 6418, Ap	c 326	16	2.2	1225	9	US-09-925-299-100	Sequence 100, App
254	17	2.4	23907	9	US-10-077-130-6	Sequence 6, Appli	c 327	16	2.2	1225	10	US-09-925-299-100	Sequence 100, App
255	17	2.4	24120	9	US-10-077-130-4	Sequence 4, Appli	c 328	16	2.2	1230	9	US-09-738-626-932	Sequence 3471, Ap
256	17	2.4	26657	10	US-09-810-673A-3	Sequence 3, Appli	c 329	16	2.2	1278	12	US-10-044-090-177	Sequence 177, App
c 257	17	2.4	32192	9	US-09-764-891-9791	Sequence 9791, Ap	330	16	2.2	1330	10	US-09-731-872-38	Sequence 38, Appl
258	17	2.4	32192	9	US-09-764-877-3657	Sequence 3657, Ap	331	16	2.2	1332	9	US-09-989-920-30	Sequence 30, Appl
c 259	17	2.4	32195	9	US-10-091-504-1605	Sequence 1605, Ap	c 332	16	2.2	1383	9	US-09-764-891-8866	Sequence 8866, Ap
c 260	17	2.4	32195	9	US-10-125-540-611	Sequence 611, App	c 333	16	2.2	1435	9	US-10-016-157A-87	Sequence 87, Appl
c 261	17	2.4	32195	9	US-10-125-540-611	Sequence 617, App	c 334	16	2.2	1455	10	US-09-801-275-3	Sequence 3, Appli
c 262	17	2.4	32195	10	US-09-764-870-611	Sequence 611, App	c 335	16	2.2	1511	9	US-09-822-846-210	Sequence 210, App
c 263	17	2.4	32195	10	US-09-764-870-611	Sequence 617, App	c 336	16	2.2	1567	10	US-09-925-300-740	Sequence 740, App
c 264	17	2.4	32195	10	US-09-764-869-1605	Sequence 1605, Ap	337	16	2.2	1583	9	US-09-892-877-23	Sequence 23, Appl
265	17	2.4	62944	10	US-09-954-456-2257	Sequence 2257, Ap	338	16	2.2	1583	9	US-09-948-783-24	Sequence 24, Appl
c 266	17	2.4	78785	9	US-09-978-167-3	Sequence 3, Appli	c 339	16	2.2	1696	9	US-10-198-846-10130	Sequence 10130, A
c 267	17	2.4	98829	9	US-10-017-724-3	Sequence 3, Appli	c 340	16	2.2	1743	9	US-10-033-174-9	Sequence 9, Appli
268	17	2.4	1691139	9	US-10-067-514-1	Sequence 1, Appli	341	16	2.2	1787	10	US-09-905-999-24	Sequence 24, Appl
269	16	2.2	20	10	US-09-735-995-52	Sequence 52, Appl	342	16	2.2	1855	10	US-09-822-849A-328	Sequence 328, App
c 270	16	2.2	25	9	US-10-098-263B-91333	Sequence 91333, A	c 343	16	2.2	1976	10	US-09-864-761-4746	Sequence 4746, Ap
c 271	16	2.2	101	10	US-09-969-373-227	Sequence 227, App	344	16	2.2	2000	9	US-09-938-842A-4062	Sequence 4062, Ap
c 272	16	2.2	101	10	US-09-969-373-296	Sequence 296, App	345	16	2.2	2002	10	US-09-922-830A-488	Sequence 488, App
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c 274	16	2.2	164	10	US-09-867-701-4739	Sequence 4739, Ap	c 347	16	2.2	2102	10	US-09-822-830A-71	Sequence 71, Appl
c 275	16	2.2	180	10	US-09-923-876-4889	Sequence 4889, Ap	c 348	16	2.2	2121	10	US-09-860-232A-1	Sequence 1, Appli
c 276	16	2.2	193	10	US-09-864-761-26367	Sequence 26367, A	349	16	2.2	2124	9	US-09-965-529-42	Sequence 42, Appl
c 277	16	2.2	204	10	US-09-923-876-5847	Sequence 5847, Ap	350	16	2.2	2142	9	US-09-776-724A-30	Sequence 30, Appl
c 278	16	2.2	212	10	US-09-294-093B-4060	Sequence 4060, Ap	c 351	16	2.2	2280	9	US-09-938-842A-833	Sequence 833, App
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c 280	16	2.2	221	10	US-09-960-352-14277	Sequence 14277, A	353	16	2.2	2446	10	US-09-801-275-1	Sequence 1, Appli
c 281	16	2.2	264	10	US-09-878-574-8734	Sequence 8734, Ap	c 354	16	2.2	2479	9	US-09-972-473-1	Sequence 1, Appli
c 282	16	2.2	283	10	US-09-772-105-48	Sequence 48, Appl	355	16	2.2	2490	9	US-10-201-310-1	Sequence 1, Appli
c 283	16	2.2	304	10	US-09-728-446-9	Sequence 9, Appli	c 356	16	2.2	2538	9	US-10-098-841-313	Sequence 313, App
c 284	16	2.2	366	10	US-09-878-574-2596	Sequence 2596, Ap	c 357	16	2.2	2586	9	US-09-905-291A-235	Sequence 235, App
c 285	16	2.2	371	10	US-09-867-701-6907	Sequence 6907, Ap	c 358	16	2.2	2586	9	US-10-063-547-7	Sequence 7, Appli
c 286	16	2.2	386	9	US-09-918-995-35009	Sequence 35009, A	c 359	16	2.2	2586	9	US-09-902-853-235	Sequence 235, App
c 287	16	2.2	393	10	US-09-864-761-3038	Sequence 3038, Ap	c 360	16	2.2	2586	9	US-09-907-824-235	Sequence 235, App
c 288	16	2.2	393	10	US-09-880-107-1074	Sequence 1074, Ap	c 361	16	2.2	2586	9	US-09-907-841-235	Sequence 235, App
c 289	16	2.2	416	10	US-09-983-965-2697	Sequence 2697, Ap	c 362	16	2.2	2586	9	US-09-904-011-235	Sequence 235, App
c 290	16	2.2	436	10	US-09-867-701-4117	Sequence 4117, Ap	c 363	16	2.2	2586	9	US-10-063-616-7	Sequence 7, Appli
c 291	16	2.2	441	9	US-09-918-995-24692	Sequence 24692, A	c 364	16	2.2	2586	9	US-09-906-712-235	Sequence 235, App
c 292	16	2.2	446	9	US-09-918-995-35118	Sequence 35118, A	c 365	16	2.2	2586	9	US-10-063-502-7	Sequence 7, Appli
c 293	16	2.2	447	9	US-09-918-995-2038	Sequence 2038, Ap	c 366	16	2.2	2586	9	US-09-906-838-235	Sequence 235, App
c 294	16	2.2	471	9	US-10-198-846-22	Sequence 22, Appl	c 367	16	2.2	2586	9	US-09-907-613-235	Sequence 235, App
c 295	16	2.2	478	9	US-09-918-995-19738	Sequence 19738, A	c 368	16	2.2	2586	9	US-09-907-942-235	Sequence 235, App
c 296	16	2.2	480	9	US-09-918-995-3101	Sequence 3101, Ap	c 369	16	2.2	2586	9	US-09-904-820-235	Sequence 235, App
c 297	16	2.2	484	9	US-09-918-995-1205	Sequence 1205, Ap	c 370	16	2.2	2586	9	US-09-904-859-235	Sequence 235, App
c 298	16	2.2	493	9	US-09-918-995-31890	Sequence 31890, A	c 371	16	2.2	2586	9	US-09-909-204-235	Sequence 235, App
c 299	16	2.2	498	9	US-10-171-581-245	Sequence 245, App	c 372	16	2.2	2586	9	US-09-904-786-235	Sequence 235, App
300	16	2.2	499	10	US-09-925-297-374	Sequence 374, App	c 373	16	2.2	2586	9	US-09-906-646-235	Sequence 235, App
301	16	2.2	507	9	US-09-918-995-31641	Sequence 31641, A	c 374	16	2.2	2586	9	US-09-906-700-235	Sequence 235, App
302	16	2.2	516	10	US-09-864-864-216	Sequence 216, App	c 375	16	2.2	2586	9	US-09-902-903-235	Sequence 235, App
c 303	16	2.2	524	10	US-09-864-761-8130	Sequence 8130, Ap	c 376	16	2.2	2586	9	US-09-903-749A-235	Sequence 235, App
c 304	16	2.2	553	9	US-09-918-995-13390	Sequence 13390, A	c 377	16	2.2	2586	9	US-09-903-786-235	Sequence 235, App
305	16	2.2	568	10	US-10-076-816-58	Sequence 58, Appl	c 378	16	2.2	2586	9	US-09-902-736-235	Sequence 235, App
306	16	2.2	569	10	US-09-734-017A-27	Sequence 27, Appl	c 379	16	2.2	2586	9	US-09-904-119-235	Sequence 235, App
c 307	16	2.2	569	10	US-09-864-761-9420	Sequence 9420, Ap	c 380	16	2.2	2586	9	US-09-904-956-235	Sequence 235, App
c 308	16	2.2	578	10	US-09-867-701-6141	Sequence 6141, Ap	c 381	16	2.2	2586	9	US-09-907-794-235	Sequence 235, App
c 309	16	2.2	579	9	US-09-738-626-1029	Sequence 1029, Ap	c 382	16	2.2	2586	9	US-10-063-518-7	Sequence 7, Appli
310	16	2.2	590	10	US-09-864-761-8014	Sequence 8014, Ap	c 383	16	2.2	2586	9	US-10-063-598-7	Sequence 7, Appli
c 311	16	2.2	594	10	US-09-864-761-16540	Sequence 16540, A	c 384	16	2.2	2586	9	US-10-227-693-7	Sequence 7, Appli

C 385	16	2.2	2586	9	US-09-902-692-235	Sequence 235, App	458	16	2.2	40645	9	US-10-216-441-3	Sequence 3, Appli
C 386	16	2.2	2586	9	US-09-903-520-235	Sequence 235, App	459	16	2.2	40645	10	US-09-818-656A-3	Sequence 3, Appli
C 387	16	2.2	2586	9	US-09-903-943-235	Sequence 235, App	C 460	16	2.2	48841	9	US-09-844-653-32	Sequence 32, Appl
C 388	16	2.2	2586	9	US-09-904-462-235	Sequence 235, App	C 461	16	2.2	60153	9	US-10-222-334-7	Sequence 7, Appli
C 389	16	2.2	2586	9	US-09-905-056-235	Sequence 235, App	C 462	16	2.2	65608	10	US-09-954-531-180	Sequence 180, App
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C 391	16	2.2	2586	9	US-09-904-553-235	Sequence 235, App	C 464	16	2.2	65608	10	US-09-962-833-119	Sequence 119, App
C 392	16	2.2	2586	9	US-09-905-381-235	Sequence 235, App	C 465	16	2.2	66686	10	US-09-736-960-86	Sequence 86, Appl
C 393	16	2.2	2586	9	US-09-909-084-235	Sequence 235, App	C 466	16	2.2	73467	9	US-10-237-859-3	Sequence 3, Appli
C 394	16	2.2	2586	9	US-10-063-567-7	Sequence 7, Appli	C 467	16	2.2	108359	9	US-10-151-807-3	Sequence 3, Appli
C 395	16	2.2	2586	9	US-09-905-088-235	Sequence 235, App	C 468	16	2.2	110096	10	US-09-880-107-1542	Sequence 1542, Ap
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C 397	16	2.2	2586	9	US-09-902-759-235	Sequence 235, App	C 470	16	2.2	116840	9	US-10-020-141-3	Sequence 3, Appli
C 398	16	2.2	2586	9	US-09-905-075-235	Sequence 235, App	C 471	16	2.2	130427	9	US-10-175-523-87	Sequence 87, Appl
C 399	16	2.2	2586	9	US-10-063-599-7	Sequence 7, Appli	C 472	16	2.2	150074	9	US-10-026-188-6	Sequence 6, Appli
C 400	16	2.2	2586	9	US-09-902-634-235	Sequence 235, App	C 473	16	2.2	170834	10	US-09-835-232-7	Sequence 7, Appli
C 401	16	2.2	2586	9	US-09-902-713-235	Sequence 235, App	C 474	16	2.2	249487	9	US-10-026-188-3	Sequence 3, Appli
C 402	16	2.2	2586	9	US-09-907-979-235	Sequence 235, App	C 475	16	2.2	513509	9	US-09-754-853A-4	Sequence 4, Appli
C 403	16	2.2	2586	9	US-10-063-595-7	Sequence 7, Appli	C 476	16	2.2	1691139	9	US-10-067-514-1	Sequence 1, Appli
C 404	16	2.2	2586	9	US-09-902-615-235	Sequence 235, App	C 477	16	2.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
C 405	16	2.2	2586	9	US-09-903-925-235	Sequence 235, App	C 478	16	2.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
C 406	16	2.2	2586	9	US-09-906-760A-235	Sequence 235, App	C 479	15	2.1	24	9	US-09-920-923-46	Sequence 46, Appl
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C 420	16	2.2	2985	10	US-09-764-853-221	Sequence 221, App	C 493	15	2.1	216	9	US-09-736-457-1210	Sequence 1210, Ap
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C 423	16	2.2	3282	10	US-09-864-864-298	Sequence 298, App	C 496	15	2.1	216	9	US-09-849-626-941	Sequence 941, App
C 424	16	2.2	3287	10	US-09-876-527-15	Sequence 15, Appl	C 497	15	2.1	216	9	US-09-849-626-1210	Sequence 1210, Ap
C 425	16	2.2	4203	9	US-09-764-891-7800	Sequence 7800, Ap	C 498	15	2.1	216	9	US-10-017-754-941	Sequence 941, App
C 426	16	2.2	4203	9	US-09-764-891-7801	Sequence 7801, Ap	C 499	15	2.1	216	9	US-10-017-754-1210	Sequence 1210, Ap
C 427	16	2.2	4465	9	US-09-984-842-1	Sequence 1, Appli	C 500	15	2.1	216	10	US-09-974-300-7706	Sequence 7706, Ap
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C 429	16	2.2	5087	10	US-09-931-704-3	Sequence 3, Appli	C 502	15	2.1	226	9	US-10-015-219-1594	Sequence 1594, Ap
C 430	16	2.2	5306	9	US-10-079-854-318	Sequence 318, App	C 503	15	2.1	226	10	US-09-777-564-1411	Sequence 1411, Ap
C 431	16	2.2	5306	10	US-09-764-878-318	Sequence 318, App	C 504	15	2.1	226	10	US-09-777-564-1594	Sequence 1594, Ap
C 432	16	2.2	6193	10	US-09-880-107-2197	Sequence 2197, Ap	C 505	15	2.1	227	9	US-10-244-633-38	Sequence 38, Appl
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C 435	16	2.2	8232	9	US-10-198-846-10976	Sequence 10976, A	C 508	15	2.1	245	10	US-09-983-965-2704	Sequence 2704, Ap
C 436	16	2.2	12930	9	US-10-214-023-4	Sequence 4, Appli	C 509	15	2.1	260	10	US-09-864-761-19724	Sequence 19724, A
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C 438	16	2.2	15186	10	US-09-822-860-3	Sequence 3, Appli	C 511	15	2.1	270	9	US-09-104-408-2	Sequence 2, Appli
C 439	16	2.2	19025	9	US-10-274-878-3	Sequence 3, Appli	C 512	15	2.1	270	10	US-10-074-095-166	Sequence 166, App
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C 445	16	2.2	31348	10	US-09-764-869-1259	Sequence 1259, Ap	C 518	15	2.1	283	9	US-10-244-633-37	Sequence 37, Appl
C 446	16	2.2	32192	9	US-10-092-1416	Sequence 1416, Ap	C 519	15	2.1	286	10	US-09-853-386-116	Sequence 116, App
C 447	16	2.2	32192	9	US-09-764-891-7945	Sequence 7945, Ap	C 520	15	2.1	299	10	US-09-867-701-3557	Sequence 3557, Ap
C 448	16	2.2	32192	9	US-09-764-891-8220	Sequence 8220, Ap	C 521	15	2.1	303	10	US-09-864-761-30389	Sequence 30389, A
C 449	16	2.2	32192	9	US-09-764-891-8319	Sequence 8319, Ap	C 522	15	2.1	309	9	US-09-796-692-6122	Sequence 6122, Ap
C 450	16	2.2	32192	10	US-09-764-847-1416	Sequence 1416, Ap	C 523	15	2.1	309	9	US-10-040-862-6122	Sequence 6122, Ap
C 451	16	2.2	32195	9	US-10-091-504-1605	Sequence 1605, App	C 524	15	2.1	310	9	US-09-918-995-18892	Sequence 18892, A
C 452	16	2.2	32195	9	US-10-125-540-611	Sequence 611, App	C 525	15	2.1	313	9	US-09-104-408-1	Sequence 1, Appli
C 453	16	2.2	32195	9	US-10-125-540-617	Sequence 617, App	C 526	15	2.1	313	10	US-09-867-701-3354	Sequence 3354, Ap
C 454	16	2.2	32195	10	US-09-764-870-611	Sequence 611, App	C 527	15	2.1	321	10	US-09-822-830A-353	Sequence 353, App
C 455	16	2.2	32195	10	US-09-764-870-617	Sequence 617, App	C 528	15	2.1	321	10	US-09-867-701-3464	Sequence 3464, Ap
C 456	16	2.2	32195	10	US-09-764-869-1605	Sequence 1605, Ap	C 529	15	2.1	331	10	US-09-912-447-19	Sequence 19, Appl
C 457	16	2.2	33023	10	US-09-880-107-3350	Sequence 3350, Ap	C 530	15	2.1	334	9	US-09-912-935-2	Sequence 2, Appli

C 531	15	2.1	341	9	US-09-764-891-1901	Sequence 1901, Ap	C 604	15	2.1	455	9	US-09-918-995-26972	Sequence 26972, A
C 532	15	2.1	341	10	US-09-983-965-3557	Sequence 3557, Ap	C 605	15	2.1	455	10	US-09-864-761-5426	Sequence 5426, Ap
C 533	15	2.1	344	10	US-09-294-903B-109	Sequence 109, Ap	C 606	15	2.1	455	10	US-09-864-761-13822	Sequence 13822, A
C 534	15	2.1	349	9	US-09-918-995-18085	Sequence 18085, A	C 607	15	2.1	458	9	US-09-918-995-13792	Sequence 13792, A
C 535	15	2.1	353	10	US-09-983-965-304	Sequence 304, Ap	C 608	15	2.1	458	9	US-09-918-995-14980	Sequence 14980, A
C 536	15	2.1	362	9	US-10-079-623-184	Sequence 184, Ap	C 609	15	2.1	458	9	US-09-918-995-26443	Sequence 26443, A
C 537	15	2.1	363	9	US-09-918-995-30092	Sequence 30092, A	C 610	15	2.1	458	10	US-09-864-761-364	Sequence 364, App
C 538	15	2.1	366	9	US-09-912-935-1	Sequence 1, Appl	C 611	15	2.1	459	9	US-09-918-995-12482	Sequence 12482, A
C 539	15	2.1	367	9	US-09-918-995-30228	Sequence 30228, Ap	C 612	15	2.1	461	9	US-09-918-995-11839	Sequence 11839, A
C 540	15	2.1	368	10	US-09-983-965-38856	Sequence 38856, Ap	C 613	15	2.1	463	10	US-09-864-761-14576	Sequence 14576, A
C 541	15	2.1	371	10	US-09-864-761-250	Sequence 250, App	C 614	15	2.1	463	10	US-09-878-574-4262	Sequence 4262, Ap
C 542	15	2.1	372	9	US-09-918-995-37696	Sequence 37696, A	C 615	15	2.1	464	9	US-09-918-995-28838	Sequence 28838, A
C 543	15	2.1	376	10	US-09-960-352-585	Sequence 585, App	C 616	15	2.1	464	9	US-09-918-995-32373	Sequence 32373, A
C 544	15	2.1	379	10	US-09-864-761-2943	Sequence 2943, Ap	C 617	15	2.1	465	9	US-09-796-692-3819	Sequence 3819, Ap
C 545	15	2.1	384	9	US-09-918-995-34217	Sequence 34217, A	C 618	15	2.1	465	9	US-10-040-862-3819	Sequence 3819, Ap
C 546	15	2.1	387	9	US-09-918-995-23224	Sequence 23224, A	C 619	15	2.1	467	9	US-09-907-969-526	Sequence 526, App
C 547	15	2.1	389	10	US-09-960-352-5350	Sequence 5350, Ap	C 620	15	2.1	468	9	US-10-101-464A-30	Sequence 30, Appl
C 548	15	2.1	397	9	US-09-764-868-402	Sequence 402, App	C 621	15	2.1	468	9	US-09-907-969-557	Sequence 557, App
C 549	15	2.1	397	9	US-09-918-995-6014	Sequence 6014, Ap	C 622	15	2.1	469	9	US-09-918-995-2440	Sequence 2440, Ap
C 550	15	2.1	397	9	US-10-198-846-12103	Sequence 12103, A	C 623	15	2.1	469	9	US-09-918-995-2804	Sequence 2804, Ap
C 551	15	2.1	401	9	US-09-946-807-917	Sequence 917, App	C 624	15	2.1	469	9	US-09-918-995-22877	Sequence 22877, A
C 552	15	2.1	401	10	US-09-795-668-917	Sequence 917, App	C 625	15	2.1	469	9	US-09-907-969-525	Sequence 525, App
C 553	15	2.1	401	10	US-09-795-668-917	Sequence 917, App	C 626	15	2.1	470	9	US-09-864-761-6264	Sequence 6264, Ap
C 554	15	2.1	402	9	US-09-738-626-1420	Sequence 1420, Ap	C 627	15	2.1	470	10	US-09-864-761-6468	Sequence 6468, Ap
C 555	15	2.1	405	9	US-10-060-036-2325	Sequence 2325, Ap	C 628	15	2.1	472	9	US-09-918-995-31690	Sequence 31690, A
C 556	15	2.1	406	9	US-09-918-995-37082	Sequence 37082, A	C 629	15	2.1	475	9	US-10-101-464A-434	Sequence 434, App
C 557	15	2.1	407	9	US-10-060-036-2835	Sequence 2835, Ap	C 630	15	2.1	476	9	US-09-918-995-26779	Sequence 26779, A
C 558	15	2.1	408	9	US-09-918-995-10555	Sequence 10555, A	C 631	15	2.1	477	9	US-09-918-995-26526	Sequence 26526, A
C 559	15	2.1	408	10	US-09-867-701-1147	Sequence 1147, Ap	C 632	15	2.1	477	10	US-09-864-761-593	Sequence 593, App
C 560	15	2.1	410	9	US-09-918-995-3946	Sequence 3946, Ap	C 633	15	2.1	478	10	US-09-864-761-456	Sequence 456, App
C 561	15	2.1	410	9	US-10-060-036-2134	Sequence 2134, Ap	C 634	15	2.1	482	9	US-09-918-995-24979	Sequence 24979, A
C 562	15	2.1	410	10	US-09-783-590-8693	Sequence 8693, Ap	C 635	15	2.1	482	9	US-09-918-995-31211	Sequence 31211, A
C 563	15	2.1	410	10	US-09-867-701-5316	Sequence 5316, Ap	C 636	15	2.1	484	9	US-10-146-574-5	Sequence 5, Appl
C 564	15	2.1	412	9	US-09-736-457-1047	Sequence 1047, Ap	C 637	15	2.1	484	9	US-10-091-483-66	Sequence 66, Appl
C 565	15	2.1	412	9	US-09-902-941-1047	Sequence 1047, Ap	C 638	15	2.1	484	9	US-10-079-854-220	Sequence 220, App
C 566	15	2.1	412	9	US-09-849-626-1047	Sequence 1047, Ap	C 639	15	2.1	484	10	US-09-764-878-220	Sequence 220, App
C 567	15	2.1	412	9	US-10-017-754-1047	Sequence 1047, Ap	C 640	15	2.1	484	10	US-09-764-878-222	Sequence 222, App
C 568	15	2.1	416	9	US-09-918-995-1517	Sequence 1517, Ap	C 641	15	2.1	484	10	US-09-764-846-66	Sequence 66, Appl
C 569	15	2.1	416	9	US-09-918-995-6441	Sequence 6441, Ap	C 642	15	2.1	485	9	US-09-907-969-544	Sequence 544, App
C 570	15	2.1	418	9	US-09-796-692-5872	Sequence 5872, Ap	C 643	15	2.1	485	9	US-09-918-995-14197	Sequence 14197, A
C 571	15	2.1	418	9	US-10-040-862-5872	Sequence 5872, Ap	C 644	15	2.1	485	9	US-09-918-995-31503	Sequence 31503, A
C 572	15	2.1	418	9	US-10-198-846-3352	Sequence 3352, Ap	C 645	15	2.1	487	10	US-09-864-761-3465	Sequence 3465, Ap
C 573	15	2.1	419	9	US-09-796-692-7030	Sequence 7030, Ap	C 646	15	2.1	489	10	US-09-918-995-2860	Sequence 2860, Ap
C 574	15	2.1	419	10	US-10-040-862-7030	Sequence 7030, Ap	C 647	15	2.1	491	10	US-09-880-107-1399	Sequence 1399, Ap
C 575	15	2.1	421	9	US-09-960-352-6987	Sequence 6987, Ap	C 648	15	2.1	493	9	US-10-040-739-542	Sequence 542, App
C 576	15	2.1	421	9	US-09-918-995-35355	Sequence 35355, A	C 649	15	2.1	493	9	US-09-918-995-14197	Sequence 14197, A
C 577	15	2.1	422	9	US-09-918-995-33996	Sequence 33996, A	C 650	15	2.1	495	9	US-09-918-995-20005	Sequence 20005, A
C 578	15	2.1	423	9	US-09-918-995-196	Sequence 196, App	C 651	15	2.1	503	9	US-09-918-995-23167	Sequence 23167, A
C 579	15	2.1	426	9	US-10-074-095-102	Sequence 102, App	C 652	15	2.1	511	9	US-10-198-846-10633	Sequence 10633, A
C 580	15	2.1	426	10	US-09-764-860-102	Sequence 102, App	C 653	15	2.1	519	10	US-09-864-761-16460	Sequence 16460, A
C 581	15	2.1	426	10	US-09-917-800A-279	Sequence 279, App	C 654	15	2.1	519	10	US-09-864-761-16485	Sequence 16485, A
C 582	15	2.1	427	10	US-09-864-761-5302	Sequence 5302, Ap	C 655	15	2.1	520	9	US-09-918-995-32839	Sequence 32839, A
C 583	15	2.1	430	9	US-09-912-935-1502	Sequence 15, Appl	C 656	15	2.1	521	9	US-09-918-995-30541	Sequence 30541, A
C 584	15	2.1	432	10	US-09-864-761-32943	Sequence 32943, A	C 657	15	2.1	524	10	US-09-864-761-13563	Sequence 13563, A
C 585	15	2.1	432	10	US-09-983-965-4149	Sequence 4149, Ap	C 658	15	2.1	524	10	US-09-920-300A-176	Sequence 176, App
C 586	15	2.1	433	9	US-10-015-219-799	Sequence 799, App	C 659	15	2.1	524	12	US-10-033-528-176	Sequence 176, App
C 587	15	2.1	433	10	US-09-777-564-799	Sequence 799, App	C 660	15	2.1	524	10	US-09-864-761-17383	Sequence 17383, A
C 588	15	2.1	436	9	US-09-918-995-34946	Sequence 34946, A	C 661	15	2.1	532	9	US-10-040-739-216	Sequence 216, App
C 589	15	2.1	439	10	US-09-815-343-1400	Sequence 1400, Ap	C 662	15	2.1	532	10	US-09-764-864-723	Sequence 723, App
C 590	15	2.1	440	9	US-09-918-995-35338	Sequence 35338, A	C 663	15	2.1	533	10	US-09-893-737-29	Sequence 29, Appl
C 591	15	2.1	441	9	US-09-907-969-43	Sequence 13, Appl	C 664	15	2.1	542	9	US-09-937-279-157	Sequence 157, App
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C 593	15	2.1	442	10	US-09-864-761-4681	Sequence 4681, Ap	C 666	15	2.1	543	9	US-09-525-978B-37	Sequence 37, Appl
C 594	15	2.1	444	9	US-09-918-995-20729	Sequence 20729, A	C 667	15	2.1	543	9	US-09-373-658-96	Sequence 96, Appl
C 595	15	2.1	445	10	US-09-880-107-2584	Sequence 2584, Ap	C 668	15	2.1	543	9	US-10-198-846-4105	Sequence 4105, Ap
C 596	15	2.1	446	9	US-09-918-995-35842	Sequence 35842, A	C 669	15	2.1	543	10	US-09-864-761-15325	Sequence 15325, A
C 597	15	2.1	447	10	US-09-864-761-681	Sequence 681, App	C 670	15	2.1	548	10	US-09-864-761-6861	Sequence 6861, Ap
C 598	15	2.1	447	10	US-09-998-598-925	Sequence 925, App	C 671	15	2.1	548	10	US-09-864-761-13461	Sequence 13461, A
C 599	15	2.1	449	10	US-09-864-761-11579	Sequence 11579, A	C 672	15	2.1	548	10		
C 600	15	2.1	451	9	US-10-114-666-28	Sequence 28, Appl	C 673	15	2.1	548	10		
C 601	15	2.1	451	9	US-09-895-828-28	Sequence 28, Appl	C 674	15	2.1	548	10		
C 602	15	2.1	453	9	US-09-918-995-14380	Sequence 14380, A	C 675	15	2.1	548	10		
C 603	15	2.1	453	10	US-09-764-877-367	Sequence 367, App	C 676	15	2.1	548	10		

677	15	2.1	549	9	US-10-060-036-2227	Sequence 2227, Ap	750	15	2.1	1049	9	US-10-007-280A-111	Sequence 111, App
678	15	2.1	550	10	US-09-864-761-12901	Sequence 12901, A	c 751	15	2.1	1051	9	US-10-037-270-312	Sequence 312, App
679	15	2.1	556	10	US-09-864-761-8509	Sequence 8509, Ap	c 752	15	2.1	1053	9	US-09-940-244-393	Sequence 393, App
680	15	2.1	557	9	US-09-918-995-14220	Sequence 14220, A	c 753	15	2.1	1060	10	US-09-791-171-113	Sequence 11, Appl
681	15	2.1	560	9	US-09-796-692-5841	Sequence 5841, Ap	754	15	2.1	1064	9	US-09-974-879-124	Sequence 124, App
682	15	2.1	560	9	US-10-040-862-5841	Sequence 5841, Ap	755	15	2.1	1064	9	US-09-305-736-126	Sequence 126, App
683	15	2.1	567	9	US-09-822-846-440	Sequence 440, App	756	15	2.1	1071	9	US-10-252-340-1	Sequence 1, Appl
684	15	2.1	569	10	US-09-867-550-1483	Sequence 1483, Ap	c 757	15	2.1	1076	9	US-10-176-847-11	Sequence 11, Appl
685	15	2.1	585	9	US-09-918-995-12161	Sequence 12161, A	c 758	15	2.1	1080	9	US-09-738-626-1741	Sequence 1741, Ap
686	15	2.1	585	10	US-09-864-761-9771	Sequence 9771, Ap	c 759	15	2.1	1107	9	US-10-174-590-595	Sequence 595, App
687	15	2.1	591	9	US-10-040-739-1442	Sequence 1442, Ap	c 760	15	2.1	1107	9	US-10-176-758-595	Sequence 595, App
688	15	2.1	593	10	US-09-864-761-9799	Sequence 9799, Ap	c 761	15	2.1	1107	9	US-10-175-737-595	Sequence 595, App
689	15	2.1	595	10	US-09-864-761-9917	Sequence 9917, Ap	c 762	15	2.1	1107	9	US-10-173-706-595	Sequence 595, App
690	15	2.1	616	10	US-09-878-574-4567	Sequence 4567, Ap	c 763	15	2.1	1107	9	US-10-175-738-595	Sequence 595, App
691	15	2.1	635	9	US-09-791-932-37	Sequence 37, Appl	c 764	15	2.1	1107	9	US-10-175-752-595	Sequence 595, App
692	15	2.1	644	9	US-09-788-773-1	Sequence 1, Appl	c 765	15	2.1	1107	9	US-10-176-482-595	Sequence 595, App
693	15	2.1	652	9	US-09-373-658-94	Sequence 94, Appl	c 766	15	2.1	1107	9	US-10-176-757-595	Sequence 595, App
694	15	2.1	654	10	US-09-974-300-8181	Sequence 8181, Ap	c 767	15	2.1	1107	9	US-10-176-913-595	Sequence 595, App
695	15	2.1	661	9	US-10-198-846-7819	Sequence 7819, Ap	c 768	15	2.1	1107	9	US-10-180-552-595	Sequence 595, App
696	15	2.1	665	9	US-08-832-139-22	Sequence 22, Appl	c 769	15	2.1	1107	9	US-10-180-557-595	Sequence 595, App
697	15	2.1	667	9	US-08-771-035A-18	Sequence 18, Appl	c 770	15	2.1	1107	9	US-10-173-700-595	Sequence 595, App
698	15	2.1	710	9	US-10-198-846-8071	Sequence 8071, Ap	c 771	15	2.1	1107	9	US-10-174-572-595	Sequence 595, App
699	15	2.1	713	9	US-10-091-483-136	Sequence 136, App	c 772	15	2.1	1107	9	US-10-174-579-595	Sequence 595, App
700	15	2.1	713	10	US-09-764-846-136	Sequence 136, App	c 773	15	2.1	1107	9	US-10-174-582-595	Sequence 595, App
701	15	2.1	719	10	US-09-964-824A-276	Sequence 276, App	c 774	15	2.1	1107	9	US-10-174-588-595	Sequence 595, App
702	15	2.1	720	9	US-10-206-901B-2	Sequence 2, Appl	c 775	15	2.1	1107	9	US-10-175-739-595	Sequence 595, App
703	15	2.1	739	10	US-09-918-171A-10	Sequence 10, Appl	c 776	15	2.1	1107	9	US-10-175-740-595	Sequence 595, App
704	15	2.1	759	10	US-09-815-242-7848	Sequence 7848, Ap	c 777	15	2.1	1107	9	US-10-175-743-595	Sequence 595, App
705	15	2.1	763	9	US-09-056-019-19	Sequence 19, Appl	c 778	15	2.1	1107	9	US-10-176-488-595	Sequence 595, App
706	15	2.1	786	9	US-09-738-626-1361	Sequence 1361, Ap	c 779	15	2.1	1107	9	US-10-176-492-595	Sequence 595, App
707	15	2.1	817	9	US-10-171-311-72	Sequence 72, Appl	c 780	15	2.1	1107	9	US-10-176-747-595	Sequence 595, App
708	15	2.1	819	10	US-09-918-686-5	Sequence 5, Appl	c 781	15	2.1	1107	9	US-10-176-750-595	Sequence 595, App
709	15	2.1	830	12	US-10-062-994-11	Sequence 11, Appl	c 782	15	2.1	1107	9	US-10-176-985-595	Sequence 595, App
710	15	2.1	830	12	US-10-062-994-11	Sequence 11, Appl	c 783	15	2.1	1107	9	US-10-176-991-595	Sequence 595, App
711	15	2.1	831	10	US-09-731-872-49	Sequence 49, Appl	c 784	15	2.1	1107	9	US-10-176-992-595	Sequence 595, App
712	15	2.1	832	10	US-09-731-872-48	Sequence 48, Appl	c 785	15	2.1	1107	9	US-10-176-993-595	Sequence 595, App
713	15	2.1	836	9	US-09-954-531-126	Sequence 126, App	c 786	15	2.1	1107	9	US-10-176-993-595	Sequence 595, App
714	15	2.1	836	9	US-09-954-531-350	Sequence 350, App	c 787	15	2.1	1107	9	US-10-184-658-595	Sequence 595, App
715	15	2.1	836	9	US-09-997-279-225	Sequence 225, App	c 788	15	2.1	1107	9	US-10-173-695-595	Sequence 595, App
716	15	2.1	836	9	US-09-997-279-226	Sequence 226, App	c 789	15	2.1	1107	9	US-10-173-697-595	Sequence 595, App
717	15	2.1	836	9	US-09-997-279-227	Sequence 227, App	c 790	15	2.1	1107	9	US-10-173-705-595	Sequence 595, App
718	15	2.1	836	10	US-09-954-456-1113	Sequence 1113, Ap	c 791	15	2.1	1107	9	US-10-174-576-595	Sequence 595, App
719	15	2.1	836	10	US-09-954-456-1788	Sequence 1788, Ap	c 792	15	2.1	1107	9	US-10-174-585-595	Sequence 595, App
720	15	2.1	836	10	US-09-880-107-1615	Sequence 1615, Ap	c 793	15	2.1	1107	9	US-10-174-586-595	Sequence 595, App
721	15	2.1	836	10	US-09-967-768A-121	Sequence 121, App	c 794	15	2.1	1107	9	US-10-175-747-595	Sequence 595, App
722	15	2.1	838	9	US-09-997-279-215	Sequence 215, App	c 795	15	2.1	1107	9	US-10-176-481-595	Sequence 595, App
723	15	2.1	838	10	US-09-813-358-215	Sequence 215, App	c 796	15	2.1	1107	9	US-10-176-485-595	Sequence 595, App
724	15	2.1	842	12	US-10-062-994-3	Sequence 3, Appl	c 797	15	2.1	1107	9	US-10-176-487-595	Sequence 595, App
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; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
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US-10-098-841-80

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; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
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; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
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; Publication No. US20030073623A1
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; FILE REFERENCE: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
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US-09-918-995-2699

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RESULT 6
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; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
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; NAME/KEY: misc feature
; LOCATION: (352)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (357)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (364)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (368)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (370)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (371)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (380)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (385)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (399)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (408)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (418)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
; LOCATION: (420)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (430)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (437)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (441)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (447)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (451)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (454)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (482)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-10224
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Query Match 2.5%; Score 18; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 497 CCTGGCCCCAGGCCCCAG 514
Db 278 CCTGGCCCCAGGCCCCAG 261
```

## RESULT 7

```
US-10-198-846-10677
; Sequence 10677, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10677
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 829, 845, 846, 847, 848
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-10677
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Query Match 2.5%; Score 18; DB 9; Length 848;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 288 CAGATGTCTTCCTGGGC 305
Db 206 CAGATGTCTTCCTGGGC 223
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RESULT 8  
US-10-198-846-1071  
; Sequence 1071, Application US/10198846  
; Publication No. US2003009974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1071  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 3, 5, 6, 7, 10, 28, 348, 429, 469, 517, 539, 573, 576, 583,  
; LOCATION: 593, 616, 645, 685, 718, 761, 769, 773, 791, 800, 821, 825,  
; LOCATION: 828, 836, 845, 850, 858, 860, 867, 879, 881, 884, 886, 889,  
; LOCATION: 893  
; OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-1071

Query Match 2.5%; Score 18; DB 9; Length 893;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 288 CAGATGCTCTCCCTGGGC 305  
DB 104 CAGATGCTCTCCCTGGGC 121

RESULT 9  
US-09-822-830A-8  
; Sequence 8, Application US/09822830A  
; Patent No. US20020142952A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics Institute, Inc.  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fachtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulkota, Kamalakur  
; APPLICANT: Graham, James R.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6402  
; CURRENT APPLICATION NUMBER: US/09/822,830A  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195,604  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 631  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 2144  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-830A-8

Query Match 2.5%; Score 18; DB 10; Length 2144;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 CAGATGCTCTCCCTGGGC 305  
DB 2127 CAGATGCTCTCCCTGGGC 2144  
  
RESULT 10  
US-09-925-301-2  
; Sequence 2, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2662  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2662)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-2

Query Match 2.5%; Score 18; DB 10; Length 2662;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 489 GCACAGAGCCTGGGCCCA 506  
DB 1184 GCACAGAGCCTGGGCCCA 1201

RESULT 11  
US-09-764-868-1440  
; Sequence 1440, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1440  
; LENGTH: 11336  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4205)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-868-1440

Query Match 2.5%; Score 18; DB 9; Length 11336;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 496 GCCTGGCCCCAGGCCCA 513  
DB 1073 GCCTGGCCCCAGGCCCA 1090

RESULT 12

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US-09-939-964-1/c
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-08-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match      2.5%; Score 18; DB 9; Length 536165;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      632 CGCATCACCCTCACCAGG 649
Db      360500 CGCATCACCCTCACCAGG 360483

RESULT 13
US-09-783-590-2233
; Sequence 2233, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2233
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (82)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (99)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
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; LOCATION: (192)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (205)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (259)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (274)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (303)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (308)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (309)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (318)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-2233
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Query Match      2.4%; Score 17; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      495 AGCCTGGCCCCAGGCC 511
Db      39 AGCCTGGCCCCAGGCC 55
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RESULT 14
US-09-803-719-1712/c
; Sequence 1712, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002
; CURRENT APPLICATION NUMBER: US/09/803,719
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1712
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; LENGTH: 350  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-803-719-1712

Query Match 2.4%; Score 17; DB 9; Length 350;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 527 TCCTGCCCTTCCTCTG 543  
|||||  
Db 217 TCCTGCCCTTCCTCTG 201

## RESULT 15

US-09-933-797-145/c  
; Sequence 145, Application US/09933797  
; Patent No. US20020155119A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert A. Sikes et al.  
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital  
; FILE REFERENCE: 9901-007-999  
; CURRENT APPLICATION NUMBER: US/09/933,797  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: US/09/482,933  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: PCT/US99/10746  
; PRIOR FILING DATE: 1999-05/14  
; PRIOR APPLICATION NUMBER: 60/085,383  
; PRIOR FILING DATE: 1998-05-14  
; NUMBER OF SEQ ID NOS: 811  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 145  
; LENGTH: 425  
; TYPE: DNA  
; ORGANISM: Murine  
US-09-933-797-145

Query Match 2.4%; Score 17; DB 9; Length 425;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 CCAGCGCGCCGATG 252  
|||||  
Db 391 CCAGCGCGCCGATG 375

Search completed: June 17, 2003, 09:59:46  
Job time : 87.5878 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 11:19:02 ; Search time 812.5 Seconds  
(without alignments)  
14252.028 Million cell updates/sec

Title: US-09-513-888C-1\_COPY\_7806\_8520

Perfect score: 715

Sequence: 1 actgcccacagagacagag.....ttccctcctagctctccag 715

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

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4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	38.9	925	12	BF338502
2	260	36.4	848	9	AL566277
3	155	21.7	326	9	AL047147
4	150	21.0	622	10	AV751885
5	142	19.9	448	14	R88008
6	99	13.8	495	14	N42784

80	19	2.7	684	10	BB866290	BB866290	BB866290	153	18	2.5	438	9	AI751163	AI751163	cn08b03.x
81	19	2.7	684	10	BE309763	BE309763	601094030	154	18	2.5	439	12	BG691697	BG691697	BG691697 340973 BA
82	19	2.7	694	10	BE133024	BE133024	601150380	155	18	2.5	434	13	BI014521	BI014521	BI014521 CM3-ET009
83	19	2.7	721	13	BI912351	BI912351	603067696	156	18	2.5	454	13	BI285833	BI285833	BI285833 CM3-ET009
84	19	2.7	722	12	BG820499	BG820499	602782819	157	18	2.5	456	10	BE292083	BE292083	BE292083 601085811
85	19	2.7	722	17	AO371661	AO371661	RPCI11-14	158	18	2.5	458	12	BF229412	BF229412	BF229412 MR1-CI002
86	19	2.7	726	13	BI599897	BI599897	603246847	159	18	2.5	461	13	BJ273862	BJ273862	BJ273862 BJ273862
87	19	2.7	744	17	AG187426	AG187426	Pan trogl	160	18	2.5	465	14	RO1367	RO1367	RO1367 ye81e06.r1
88	19	2.7	747	17	BH024855	BH024855	RPCI-24-3	161	18	2.5	466	17	AQ667259	AQ667259	AQ667259 HS-2109 A
89	19	2.7	760	17	AG032084	AG032084	Pan trogl	162	18	2.5	472	12	BF394965	BF394965	BF394965 UI-R-CA0-
90	19	2.7	788	12	BG163536	BG163536	602338563	163	18	2.5	479	17	AQ112930	AQ112930	AQ112930 CIT-RSP-2
91	19	2.7	851	14	BQ948941	BQ948941	AGENCOURT	164	18	2.5	481	13	BJ201155	BJ201155	BJ201155 DKZP4341
92	19	2.7	870	12	BG395237	BG395237	602457748	165	18	2.5	493	9	AL045237	AL045237	AL045237 DKZP4341
93	19	2.7	880	14	QO213511	QO213511	AGENCOURT	166	18	2.5	491	17	AQ522959	AQ522959	AQ522959 HS-5202 A
94	19	2.7	884	12	BG396457	BG396457	602459175	167	18	2.5	504	17	AQ212184	AQ212184	AQ212184 HS-3073 A
95	19	2.7	884	10	BE231225	BE231225	HVSMG001	168	18	2.5	505	17	AQ055922	AQ055922	AQ055922 CIT-RSP-2
96	19	2.7	884	14	BQ649665	BQ649665	AGENCOURT	169	18	2.5	508	10	AM106768	AM106768	AM106768 um33d04.Y
97	19	2.7	901	14	BQ679778	BQ679778	AGENCOURT	170	18	2.5	510	10	BE480668	BE480668	BE480668 165861 BA
98	19	2.7	906	12	BG330663	BG330663	602430070	171	18	2.5	515	10	BE430822	BE430822	BE430822 SUN006.B0
99	19	2.7	920	14	BQ888031	BQ888031	AGENCOURT	172	18	2.5	517	12	BF591215	BF591215	BF591215 7b43e12.x
100	19	2.7	923	14	EQ927585	EQ927585	AGENCOURT	173	18	2.5	519	12	BF192274	BF192274	BF192274 244037 MA
101	19	2.7	929	12	BG174319	BG174319	602336327	174	18	2.5	519	13	BI345001	BI345001	BI345001 373677 MA
102	19	2.7	945	14	BQ649665	BQ649665	AGENCOURT	175	18	2.5	519	17	AQ810155	AQ810155	AQ810155 HS-4787 A
103	19	2.7	949	12	BF314376	BF314376	601901125	176	18	2.5	526	13	BJ273905	BJ273905	BJ273905 RPCI-11-3
104	19	2.7	966	14	BQ668492	BQ668492	AGENCOURT	177	18	2.5	526	17	AQ544183	AQ544183	AQ544183 RPCI-11-3
105	19	2.7	1019	12	BG565019	BG565019	602583807	178	18	2.5	527	9	AL041355	AL041355	AL041355 DKZP434A
106	19	2.7	1088	12	BF345938	BF345938	602017942	179	18	2.5	536	10	AM049386	AM049386	AM049386 UI-M-BH1-
107	19	2.7	1094	12	BF314647	BF314647	601900678	180	18	2.5	537	12	BG512838	BG512838	BG512838 dad63a09.
108	19	2.7	1117	12	BF311014	BF311014	601988330	181	18	2.5	537	17	AZ626768	AZ626768	AZ626768 1M0467007
109	19	2.7	1118	12	BF348179	BF348179	602022085	182	18	2.5	539	12	BF705614	BF705614	BF705614 228134 MA
110	18	2.5	125	17	AZ252472	AZ252472	RPCI-23-2	183	18	2.5	540	13	BI010491	BI010491	BI010491 MR2-EN009
111	18	2.5	189	14	FL5970	FL5970	HSPD00446 H	184	18	2.5	543	13	BJ194728	BJ194728	BJ194728 BJ194728
112	18	2.5	191	14	BQ380476	BQ380476	RC3-UT008	185	18	2.5	544	9	AL672947	AL672947	AL672947 AL672947
113	18	2.5	243	9	AU059880	AU059880	AU059880	186	18	2.5	544	14	BQ211679	BQ211679	BQ211679 UI-R-DZ1-
114	18	2.5	253	10	AM823661	AM823661	uf57c11.x	187	18	2.5	546	10	AM951566	AM951566	AM951566 EST363636
115	18	2.5	264	10	BE579462	BE579462	BB579462	188	18	2.5	549	12	BF705694	BF705694	BF705694 244538 MA
116	18	2.5	275	17	AO637463	AO637463	RPCI-11-4	189	18	2.5	549	17	AQ174681	AQ174681	AQ174681 HS-3205 B
117	18	2.5	288	10	BE202421	BE202421	BB202421	190	18	2.5	550	17	AZ298218	AZ298218	AZ298218 RPCI-23-1
118	18	2.5	297	10	BE031980	BE031980	130769 MA	191	18	2.5	550	17	AZ467636	AZ467636	AZ467636 1M0279H10
119	18	2.5	298	10	AM242848	AM242848	xm26904.x	192	18	2.5	553	9	AL676383	AL676383	AL676383
120	18	2.5	308	9	AA789342	AA789342	vv93a09.r	193	18	2.5	554	13	BJ169644	BJ169644	BJ169644 BJ169644
121	18	2.5	312	10	AM076439	AM076439	683018C04	194	18	2.5	555	12	BE845925	BE845925	BE845925 232597 BA
122	18	2.5	313	10	BB549601	BB549601	BB549601	195	18	2.5	555	13	BJ424293	BJ424293	BJ424293 BJ424293
123	18	2.5	314	10	BB194657	BB194657	BB194657	196	18	2.5	555	13	AQ925729	AQ925729	AQ925729 RPCI-23-2
124	18	2.5	323	9	AA372341	AA372341	ESR84430	197	18	2.5	565	17	AQ321266	AQ321266	AQ321266 RPCI11-10
125	18	2.5	341	9	AI324098	AI324098	mh06910.x	198	18	2.5	569	13	BJ396817	BJ396817	BJ396817 BJ396817
126	18	2.5	341	9	AA344167	AA344167	EST50077	199	18	2.5	572	12	BG512119	BG512119	BG512119 G8d25e12.
127	18	2.5	345	10	AM183341	AM183341	xj76c12.x	200	18	2.5	579	13	BJ005471	BJ005471	BJ005471 370643 MA
128	18	2.5	353	10	AM336125	AM336125	23681 MAR	201	18	2.5	579	13	BJ005471	BJ005471	BJ005471 BJ005471
129	18	2.5	353	17	AQ018416	AQ018416	CIT-RSP-2	202	18	2.5	579	13	BJ172742	BJ172742	BJ172742 BJ172742
130	18	2.5	359	9	AL628789	AL628789	AL628789	203	18	2.5	582	17	AZ653781	AZ653781	AZ653781 1M0527C10
131	18	2.5	365	13	BI040069	BI040069	CM4-N7028	204	18	2.5	586	13	BJ009877	BJ009877	BJ009877 BJ009877
132	18	2.5	374	13	BM432599	BM432599	1UEJ11F3.	205	18	2.5	590	17	BH036367	BH036367	BH036367 RPCI-24-2
133	18	2.5	375	13	BM431973	BM431973	1UEJ11F3.	206	18	2.5	592	9	AL682686	AL682686	AL682686 AL682686
134	18	2.5	375	13	BM432641	BM432641	1UEJ12B7.	207	18	2.5	593	9	AL595604	AL595604	AL595604 AL595604
135	18	2.5	377	13	BM481901	BM481901	534522 MA	208	18	2.5	593	17	AQ544199	AQ544199	AQ544199 RPCI-11-3
136	18	2.5	387	13	BI334653	BI334653	602998609	209	18	2.5	595	13	BI849747	BI849747	BI849747 477676 MA
137	18	2.5	395	10	BE592140	BE592140	WS185.A0	210	18	2.5	597	17	AQ162155	AQ162155	AQ162155 mxb0011L
138	18	2.5	399	9	AI503281	AI503281	wn13d09.x	211	18	2.5	600	17	AQ473623	AQ473623	AQ473623 CITRBI-E1-
139	18	2.5	400	17	AQ090077	AQ090077	HS-3000 B	212	18	2.5	601	10	BE588741	BE588741	BE588741 194358 BA
140	18	2.5	400	17	BH366290	BH366290	CH230-75H	213	18	2.5	603	12	BG08756	BG08756	BG08756 Talr1171A
141	18	2.5	402	10	BE480670	BE480670	165863 BA	214	18	2.5	611	13	BI966577	BI966577	BI966577 id56a04.x
142	18	2.5	405	13	BM46118	BM46118	1L13G8.ab	215	18	2.5	627	12	BF530123	BF530123	BF530123 602040302
143	18	2.5	405	17	AZ261683	AZ261683	RPCI-23-1	216	18	2.5	629	13	BI159765	BI159765	BI159765 602863520
144	18	2.5	406	12	BF870809	BF870809	CM3-ET009	217	18	2.5	632	9	AA625525	AA625525	AA625525 af72f06.r
145	18	2.5	407	17	AQ082223	AQ082223	RPCI11-55	218	18	2.5	637	9	AL683185	AL683185	AL683185 AL683185
146	18	2.5	412	12	BF955446	BF955446	MR4-NN018	219	18	2.5	639	14	BQ195125	BQ195125	BQ195125 UI-R-CN1-
147	18	2.5	413	9	AA027233	AA027233	zj99a12.s	220	18	2.5	642	10	AV733321	AV733321	AV733321 AV733321
148	18	2.5	428	10	AA297549	AA297549	UI-H-EW0-	221	18	2.5	642	17	BH109550	BH109550	BH109550 RPCI-24-2
149	18	2.5	431	9	AL044298	AL044298	DKZP434N	222	18	2.5	644	17	BH350360	BH350360	BH350360 CH230-320
150	18	2.5	432	10	BE487382	BE487382	176094 BA	223	18	2.5	647	9	AI147208	AI147208	AI147208 qa89b12.x
151	18	2.5	433	17	FR0017362	FR0017362	FR0017362	224	18	2.5	654	13	BJ243844	BJ243844	BJ243844 BJ243844
152	18	2.5	435	13	BI065452	BI065452	pgfin.pk0	225	18	2.5	657	12	BG770038	BG770038	BG770038 602745156



226	18	2.5	660	10	AV610110	AV610110 AV610110	c 299	18	2.5	921	17	CNS049VL	AL281082 Tetraodon
227	18	2.5	663	9	AL790318	AL790318 AL790318	300	18	2.5	924	12	BG335921	BG335921 602404653
228	18	2.5	663	13	BJ168051	BJ168051 B168051	301	18	2.5	924	14	BQ689965	BQ689965 AGENCOURT
229	18	2.5	666	17	AZ120164	AZ120164 RPCI-23-4	302	18	2.5	928	13	BM453383	BM453383 AGENCOURT
230	18	2.5	668	13	BJ273890	BJ273890 B273890	303	18	2.5	930	14	BQ644914	BQ644914 AGENCOURT
231	18	2.5	675	10	BB383556	BB383556 BB383556	304	18	2.5	930	14	BQ939534	BQ939534 AGENCOURT
232	18	2.5	675	10	BE615267	BE615267 601280626	305	18	2.5	931	12	BG742213	BG742213 602631213
233	18	2.5	676	12	BG332222	BG332222 602430939	306	18	2.5	932	12	BG109806	BG109806 602280962
234	18	2.5	687	13	BM007737	BM007737 603617185	307	18	2.5	932	14	BQ939826	BQ939826 AGENCOURT
235	18	2.5	687	17	AZ716197	AZ716197 RPCI-24-1	308	18	2.5	935	14	BQ675120	BQ675120 AGENCOURT
236	18	2.5	687	17	AG121604	AG121604 Pan trogl	c 309	18	2.5	935	14	BQ923647	BQ923647 AGENCOURT
237	18	2.5	688	10	BB619790	BB619790 BB619790	310	18	2.5	938	12	BG386273	BG386273 602455465
238	18	2.5	691	12	BG762768	BG762768 602734685	311	18	2.5	950	17	CNS04NMV	AL2992275 Tetraodon
239	18	2.5	694	10	BE570835	BE570835 601329336	312	18	2.5	957	12	BF339803	BF339803 602038809
240	18	2.5	695	10	BB344077	BB344077 BB344077	313	18	2.5	960	14	BQ951227	BQ951227 AGENCOURT
241	18	2.5	697	9	AL653433	AL653433 AL653433	314	18	2.5	961	13	BM475687	BM475687 AGENCOURT
242	18	2.5	700	12	BE917382	BE917382 601664213	c 315	18	2.5	965	12	BF299687	BF299687 602029377
243	18	2.5	700	13	BI116671	BI116671 602868349	316	18	2.5	965	13	BI411929	BI411929 602966315
244	18	2.5	704	12	BG748190	BG748190 602705814	c 317	18	2.5	972	14	BQ891229	BQ891229 AGENCOURT
245	18	2.5	719	13	BM016518	BM016518 603642144	c 318	18	2.5	977	14	BQ933450	BQ933450 AGENCOURT
246	18	2.5	720	17	AZ961286	AZ961286 2M0229111	319	18	2.5	983	14	BQ936084	BQ936084 AGENCOURT
247	18	2.5	728	13	BI857728	BI857728 603388360	320	18	2.5	993	12	BG330768	BG330768 602430289
248	18	2.5	734	10	BE273443	BE273443 601143138	321	18	2.5	1012	14	BM917847	BM917847 AGENCOURT
249	18	2.5	736	17	AZ721209	AZ721209 RPCI-24-9	322	18	2.5	1035	13	BM559810	BM559810 AGENCOURT
250	18	2.5	738	12	BG392323	BG392323 602410477	323	18	2.5	1035	13	BM559810	BM559810 AGENCOURT
251	18	2.5	745	9	AU116843	AU116843 AU116843	324	18	2.5	1022	14	BM054393	BQ543933 AGENCOURT
252	18	2.5	751	12	BG478754	BG478754 602525681	325	18	2.5	1022	14	BM06168	BM06168 AGENCOURT
253	18	2.5	751	12	BG824539	BG824539 602728436	326	18	2.5	1033	14	BQ058335	BQ058335 AGENCOURT
254	18	2.5	762	12	BG743862	BG743862 602722617	327	18	2.5	1042	12	BF306771	BF306771 601891753
255	18	2.5	762	13	BI686675	BI686675 603312902	328	18	2.5	1051	14	BQ059399	BQ059399 AGENCOURT
256	18	2.5	772	9	AL521157	AL521157 AL521157	329	18	2.5	1056	14	BQ051964	BQ051964 AGENCOURT
257	18	2.5	775	17	BH312500	BH312500 CH230-119	330	18	2.5	1071	12	BF690553	BF690553 602187054
258	18	2.5	776	12	CNS02Y2Q	AL219131 Tetraodon	331	18	2.5	1081	14	BM916591	BM916591 AGENCOURT
259	18	2.5	779	12	BG871365	BG871365 602790543	332	18	2.5	1082	14	BQ054920	BQ054920 AGENCOURT
260	18	2.5	781	12	BF342396	BF342396 602013192	c 333	18	2.5	1100	14	BM917087	AL344427 Tetraodon
261	18	2.5	782	17	AZ520242	AZ520242 RPCI-11-2	334	18	2.5	1115	14	BQ059011	BM917087 AGENCOURT
262	18	2.5	784	9	AU119143	AU119143 AU119143	335	18	2.5	1115	14	BF971937	BQ590111 AGENCOURT
263	18	2.5	792	12	BG733718	BG733718 601568230	336	18	2.5	1149	12	BF971937	BF971937 602240341
264	18	2.5	797	12	BG863933	BG863933 602797171	c 337	18	2.5	1168	17	CNS0671A	AL731372 T3 end of
265	18	2.5	798	17	CNS04TD6	AL306339 Tetraodon	338	18	2.5	1194	14	BQ933053	BQ933053 AGENCOURT
266	18	2.5	799	10	AW045021	AW045021 um16906.Y	339	18	2.5	1221	13	BM564098	BM564098 AGENCOURT
267	18	2.5	801	12	BG761029	BG761029 602717539	340	18	2.5	1324	14	BM806169	BM806169 AGENCOURT
268	18	2.5	803	10	BE613560	BE613560 601504325	341	18	2.5	1493	12	BG622685	BG622685 602647449
269	18	2.5	811	9	AL521158	AL521158 AL521158	342	18	2.5	1612	14	BM927011	BM927011 AGENCOURT
270	18	2.5	813	13	BI261586	BI261586 602953653	343	17	2.4	82	17	AZ777035	BM927011 2M0011J12
271	18	2.5	823	13	BM018838	BM018838 603646757	c 344	17	2.4	100	9	AA542233	AA542233 vk28b02.r
272	18	2.5	826	12	BG675934	BG675934 602622286	c 345	17	2.4	133	17	BH324346	BH324346 CH230-133
273	18	2.5	830	14	BQ961311	BQ961311 AGENCOURT	346	17	2.4	136	13	BJ479338	BJ479338 BU479338
274	18	2.5	838	12	BF678125	BF678125 602085177	347	17	2.4	141	12	BF857780	BF857780 QV1-F7020
275	18	2.5	840	17	AQ745383	AQ745383 HS 2276.A	348	17	2.4	154	10	BE158193	BE158193 MR2-HT038
276	18	2.5	842	12	BG490860	BG490860 602520044	349	17	2.4	156	12	BF411739	BF411739 UT-R-BT1-
277	18	2.5	848	12	BE781631	BE781631 601467488	c 350	17	2.4	157	14	T23990	T23990 seq2146 NHB
278	18	2.5	853	17	CNS04HYT	AL291566 Tetraodon	351	17	2.4	158	17	AZ730710	AZ730710 RPCI-24-1
279	18	2.5	855	14	BQ642584	BQ642584 AGENCOURT	352	17	2.4	159	17	CNS04ETP	AL287494 Tetraodon
280	18	2.5	858	14	BQ924903	BQ924903 AGENCOURT	c 353	17	2.4	183	13	BI751683	BI751683 TA01_13c0
281	18	2.5	858	9	AA203200	AA203200 x57a04.r	354	17	2.4	183	13	BI751784	BI751784 TA01_12b1
282	18	2.5	863	12	BG763365	BG763365 602735427	c 355	17	2.4	183	14	BQ901380	BQ901380 TA02_18h0
283	18	2.5	871	12	BE961683	BE961683 601647959	c 356	17	2.4	183	14	BQ901459	BQ901459 TA02_15f0
284	18	2.5	877	12	BE900734	BE900734 601673902	357	17	2.4	183	14	BQ901772	BQ901772 TA02_11f0
285	18	2.5	879	14	BQ721722	BQ721722 AGENCOURT	c 358	17	2.4	183	14	BQ902249	BQ902249 TA02_06f0
286	18	2.5	883	12	BG479515	BG479515 602526046	c 359	17	2.4	192	9	AA038584	AA038584 mi195e09.r
287	18	2.5	885	13	BQ962515	BQ962515 AGENCOURT	360	17	2.4	192	14	BQ901457	BQ901457 TA02_19h0
288	18	2.5	887	11	BI870592	BI870592 603394077	c 361	17	2.4	203	12	BF763978	BF763978 CM0-CS004
289	18	2.5	889	14	BQ227906	BQ227906 AGENCOURT	c 362	17	2.4	208	10	BE158194	BE158194 MR2-HT038
290	18	2.5	893	17	CNS02UOI	AL214731 Tetraodon	363	17	2.4	212	12	BF752577	BF752577 RCO-EN041
291	18	2.5	896	14	BQ898880	BQ898880 AGENCOURT	c 364	17	2.4	214	10	BM227412	BM227412 BB227412
292	18	2.5	900	13	BQ723195	BQ723195 AGENCOURT	365	17	2.4	215	17	AZ733211	AZ733211 RPCI-24-1
293	18	2.5	902	13	BM451269	BM451269 AGENCOURT	c 366	17	2.4	217	17	AZ774967	AZ774967 2M0004A20
294	18	2.5	907	14	BQ051460	BQ051460 AGENCOURT	367	17	2.4	222	10	BB523092	BB523092 BB523092
295	18	2.5	911	12	BG762117	BG762117 602717704	368	17	2.4	223	12	BE999962	BE999962 7h20h09.x
296	18	2.5	914	14	BQ653698	BQ653698 AGENCOURT	369	17	2.4	224	12	BF800062	BF800062 MR1-C1002
297	18	2.5	915	12	BF306251	BF306251 601893110	c 370	17	2.4	225	9	A1566424	A1566424 tr95d01.x
298	18	2.5	918	14	BQ720407	BQ720407 AGENCOURT	371	17	2.4	231	10	AW407398	AW407398 UT-HF-BM0

C 372	17	2.4	233	10	BB169472	BB169472	BB169472	445	17	2.4	354	13	BM253857	BM253857	BM253857	515063	MA
C 373	17	2.4	236	9	AV241776	AV241776	AV241776	446	17	2.4	355	9	AA863865	AA863865	AA863865	VX15b10.r	
C 374	17	2.4	237	9	AV229732	AV229732	AV229732	C 447	17	2.4	356	9	AU161496	AU161496	AU161496	1A161496	
C 375	17	2.4	238	10	AV377039	AV377039	AV377039	C 448	17	2.4	356	12	BG907360	BG907360	BG907360	TALR1159D	
C 376	17	2.4	238	10	AW376284	AW376284	AW376284	C 449	17	2.4	357	12	BF285684	BF285684	BF285684	EST450275	
C 377	17	2.4	240	10	BB178438	BB178438	BB178438	C 450	17	2.4	357	14	BQ749904	BQ749904	BQ749904	SDST4a73	
C 378	17	2.4	243	10	AV376815	AV376815	AV376815	C 451	17	2.4	358	14	BQ337322	BQ337322	BQ337322	IL2-WT018	
C 379	17	2.4	249	9	AV105028	AV105028	AV105028	C 452	17	2.4	358	14	BQ337322	BQ337322	BQ337322	IL2-WT018	
C 380	17	2.4	249	10	AW563223	AW563223	AW563223	C 453	17	2.4	359	9	AI892028	AI892028	AI892028	u158d04.y	
C 381	17	2.4	256	9	A1872565	A1872565	A1872565	C 454	17	2.4	360	14	BQ659591	BQ659591	BQ659591	HE01F21u	
C 382	17	2.4	266	10	BB259009	BB259009	BB259009	C 455	17	2.4	361	14	BQ659591	BQ659591	BQ659591	HE01F21u	
C 383	17	2.4	269	13	BQ459519	BQ459519	BQ459519	C 456	17	2.4	362	12	BG313726	BG313726	BG313726	WHE2057.G	
C 384	17	2.4	270	12	BF054374	BF054374	BF054374	C 457	17	2.4	362	12	BG907182	BG907182	BG907182	TALR1157G	
C 385	17	2.4	272	12	BF799932	BF799932	BF799932	C 458	17	2.4	363	13	BI873998	BI873998	BI873998	963112F12	
C 386	17	2.4	273	9	A1928661	A1928661	A1928661	C 459	17	2.4	364	10	BE365951	BE365951	BE365951	P11.2.E10	
C 387	17	2.4	277	12	BF880720	BF880720	BF880720	C 460	17	2.4	365	13	BQ842841	BQ842841	BQ842841	BU042841	
C 388	17	2.4	281	9	AA506315	AA506315	AA506315	C 461	17	2.4	366	13	AW820483	AW820483	AW820483	QV2-ST029	
C 389	17	2.4	281	10	BB402834	BB402834	BB402834	C 462	17	2.4	367	13	BG907181	BG907181	BG907181	TALR1157G	
C 390	17	2.4	282	13	BJ451424	BJ451424	BJ451424	C 463	17	2.4	368	10	AW427695	AW427695	AW427695	64034.MAR	
C 391	17	2.4	283	10	BB182728	BB182728	BB182728	C 464	17	2.4	369	12	BG692516	BG692516	BG692516	342232.BA	
C 392	17	2.4	285	9	AA507298	AA507298	AA507298	C 465	17	2.4	370	10	AW478610	AW478610	AW478610	21191.MAR	
C 393	17	2.4	285	14	BM845045	BM845045	BM845045	C 466	17	2.4	371	9	AI180542	AI180542	AI180542	uc70c11.f	
C 394	17	2.4	289	17	BH089789	BH089789	BH089789	C 467	17	2.4	372	12	BF016798	BF016798	BF016798	ux16h07.y	
C 395	17	2.4	291	10	BB038001	BB038001	BB038001	C 468	17	2.4	373	9	AI1797513	AI1797513	AI1797513	we8h11.x	
C 396	17	2.4	291	12	BE722956	BE722956	BE722956	C 469	17	2.4	374	10	BE291545	BE291545	BE291545	601084356	
C 397	17	2.4	291	12	BE722957	BE722957	BE722957	C 470	17	2.4	375	14	BQ659880	BQ659880	BQ659880	HG01A13u	
C 398	17	2.4	291	14	W79279	W79279	W79279	C 471	17	2.4	376	10	AW406894	AW406894	AW406894	UT-HF-BK0	
C 399	17	2.4	292	10	BB607762	BB607762	BB607762	C 472	17	2.4	377	10	BF731935	BF731935	BF731935	BU731935	
C 400	17	2.4	293	12	BF711571	BF711571	BF711571	C 473	17	2.4	378	13	BJ457125	BJ457125	BJ457125	BU457125	
C 401	17	2.4	294	10	BB555912	BB555912	BB555912	C 474	17	2.4	379	9	AV011765	AV011765	AV011765	AV011765	
C 402	17	2.4	294	12	BF947188	BF947188	BF947188	C 475	17	2.4	380	10	AW137002	AW137002	AW137002	UT-H-B11-	
C 403	17	2.4	297	12	BE751413	BE751413	BE751413	C 476	17	2.4	381	13	BI396959	BI396959	BI396959	K64401.Y	
C 404	17	2.4	298	14	F12536	F12536	F12536	C 477	17	2.4	382	10	BB803125	BB803125	BB803125	BB803125	
C 405	17	2.4	299	17	AZ655768	AZ655768	AZ655768	C 478	17	2.4	383	12	BF095532	BF095532	BF095532	IL2-UT007	
C 406	17	2.4	300	9	AU276116	AU276116	AU276116	C 479	17	2.4	384	12	AA310284	AA310284	AA310284	EST18111	
C 407	17	2.4	300	10	BE401201	BE401201	BE401201	C 480	17	2.4	385	9	AW315107	AW315107	AW315107	12000.MAR	
C 408	17	2.4	307	17	B44134	B44134	B44134	C 481	17	2.4	386	12	BG908200	BG908200	BG908200	TALR1166D	
C 409	17	2.4	308	12	BF933677	BF933677	BF933677	C 482	17	2.4	387	17	AQ482414	AQ482414	AQ482414	RPCI-11-2	
C 410	17	2.4	310	13	BI02936	BI02936	BI02936	C 483	17	2.4	388	9	AT004167	AT004167	AT004167	AT004167	
C 411	17	2.4	311	12	BF365944	BF365944	BF365944	C 484	17	2.4	389	10	AW907153	AW907153	AW907153	EST343276	
C 412	17	2.4	314	9	A1917235	A1917235	A1917235	C 485	17	2.4	390	9	AI615610	AI615610	AI615610	V122h01.Y	
C 413	17	2.4	317	10	BE638697	BE638697	BE638697	C 486	17	2.4	391	10	BB817236	BB817236	BB817236	BB817236	
C 414	17	2.4	318	13	BI052798	BI052798	BI052798	C 487	17	2.4	392	13	BI053046	BI053046	BI053046	RCO-GN027	
C 415	17	2.4	319	9	AA576259	AA576259	AA576259	C 488	17	2.4	393	17	AQ121303	AQ121303	AQ121303	HS.3075.A	
C 416	17	2.4	320	10	BE245363	BE245363	BE245363	C 489	17	2.4	394	12	BF774472	BF774472	BF774472	284152.MA	
C 417	17	2.4	322	12	EG012863	EG012863	EG012863	C 490	17	2.4	395	13	BI360883	BI360883	BI360883	388961.MA	
C 418	17	2.4	323	13	BM286919	BM286919	BM286919	C 491	17	2.4	396	13	BI360885	BI360885	BI360885	388963.MA	
C 419	17	2.4	324	12	BF991156	BF991156	BF991156	C 492	17	2.4	397	10	AW501800	AW501800	AW501800	UT-HF-BR0	
C 420	17	2.4	324	14	T08803	T08803	T08803	C 493	17	2.4	398	9	AA761019	AA761019	AA761019	nw08G04.s	
C 421	17	2.4	326	10	BB208793	BB208793	BB208793	C 494	17	2.4	399	10	AW406797	AW406797	AW406797	UT-HF-BL0	
C 422	17	2.4	328	10	AW503020	AW503020	AW503020	C 495	17	2.4	400	12	BG276868	BG276868	BG276868	uv08G04.Y	
C 423	17	2.4	329	9	AL838282	AL838282	AL838282	C 496	17	2.4	401	13	BJ458918	BJ458918	BJ458918	BU458918	
C 424	17	2.4	330	10	BB101817	BB101817	BB101817	C 497	17	2.4	402	14	BQ661277	BQ661277	BQ661277	HM02M11u	
C 425	17	2.4	333	10	AW958256	AW958256	AW958256	C 498	17	2.4	403	17	AQ031485	AQ031485	AQ031485	HS.2223.A	
C 426	17	2.4	334	13	BJ454793	BJ454793	BJ454793	C 499	17	2.4	404	12	BG406635	BG406635	BG406635	g4c14g12.	
C 427	17	2.4	335	13	BI363678	BI363678	BI363678	C 500	17	2.4	405	13	BJ449707	BJ449707	BJ449707	BU449707	
C 428	17	2.4	336	13	EG941480	EG941480	EG941480	C 501	17	2.4	406	14	BQ632668	BQ632668	BQ632668	il26c05.Y	
C 429	17	2.4	338	12	BF892520	BF892520	BF892520	C 502	17	2.4	407	9	AL837331	AL837331	AL837331	AL837331	
C 430	17	2.4	338	13	BJ459564	BJ459564	BJ459564	C 503	17	2.4	408	9	AV102465	AV102465	AV102465	AV102465	
C 431	17	2.4	340	9	AA414544	AA414544	AA414544	C 504	17	2.4	409	9	AA758083	AA758083	AA758083	ah68a03.s	
C 432	17	2.4	340	13	BI342660	BI342660	BI342660	C 505	17	2.4	410	9	AU197751	AU197751	AU197751	AU197751	
C 433	17	2.4	340	17	AZ101591	AZ101591	AZ101591	C 506	17	2.4	411	13	BI799682	BI799682	BI799682	HL38B09.E	
C 434	17	2.4	344	12	BF333604	BF333604	BF333604	C 507	17	2.4	412	14	BQ463646	BQ463646	BQ463646	HG01A01r	
C 435	17	2.4	344	17	AQ242049	AQ242049	AQ242049	C 508	17	2.4	413	10	AW282788	AW282788	AW282788	LGI.290.D	
C 436	17	2.4	345	13	BI722762	BI722762	BI722762	C 509	17	2.4	414	10	AW282931	AW282931	AW282931	LGI.304.D	
C 437	17	2.4	347	13	BG959143	BG959143	BG959143	C 510	17	2.4	415	17	B94209	B94209	B94209	CIT-HSP-217	
C 438	17	2.4	348	14	BQ657204	BQ657204	BQ657204	C 511	17	2.4	416	17	AQ341494	AQ341494	AQ341494	RPCI11-12	
C 439	17	2.4	349	12	BF737159	BF737159	BF737159	C 512	17	2.4	417	10	AV910267	AV910267	AV910267	AV910267	
C 440	17	2.4	349	14	N4832	N4832	N4832	C 513	17	2.4	418	10	AW284719	AW284719	AW284719	LGI.214.F	
C 441	17	2.4	351	10	BB725329	BB725329	BB725329	C 514	17	2.4	419	17	AQ515749	AQ515749	AQ515749	HS.5235.A	
C 442	17	2.4	351	17	AZ052843	AZ052843	AZ052843	C 515	17	2.4	420	17	BF557617	BF557617	BF557617	UI-R-E1-9	
C 443	17	2.4	351	17	AZ734573	AZ734573	AZ734573	C 516	17	2.4	421	13	BG959585	BG959585	BG959585	PM4-CT080	
C 444	17	2.4	353	13	BM002												

C 518	17	2.4	407	13	BJ447290	BJ447290	BJ447290	BJ447290	C 591	17	2.4	449	13	BM218099	BM218099	BM218099	C0306D06-
C 519	17	2.4	407	17	TA8G07P	AL452629	T. brucei	AL452629	C 592	17	2.4	450	9	AA612010	AA612010	AA612010	vo02c12.r
C 520	17	2.4	408	12	BG907840	TA8G07P	TA8G07P	TA8G07P	C 593	17	2.4	450	13	BG995163	BG995163	CMO-HT129	
C 521	17	2.4	409	10	BM897233	CMO-NM005	CMO-NM005	CMO-NM005	C 594	17	2.4	450	17	QA073123	QA073123	CITR1-EL-	
C 522	17	2.4	409	13	BM328261	PICL-23.A	PICL-23.A	PICL-23.A	C 595	17	2.4	451	9	AA253758	AA253758	mw03b07.r	
C 523	17	2.4	409	14	BO659872	HGO1A01u	HGO1A01u	HGO1A01u	C 596	17	2.4	451	14	BO908096	BO908096	T002D10.O	
C 524	17	2.4	410	9	AA047661	zfl4a05.s	zfl4a05.s	zfl4a05.s	C 597	17	2.4	451	14	R64014	R64014	Y119603.r1	
C 525	17	2.4	411	12	BF725949	bx22a10.Y	bx22a10.Y	bx22a10.Y	C 598	17	2.4	451	17	QA111777	QA111777	CIT-HSP-2	
C 526	17	2.4	412	10	AW437355	78363.MAR	78363.MAR	78363.MAR	C 599	17	2.4	451	17	AQ111777	AQ111777	CIT-HSP-2	
C 527	17	2.4	412	12	BF011939	u37h09.Y	u37h09.Y	u37h09.Y	C 600	17	2.4	451	9	AZ950059	AZ950059	2M0214A06	
C 528	17	2.4	414	17	AZ281849	RPCI-23-1	RPCI-23-1	RPCI-23-1	C 601	17	2.4	453	9	AI095114	AI095114	QA19a10.x	
C 529	17	2.4	415	10	AV667195	AV667195	AV667195	AV667195	C 602	17	2.4	453	10	AV910686	AV910686	AV910686	
C 530	17	2.4	415	12	BE816031	MRO-BN018	MRO-BN018	MRO-BN018	C 603	17	2.4	453	13	BI359612	BI359612	384209.MA	
C 531	17	2.4	415	13	BG996752	CMO-HT129	CMO-HT129	CMO-HT129	C 604	17	2.4	454	10	BB755186	BB755186	BB755186	
C 532	17	2.4	416	12	BF897207	IL2-MT018	IL2-MT018	IL2-MT018	C 605	17	2.4	454	12	BF468543	BF468543	BF468543	
C 533	17	2.4	416	17	AZ369732	1M0120022	1M0120022	1M0120022	C 606	17	2.4	455	14	R48905	R48905	Y169F06.r1	
C 534	17	2.4	417	10	AM204275	UI-H-B11-	UI-H-B11-	UI-H-B11-	C 607	17	2.4	455	17	AQ338818	AQ338818	HS-3118.B	
C 535	17	2.4	417	12	BF709310	MI-P-AY0-	MI-P-AY0-	MI-P-AY0-	C 608	17	2.4	456	10	BB751485	BB751485	BB751485	
C 536	17	2.4	418	12	BF229432	MRI-C1002	MRI-C1002	MRI-C1002	C 609	17	2.4	456	12	BF229415	BF229415	BF229415	
C 537	17	2.4	420	9	AL796516	AL796516	AL796516	AL796516	C 610	17	2.4	457	9	AA656845	AA656845	vr24e03.r	
C 538	17	2.4	420	12	BF292631	WHE2216.A	WHE2216.A	WHE2216.A	C 611	17	2.4	457	10	AM200197	AM200197	da12912.Y	
C 539	17	2.4	420	14	N30487	YX48F05.r1	YX48F05.r1	YX48F05.r1	C 612	17	2.4	457	17	AZ583746	AZ583746	IM037BP17	
C 540	17	2.4	420	17	AZ323358	1M0044007	1M0044007	1M0044007	C 613	17	2.4	457	17	BH749768	BH749768	SALK-0301	
C 541	17	2.4	421	10	AM909828	ur74f10.Y	ur74f10.Y	ur74f10.Y	C 614	17	2.4	458	10	AV910822	AV910822	AV910822	
C 542	17	2.4	421	12	BF941718	na092c03.	na092c03.	na092c03.	C 615	17	2.4	458	10	BB703108	BB703108	BB703108	
C 543	17	2.4	421	13	BJ458079	BJ458079	BJ458079	BJ458079	C 616	17	2.4	459	10	BB795732	BB795732	BB795732	
C 544	17	2.4	421	14	BO659923	HGO1D13u	HGO1D13u	HGO1D13u	C 617	17	2.4	460	9	AI060291	AI060291	UI-R-C1-1	
C 545	17	2.4	424	17	TA76H09P	AL460760	T. brucei	AL460760	C 618	17	2.4	460	9	AL822851	AL822851	AL822851	
C 546	17	2.4	426	10	AM283727	LGI-222.G	LGI-222.G	LGI-222.G	C 619	17	2.4	460	13	BM038728	BM038728	V009A03.O	
C 547	17	2.4	426	12	BF810963	CM2-C1017	CM2-C1017	CM2-C1017	C 620	17	2.4	460	14	BM761644	BM761644	K-EST0042	
C 548	17	2.4	427	10	BE014084	125664.MA	125664.MA	125664.MA	C 621	17	2.4	461	9	AA683338	AA683338	ah51a09.s	
C 549	17	2.4	427	14	BO335141	CM3-MT029	CM3-MT029	CM3-MT029	C 622	17	2.4	461	10	BE246438	BE246438	TCBAP1E46	
C 550	17	2.4	428	9	AU094557	AU094557	AU094557	AU094557	C 623	17	2.4	461	12	BF958307	BF958307	CM2-NM024	
C 551	17	2.4	428	12	BF841025	RC3-HT097	RC3-HT097	RC3-HT097	C 624	17	2.4	461	17	AZ741302	AZ741302	RPCI-23-7	
C 552	17	2.4	429	12	BF43537	261055.MA	261055.MA	261055.MA	C 625	17	2.4	462	9	AI419507	AI419507	tf22a03.x	
C 553	17	2.4	429	12	BF800053	MRI-C1002	MRI-C1002	MRI-C1002	C 626	17	2.4	462	14	BQ447189	BQ447189	UI-H-EU1-	
C 554	17	2.4	431	9	AA030087	mi27c03.r	mi27c03.r	mi27c03.r	C 627	17	2.4	462	14	H09911	H09911	ym05902.r1	
C 555	17	2.4	431	17	AL827401	AL827401	AL827401	AL827401	C 628	17	2.4	464	10	AW742197	AW742197	UV53e10.Y	
C 556	17	2.4	431	17	AZ818697	2M0088E24	2M0088E24	2M0088E24	C 629	17	2.4	464	12	BF880518	BF880518	QV3-ET017	
C 557	17	2.4	432	9	A1275074	ql65b02.x	ql65b02.x	ql65b02.x	C 630	17	2.4	464	12	AW252896	AW252896	UI-R-BJ0-	
C 558	17	2.4	432	12	BG360140	da992h05.	da992h05.	da992h05.	C 631	17	2.4	465	17	B38918	B38918	HS-1048-B1-	
C 559	17	2.4	432	12	BE765760	IL3-NT010	IL3-NT010	IL3-NT010	C 632	17	2.4	466	9	AI326502	AI326502	mq34d05.Y	
C 560	17	2.4	432	14	BO661772	HP01D15w	HP01D15w	HP01D15w	C 633	17	2.4	467	17	TA372F12Q	TA372F12Q	TA372F12Q	
C 561	17	2.4	432	14	T49530	ya76f09.s1	ya76f09.s1	ya76f09.s1	C 634	17	2.4	468	10	BE159570	BE159570	MRO-HT040	
C 562	17	2.4	435	17	AO812286	HS-5263.A	HS-5263.A	HS-5263.A	C 635	17	2.4	468	12	BG313982	BG313982	WHE2065.E	
C 563	17	2.4	436	9	AA801029	ESTI90526	ESTI90526	ESTI90526	C 636	17	2.4	470	10	BE247311	BE247311	TCBAP1E37	
C 564	17	2.4	437	9	AI182542	AU182542	AU182542	AU182542	C 637	17	2.4	470	10	BE247311	BE247311	TCBAP1E37	
C 565	17	2.4	438	13	BG996753	CMO-HT129	CMO-HT129	CMO-HT129	C 638	17	2.4	470	12	BG275110	BG275110	WHE2117.H	
C 566	17	2.4	438	13	BI809216	F002F08.O	F002F08.O	F002F08.O	C 639	17	2.4	471	12	BF485332	BF485332	WHE2310.C	
C 567	17	2.4	438	13	BM087101	499771.MA	499771.MA	499771.MA	C 640	17	2.4	471	13	BJ451959	BJ451959	BJ451959	
C 568	17	2.4	439	9	AA310446	ESTI181260	ESTI181260	ESTI181260	C 641	17	2.4	471	14	W99993	W99993	mq27d06.r1	
C 569	17	2.4	439	9	AA611692	vo2c04.r	vo2c04.r	vo2c04.r	C 642	17	2.4	472	10	AV703800	AV703800	AV703800	
C 570	17	2.4	439	12	BF529470	602043223	602043223	602043223	C 643	17	2.4	472	12	EG905996	EG905996	Taur11444	
C 571	17	2.4	440	9	AA590179	vm23c01.r	vm23c01.r	vm23c01.r	C 644	17	2.4	472	12	BF811935	BF811935	QV1-C1017	
C 572	17	2.4	440	12	BF841033	RC3-HT097	RC3-HT097	RC3-HT097	C 645	17	2.4	474	12	BF293158	BF293158	WHE2164.C	
C 573	17	2.4	440	13	BM527026	sal148f06.	sal148f06.	sal148f06.	C 646	17	2.4	474	14	BM837081	BM837081	K-EST0113	
C 574	17	2.4	440	14	R49154	Y957b10.s1	Y957b10.s1	Y957b10.s1	C 647	17	2.4	475	10	BE425743	BE425743	WHE0316.F	
C 575	17	2.4	441	13	BI806358	S062B01.S	S062B01.S	S062B01.S	C 648	17	2.4	475	13	BI806822	BI806822	S078A08-S	
C 576	17	2.4	441	17	AQ695578	HS-2148.A	HS-2148.A	HS-2148.A	C 649	17	2.4	476	9	AI832623	AI832623	ac70h05.x	
C 577	17	2.4	442	9	AI182488	AU182488	AU182488	AU182488	C 650	17	2.4	476	10	BE206737	BE206737	ba02d01.Y	
C 578	17	2.4	442	10	AV737548	AV737548	AV737548	AV737548	C 651	17	2.4	476	12	EG907968	EG907968	Taur1164C	
C 579	17	2.4	445	14	W40652	mc45a08.r1	mc45a08.r1	mc45a08.r1	C 652	17	2.4	477	10	BE498414	BE498414	WHE0963.H	
C 580	17	2.4	445	14	W80014	me90c08.r1	me90c08.r1	me90c08.r1	C 653	17	2.4	477	13	BJ455086	BJ455086	BJ455086	
C 581	17	2.4	446	14	BM837931	K-EST0114	K-EST0114	K-EST0114	C 654	17	2.4	477	14	W78309	W78309	me78a12.r1	
C 582	17	2.4	446	14	R41549	yf88b06.s1	yf88b06.s1	yf88b06.s1	C 655	17	2.4	478	9	AA139676	AA139676	mq34d05.r	
C 583	17	2.4	446	17	BH590055	BOH0794TR	BOH0794TR	BOH0794TR	C 656	17	2.4	478	12	BF776790	BF776790	288513.MA	
C 584	17	2.4	447	9	AI182976	AU182976	AU182976	AU182976	C 657	17	2.4	479	10	AW322976	AW322976	uo54906.Y	
C 585	17	2.4	448	12	BF442448	259169.MA	259169.MA	259169.MA	C 658	17	2.4	479	17	AZ338978	AZ338978	IM0070G14	
C 586	17	2.4	448	12	BF803570	QV1-C1017	QV1-C1017	QV1-C1017	C 659	17	2.4	480	9	AI901966	AI901966	618013A08	
C 587	17	2.4	448	13	BJ450655	BJ450655	BJ450655	BJ450655	C 660	17	2.4	480	10	BE426332	BE426332	WHE0330.A	
C 588	17	2.4	448	17	AQ988396	RPCI-23-3	RPCI-23-3	RPCI-23-3	C 661	17	2.4	480	10	BE490097	BE490097	WHE0365.E	
C 589	17	2.4	449	9	AL506352	AL506352	AL506352	AL506352	C 662	17	2.4	480	17	AQ148012	AQ148012	HS-3110.A	
C 590	17	2.4															

664	17	2.4	481	13	BG988496	BG988496 RC4-HT109
C 665	17	2.4	481	14	T74062	T74062 YC81f01.r1
C 666	17	2.4	481	17	TA233A06Q	AL483062 T. brucei
C 667	17	2.4	482	9	AA220140	AA220140 my01e12.r
668	17	2.4	482	12	BG560805	BG560805 D108 SSH-
669	17	2.4	482	14	BM986485	BM986485 EST594079
C 670	17	2.4	482	17	AQ693921	AQ693921 HS 5466.B
C 671	17	2.4	482	17	AQ971413	AQ971413 EST383502
C 672	17	2.4	483	10	BM971413	BM971413 EST383502
C 673	17	2.4	483	13	B1647003	B1647003 60327877A
C 674	17	2.4	484	10	BE497071	BE497071 WHE0764.A
C 675	17	2.4	484	10	BE499884	BE499884 WHE079.B
C 676	17	2.4	485	17	AQ702465	AQ702465 HS 5429.A
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c 994 17 2.4 611 12 EG909135
c 995 17 2.4 611 12 EG909135
c 996 17 2.4 611 12 EG909135
c 997 17 2.4 611 12 EG909135
c 998 17 2.4 611 12 EG909135
c 999 17 2.4 611 12 EG909135
1000 17 2.4 611 12 EG909135

```

## ALIGNMENTS

```

RESULT 1
BF338502
LOCUS BF338502
DEFINITION BF338502
5', mRNA sequence.
ACCESSION BF338502
VERSION BF338502.1 GI:11284905
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 925)
JOURNAL NIH-MGC http://mgs.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

```

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 674.
Location/Qualifiers
source 1. 925
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4182233"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 212 a 251 c 273 g 188 t 1 others
ORIGIN
Query Match 38.9%; Score 278; DB 12; Length 925;
Best Local Similarity 100.0%; Pred. NO. 6.8e-109;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 438 TGCAGATTCTGCTCTCTGGAAGAGGCTCTGGACAGAGAGCTTCCCAAGCAGAGC 497
Db 1 TGCAGATTCTGCTCTCTGGAAGAGGCTCTGGACAGAGAGCTTCCCAAGCAGAGC 60
Oy 498 CTGCCCCAGGCCCGACAGAGGCTTCTGCTCCCTCTGCGGACGCTGTGGTGG 557
Db 61 CTGCCCCAGGCCCGACAGAGGCTTCTGCTCCCTCTGCGGACGCTGTGGTGG 120
Oy 558 CCGACCCACTGACCCACTCGGATGGAGCAACCTCTGTCCCAAGGAGCGCTGGAG 617
Db 121 CCGACCCACTGACCCACTCGGATGGAGCAACCTCTGTCCCAAGGAGCGCTGGAG 180
Oy 618 AGAGAGCAGACTCCGATCACCTCACCAAGGATCGGACTCTGCCCCCTGGACCTGGGAAC 677
Db 181 AGAGAGCAGACTCCGATCACCTCACCAAGGATCGGACTCTGCCCCCTGGACCTGGGAAC 240
Oy 678 GACTGGACTGTACGGGGTTCCTCTCTAGCTCTCCAG 715
Db 241 GACTGGACTGTACGGGGTTCCTCTCTAGCTCTCCAG 278
RESULT 2
AL566277/c
LOCUS AL566277
DEFINITION AL566277 LTI FL013 FBrnl Homo sapiens cDNA clone CS0DF014YH20 3
prime, mRNA sequence.
ACCESSION AL566277
VERSION AL566277.1 GI:12918488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 848)
JOURNAL Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
source 1. 848
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF014YH20"
/lab_host="LTI FL013 FBrnl"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"

```

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 161 a 230 c 294 g 161 t 2 others  
ORIGIN

Query Match 36.4%; Score 260; DB 9; Length 848;  
Best Local Similarity 99.3%; Pred. No. 3.7e-101;  
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 303 GGCTGCCACACAGCCCGCCAGAGTGGCCACCGTGGCACTAGATGCAAGTATCCTG 362  
Db 799 GGCTGCCACACAGCCCGCCAGAGTGGCCACCGTGGCACTAGATGCAAGTATCCTG 740  
Qy 363 CGACTTGTCAACCTCACCTTCTGTGGGTGTTCTTCTGCGCTGTCCAAAGCGCCCTC 422  
Db 739 CGACTTGTCAACCTCACCTTCTGTGGGTGTTCTTCTGCGCTGTCCAAAGCGCCCTC 680  
Qy 423 ACTATTCTTGACCATGCGATTCCTCTCTGGAAGAGGCTCTGGACAGCAGAGC 482  
Db 679 ACTATTCTTGACCATGCGATTCCTCTCTGGAAGAGGCTCTGGACAGCAGAGC 620  
Qy 483 CTCAAGCAGACAGCTGGCCCGCCAGGCCCCAGACAGGTTGGCTCTTCCCTTCCCTCT 542  
Db 619 CTCAAGCAGACAGCTGGCCCGCCAGGCCCCAGACAGGTTGGCTCTTCCCTTCCCTCT 560  
Qy 543 GGGCAGCGCTCTGGCCGACCACTGACCCACTCGGATGGACCACTGCTGTGCCCA 602  
Db 559 GGGCAGCGCTCTGGCCGACCACTGACCCACTCGGATGGACCACTGCTGTGCCCA 500  
Qy 603 AAGGACGCTCTGAGGAGAGCAGCAGCTCCGCATCACCTCACCAGGATCGGACTCTGCC 662  
Db 499 AAGGACGCTCTGAGGAGAGCAGCAGCTCCGCATCACCTCACCAGGATCGGACTCTGCC 440  
Qy 663 CTGACCTGGAGACGACTGACTGTACGGGGTTCCTCTAGTCTCCCGAG 715  
Db 439 CTGACCTGGAGACGACTGACTGTACGGGGTTCCTCTAGTCTCCCGAG 387

RESULT 3  
AL047147  
LOCUS AL047147 326 bp mRNA linear EST 29-FEB-2000  
DEFINITION DKFZp586E1518 r1 586 (synonym: hutel) Homo sapiens cDNA clone  
ACCESSION DKFZp586E1518 5', mRNA sequence.  
VERSION AL047147.1 GI:5435179  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 326)  
REFERENCE Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
AUTHORS EST (Koehrer, et al.)  
TITLE Unpublished (1999)  
JOURNAL Contact: Koehrer K  
COMMENT MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Sequenced by BMFZ (Biomedical Research Center at the Charite,  
Berlin/Germany) within the cDNA sequencing consortium of the German  
Genome Project.  
No sl sequence available.  
This clone (DKFZp586E1518) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source

1..326  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp586E1518"  
/clone\_lib="586 (synonym: hutel)"  
/tissue\_type="uterus"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="vector: pSPORT1; Site\_1: NotI; Site\_2: SalI/MluI"  
64 a 110 c 67 t 1 others

Query Match 21.7%; Score 155; DB 9; Length 326;  
Best Local Similarity 100.0%; Pred. No. 4.8e-56;  
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 54 CCCCCCACTCCAGGAAGAGCAGTCCAGTCCAGTCTCTGCTCAGACGTTGCCCTG 113  
Db 140 CCCCCCACTCCAGGAAGAGCAGTCCAGTCCAGTCTCTGCTCAGACGTTGCCCTG 199  
Qy 114 AGAAGAAGTGGTCCACACCCAGGAGGCCCTGAGGCGGAGCTGTGCTCCGCAATG 173  
Db 200 AGAAGAAGTGGTCCACACCCAGGAGGCCCTGAGGCGGAGCTGTGCTCCGCAATG 259  
Qy 174 GTGTCCCGGTACCTTCCATACACAGAGGAGTGCAG 208  
Db 260 GTGTCCCGGTACCTTCCATACACAGAGGAGTGCAG 294

RESULT 4

AV751885  
LOCUS AV751885 622 bp mRNA linear EST 19-OCT-2000  
DEFINITION AV751885 NPD Homo sapiens cDNA clone NPD8HA02 5', mRNA sequence.  
ACCESSION AV751885  
VERSION AV751885.1 GI:10909733  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 622)

REFERENCE Song H., Peng Y., Gu J., Yang Y., Gao G., Xiao H., Xu X., Li N.,  
AUTHORS Qian B., Liu F., Qu J., Gao X., Cheng Z., Xu Z., Zeng L., Xu S., Gu  
W., Tu Y., Jia J., Fu G., Ren S., Zhong M., Lu G., Ye M., Zhang, Q.  
Han Z., Chen Z., Hu R. and Chen J.  
Homo sapiens NPD library cDNA clones  
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Qinghua Zhang  
Shanghai Institute of Endocrinology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64370045(ex.663332)  
Fax: 86-21-64743206

Email: mbshi@ms.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in  
Shanghai.

Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers

FEATURES  
source

1..622  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NPD8HA02"  
/clone\_lib="NPD"  
/tissue\_type="pituitary"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 130 a 214 c 158 g 120 t  
ORIGIN











**AUTHORS**  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,  
Goldman,G.H., Galvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

**TITLE**  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

**JOURNAL**  
**MEDLINE**  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663

**COMMENT**  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&t2=MR4-MT0255-  
140201-203-c09&t3=2001-02-14&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 471.  
Location/Qualifiers  
1. .471  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="MT0255"  
/dev\_stages="Adult"  
/note="Organ: marrow; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 98 a 144 c 140 g 87 t 2 others  
ORIGIN

Query Match 7.1%; Score 51; DB 13; Length 471;  
Best Local Similarity 100.0%; Pred. No. 2.2e-11;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 665 TGGACCTGGGAACGACTGTACCGGGGTTCCTCTAGCTCTCCAG 715  
|||||  
|||||

**Db** 454 TGGACCTGGGAACGACTGTACCGGGGTTCCTCTAGCTCTCCAG 404  
|||||  
|||||

**RESULT 12**  
**F11822**  
**LOCUS** F11822 302 bp mRNA linear EST 12-MAR-1995  
**DEFINITION** HS32A091 normalized infant brain cDNA Homo sapiens CDNA clone  
c-32a09, mRNA sequence.  
**ACCESSION** F11822  
**VERSION** F11822.1 GI:706134  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 302)  
**REFERENCE**  
**AUTHORS** Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes  
,M.D., Duprat,S., Houllatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,  
Michell,H., Mariage-Samson,R., Pietu,G., Foullet,Y.,  
Sebastien-Kabaktchis,C. and Tessier,A.  
**TITLE** IMAGE: molecular integration of the analysis of the human genome  
and its expression  
**JOURNAL** C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
**MEDLINE** 95277534  
**COMMENT** Contact: Genethon  
Genexpress-Genethon  
Genethon Centre de recherche sur le Genome Humain

1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpress@genethon.fr  
Single read  
Genexpress\_library\_id: C; Genexpress\_sequence\_id: y1c-32a09  
Seq primer: (-21)MT3 universal.  
Location/Qualifiers  
1. .302  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="c-32a09"  
/clone\_lib="normalized infant brain cDNA"  
/sex="Female"  
/tissue\_type="total brain"  
/dev\_stages="3 months old"  
/note="Organ: brain; Vector: lafmid BA; Site\_1: HindIII;  
Site\_2: NotI; sex:female; dev\_stage=3 months old;  
isolate=muscular atrophy patient; tissue\_type=total brain  
; total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Soaeres, Psychiatry  
Dept. Columbia University, USA. Normalization\_method:  
Bento Soares, P.N.A.S in press"  
BASE COUNT 67 a 97 c 65 g 72 t 1 others  
ORIGIN

Query Match 4.6%; Score 33; DB 14; Length 302;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 ACTGCCCCACGACAGACAGAGGAGGGCTGGCT 33  
|||||  
|||||

**Db** 270 ACTGCCCCACGACAGACAGAGGAGGGCTGGCT 302  
|||||  
|||||

**RESULT 13**  
**N31948/c**  
**LOCUS** N31948 599 bp mRNA linear EST 10-JAN-1996  
**DEFINITION** VY22g12.s1 Soares melanocyte 2NDHM Homo sapiens CDNA clone  
IMAGE:272038 3', mRNA sequence.  
**ACCESSION** N31948  
**VERSION** N31948.1 GI:1152347  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 599)  
**REFERENCE**  
**AUTHORS** Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M., Parsons,J.,  
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston  
,R., Williamson,A., Wohlmann,P. and Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Willson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 345  
Source: IMAGE Consortium LNL  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: ml3 -40 forward  
High quality sequence stop: 345.  
Location/Qualifiers  
1. .599  
/organism="Homo sapiens"  
/db\_xref="GDB:3881680"  
/db\_xref="taxon:9606"  
/clone="IMAGE:272038"

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/clone_lib="Soares melanocyte 2N6HM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGCGCGCGAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      159 a 162 c 159 g 116 t
ORIGIN
Query Match      4.2%; Score 30; DB 14; Length 599;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 665 TGGACCTGGGAACGACTGCTGTCACGGG 694
Db 574 TGGACCTGGGAACGACTGCTGTCACGGG 545
RESULT 14
BM471442      1044 bp mRNA linear EST 05-FEB-2002
LOCUS      AGENCOUNT 6478304 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5563262
DEFINITION      5' mRNA sequence.
ACCESSION      BM471442
VERSION      BM471442.1 GI:18520484
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1. (bases 1 to 1044)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12293 row: p column: 15
High quality sequence stop: 238.
Location/Qualifiers
1. 1044
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5563262"
/clone_lib="NIH MGC 72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT      251 a 326 c 266 g 196 t 5 others
ORIGIN
Query Match      3.8%; Score 27; DB 13; Length 1044;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 35 CCCTCCCGGCTGGAGACCCCGCC 61
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Db 225 CCCTCCCGGCTGGAGACCCCGCC 251
RESULT 15
BE014383
LOCUS      541 bp mRNA linear EST 09-JUL-2000
DEFINITION      125972 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION      BE014383
VERSION      BE014383.1 GI:8275324
KEYWORDS      EST.
SOURCE      pig.
ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE      1. (bases 1 to 541)
AUTHORS      Stone,R.T., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Fahrenkrug,S.C., Freking,W.M., Bennett,G.A., Laegreid,W.W.,
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 53 row: N column: 21
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 541
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      110 a 188 c 132 g 111 t
ORIGIN
Query Match      2.9%; Score 21; DB 10; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 37 CCTCCCGGCTGGAGACCCCGCC 57
Db 380 CCTCCCGGCTGGAGACCCCGCC 400
Search completed: June 17, 2003, 06:27:15
Job time : 863.75 secs
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